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OM protein - protein search, using sw model

Run on: September 15, 2003, 17:16:01 ; Search time 36.7714 Seconds  
(without alignments)  
112.231 Million cell updates/sec

Title: US-09-544-664-1

Perfect score: 138  
Sequence: 1 NLWAAQYGRLELRMSDFEGSKGL (26)

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_19Jun03.\*

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- 3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*
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- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	138	100.0	26	21	AAB37001		Bcl2 polypeptide B
2	138	100.0	26	21	AAB37002		Bcl2 polypeptide B
3	138	100.0	27	21	AAB37003		Bcl2 polypeptide B
4	138	100.0	27	21	AAB37056		Bcl2 polypeptide B
5	138	100.0	28	21	AAB37055		Bcl2 polypeptide B
6	138	100.0	162	22	AAR70370		Shorter murine BAD
7	138	100.0	204	17	AAR95168		bcl-x(L)/bcl-2 ass
8	138	100.0	204	19	AAW61315		Murine BCL-XL/BCL-
9	138	100.0	204	19	AAW61316		Mutant BCL-XL/BCL-

SEQ UPDATE 1-3,55-56

(38-29 - Not Reported)

10	138	100.0	138	19	AAW61317	Mutant BCL-XL/BCL-
11	138	100.0	138	19	AAW61318	Mutant BCL-XL/BCL-
12	138	100.0	138	19	AAW58832	Murine BAD protein
13	138	100.0	138	22	AAW70369	Longer murine BAD
14	138	100.0	138	24	ABR39082	Murine BAD protein
15	138	100.0	138	22	AAU00220	Bad-DTR apoptosis
16	114	82.6	114	24	AAU78627	Human Bad peptide
17	114	82.6	114	25	ABP56161	PPC-interacting r
18	114	82.6	114	25	ABG78484	Mutant Bcl2 compet
19	114	82.6	114	25	ABG78493	Mutant Bcl2 compet
20	114	82.6	114	25	AAU78610	Human Bad peptide
21	114	82.6	114	25	AAU78620	Human Bad peptide
22	114	82.6	166	18	AAW32476	BBC6 protein for r
23	114	82.6	168	19	AAW55779	Human Bcl-XL/Bcl-2
24	114	82.6	168	21	AAW13512	Human cell prolif
25	114	82.6	168	22	AAW70368	Human BAD mutant a
26	114	82.6	168	22	AAW48287	Human BAD protein.
27	114	82.6	168	22	AAW67688	Amino acid sequenc
28	114	82.6	168	24	ABR39081	Human BAD protein
29	114	82.6	201	23	ABP41830	Human ovarian anti
30	113	81.9	23	17	AAW95166	bcl-x(L)/bcl-2 ass
31	111	80.4	25	23	ABG78490	Mutant Bcl2 compet
32	111	80.4	25	23	AAU78617	Human Bad peptide
33	110	79.7	25	23	ABG78488	Mutant Bcl2 compet
34	110	79.7	25	23	ABG78489	Human Bad peptide
35	110	79.7	25	23	AAU78615	Human Bad peptide
36	110	79.7	25	23	AAU78616	Human Bad peptide
37	109	79.0	23	23	AAU78628	Human Bad peptide
38	109	79.0	25	23	ABG78486	Mutant Bcl2 compet
39	109	79.0	25	23	ABG78492	Mutant Bcl2 compet
40	109	79.0	25	23	ABG78497	Mutant Bcl2 compet
41	109	79.0	25	23	AAU78612	Human Bad peptide
42	109	79.0	25	23	AAU78619	Human Bad peptide
43	109	79.0	25	23	AAU78624	Human Bad peptide
44	108	78.3	25	23	ABG78485	Mutant Bcl2 compet
45	108	78.3	25	23	AAU78611	Human Bad peptide

ALIGNMENTS

RESULT 1

AAB37001  
ID AAB37001 standard; peptide; 26 AA.

XX AAB37001;

AC AAB37001;

XX 28-FEB-2001 (first entry)

XX Bcl2 polypeptide BH3 domain peptide #1.

DE Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;

XX Cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;

KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;

KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;

KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;

KW stroke; myocardial infarction.

XX Homo sapiens.

OS WO200059526-A1.

XX 12-OCT-2000.

XX 06-APR-2000; 2000WO-US09352.

XX 07-APR-1999; 93US-0128202.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Huang Z, Wang J, Zhang Z, Shan S, Lu Z;

XX WPI; 2000-679325/66.

XX PT New peptide conjugates for modulating apoptosis or for inhibiting B  
 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for  
 PT treating neurodegenerative disorders, stroke, or cancer  
 XX PS Claim 18; Page 17; 74pp; English.  
 XX CC The invention relates to a peptide conjugate having the formula:  
 CC (R-X)n-peptide where n = 1-10; X = C=O, when the R-X group is attached  
 CC to the N-terminus of the peptide, or a side chain of the peptide where  
 CC the functional group of the side chain is NH2 or OH; or X = O or NH,  
 CC when the R-X group is attached to the C-terminus of the peptide, or a  
 CC side chain of the peptide, where the side chain functional group is COOH  
 CC or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylene containing one  
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally  
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,  
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain  
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples  
 CC of the peptide portion of the conjugate. The peptides represent analogues  
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of  
 CC the BH3 domain of the cell death agonist Bad. The peptide conjugate is  
 CC useful for modulating apoptosis in the cells of a subject, or for  
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of  
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2  
 CC function. In particular, the peptide conjugate is useful for treating a  
 CC subject afflicted with a cancer characterized by cancer cells that  
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,  
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or  
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide  
 CC conjugate is also useful for treating disorders characterized by  
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired  
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.  
 XX SQ Sequence 26 AA;  
 Query Match 100.0%; Score 138; DB 21; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 2e-14;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 NLWAAQRYGRELRMSDFEGSPKGL 26  
 Db 1 NLWAAQRYGRELRMSDFEGSPKGL 26  
 RESULT 2  
 AAB37002  
 ID AAB37002 standard; peptide; 26 AA.  
 XX AC AAB37002;  
 XX DT 28-FEB-2001 (first entry)  
 XX DE Bcl2 polypeptide BH3 domain peptide #2.  
 XX KW Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;  
 KW cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;  
 KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;  
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;  
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;  
 KW stroke; myocardial infarction.  
 XX OS Homo sapiens.  
 XX PN WO200059526-A1.  
 XX PD 12-OCT-2000.  
 XX PF 06-APR-2000; 2000WO-US09352.  
 XX PR 07-APR-1999; 99US-0128202.  
 XX PA (UYJE-) UNIV JEFFERSON THOMAS.  
 XX

PI Huang Z, Wang J, Zhang Z, Shan S, Lu Z;  
 XX WPI; 2000-679325/66.  
 DR  
 XX  
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 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for  
 PT treating neurodegenerative disorders, stroke, or cancer  
 XX PS Claim 18; Page 17; 74pp; English.  
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 CC to the N-terminus of the peptide, or a side chain of the peptide where  
 CC the functional group of the side chain is NH2 or OH; or X = O or NH,  
 CC when the R-X group is attached to the C-terminus of the peptide, or a  
 CC side chain of the peptide, where the side chain functional group is COOH  
 CC or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylene containing one  
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally  
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,  
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain  
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples  
 CC of the peptide portion of the conjugate. The peptides represent analogues  
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 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide  
 CC conjugate is also useful for treating disorders characterized by  
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired  
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.  
 XX SQ Sequence 26 AA;  
 Query Match 100.0%; Score 138; DB 21; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 2e-14;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 NLWAAQRYGRELRMSDFEGSPKGL 26  
 Db 1 NLWAAQRYGRELRMSDFEGSPKGL 26  
 RESULT 3  
 AAB37003  
 ID AAB37003 standard; peptide; 27 AA.  
 XX AC AAB37003;  
 XX DT 28-FEB-2001 (first entry)  
 XX DE Bcl2 polypeptide BH3 domain peptide #3.  
 XX KW Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;  
 KW cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;  
 KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;  
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;  
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;  
 KW stroke; myocardial infarction.  
 XX OS Homo sapiens.  
 XX PN WO200059526-A1.  
 XX PD 12-OCT-2000.  
 XX PF 06-APR-2000; 2000WO-US09352.  
 XX PR 07-APR-1999; 99US-0128202.

XX PA (UYJE-) UNIV JEFFERSON THOMAS.

XX PI Huang Z, Wang J, Zhang Z, Shan S, Lu Z;

XX XX WPI; 2000-679325/66.

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CC the functional group of the side chain is NH<sub>2</sub> or OH; or X = O or NH,

CC when the R-X group is attached to the C-terminus of the peptide, or a

CC side chain of the peptide, where the side chain functional group is COOH

CC or CONH<sub>2</sub>; and R = 2-18C alkyl or alkoxy, 2-14C alkylene containing one

CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally

CC monosubstituted with a 1-5C straight or branched chain alkyl group,

CC phenyl optionally monosubstituted with a 1-5C straight or branched chain

CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples

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CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2

CC function. In particular, the peptide conjugate is useful for treating a

CC subject afflicted with a cancer characterized by cancer cells that

CC express Bcl-2. The cancer includes prostate, colorectal, gastric,

CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or

CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide

CC conjugate is also useful for treating disorders characterized by

CC increased apoptosis, e.g. neurodegenerative disorders, acquired

CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.

XX SQ Sequence 27 AA;

Query Match 100.0%; Score 138; DB 21; Length 27;

Best Local Similarity 100.0%; Pred. No. 2.1e-14;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFGSKGL 26

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DB 1 NLWAAQRYGRELRRMSDEFGSKGL 26

RESULT 4

AAB37056

XX ID AAB37056 standard; peptide; 27 AA.

XX AC AAB37056;

XX XX 28-FEB-2001 (first entry)

XX DE Bcl2 polypeptide BH3 domain peptide #56.

XX KW Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;

XX KW cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;

XX KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;

XX KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;

XX KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;

XX KW stroke; myocardial infarction.

XX OS Homo sapiens.

XX XX WO200059526-A1.

XX PN 12-OCT-2000.

XX PD

PF 06-APR-2000; 2000WO-US09352.

XX 07-APR-1999; 99US-0128202.

PR (UYJE-) UNIV JEFFERSON THOMAS.

XX PI Huang Z, Wang J, Zhang Z, Shan S, Lu Z;

XX XX WPI; 2000-679325/66.

XX PT New peptide conjugates for modulating apoptosis or for inhibiting B

XX PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for

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CC when the R-X group is attached to the C-terminus of the peptide, or a

CC side chain of the peptide, where the side chain functional group is COOH

CC or CONH<sub>2</sub>; and R = 2-18C alkyl or alkoxy, 2-14C alkylene containing one

CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally

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XX SQ Sequence 27 AA;

Query Match 100.0%; Score 138; DB 21; Length 27;

Best Local Similarity 100.0%; Pred. No. 2.1e-14;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFGSKGL 26

|||||

DB 2 NLWAAQRYGRELRRMSDEFGSKGL 27

RESULT 5

AAB37055

XX ID AAB37055 standard; peptide; 28 AA.

XX AC AAB37055;

XX XX 28-FEB-2001 (first entry)

XX DE Bcl2 polypeptide BH3 domain peptide #55.

XX KW Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;

XX KW cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;

XX KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;

XX KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;

XX KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;

XX KW stroke; myocardial infarction.

XX OS Homo sapiens.

XX XX WO200059526-A1.

XX PN

XX PD 12-OCT-2000.  
 XX PF 06-APR-2000; 2000WO-US09352.  
 XX PR 07-APR-1999; 99US-0128202.  
 XX PA (UYJE-) UNIV JEFFERSON THOMAS.  
 XX PI Huang Z, Wang J, Zhang Z, Shan S, Lu Z;  
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 XX PT New peptide conjugates for modulating apoptosis or for inhibiting B  
 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for  
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 CC to the N-terminus of the peptide, or a side chain of the peptide where  
 CC the functional group of the side chain is NH<sub>2</sub> or OH; or X = O or NH,  
 CC when the R-X group is attached to the C-terminus of the peptide, or a  
 CC side chain of the peptide, where the side chain functional group is COOH  
 CC or CONH<sub>2</sub>; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl containing one  
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally  
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,  
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain  
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 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of  
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2  
 CC function. In particular, the peptide conjugate is useful for treating a  
 CC subject afflicted with a cancer characterized by cancer cells that  
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,  
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or  
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide  
 CC conjugate is also useful for treating disorders characterized by  
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired  
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.  
 XX SQ Sequence 28 AA;

Query Match 100.0%; Score 138; DB 21; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-14;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFGSFKGL 26  
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 Db 2 NLWAAQRYGRELRRMSDEFGSFKGL 27

RESULT 6  
 AAB70370  
 ID AAB70370 standard; protein; 162 AA.  
 XX AC AAB70370;  
 XX DT 02-MAY-2001 (first entry)  
 XX DE Shorter murine BAD mutant amino acid sequence SEQ ID NO:3.  
 XX KW Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;  
 KW immunostimulant; neuroprotective; nontropic; antiischaemic; vulnary;  
 KW cyostatic; antiviral; antiarthritic; antiinflammatory; wound healing;  
 KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;  
 KW immunodeficiency disease; neurodegenerative disease; viral infection;  
 KW ischaemic cell death; reperfusion cell death; arthritis; infertility;  
 KW lymphoproliferative condition; inflammation; autoimmune disease.

XX OS Mus musculus.  
 OS Synthetic.  
 XX PN WO200110888-A1.  
 XX PD 15-FEB-2001.  
 XX PF 30-MAY-2000; 2000WO-US11864.  
 XX PR 28-MAY-1999; 99US-0136783.  
 XX PA (APOP-) APOPTOSIS TECHNOLOGY INC.  
 XX PI Zhou X;  
 XX WPI; 2001-138734/14.  
 XX PT New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,  
 PT useful for screening for candidate compounds which induce or inhibit  
 PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or  
 PT Ser113 -  
 XX PS Claim 7; Page 148-149; 157pp; English.  
 XX CC The present invention describes an isolated or synthetic polypeptide  
 CC (I) comprising a less than full length amino acid sequence of a mutant  
 CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its  
 CC fragment, which contains amino acid substitutions at Ser118 of a human  
 CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine  
 CC BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,  
 CC antitropic, antiischaemic, vulnary, cyostatic, antiviral,  
 CC antiarthritic, antiinflammatory and immunosuppressive activities, and  
 CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and  
 CC polynucleotides can be used for screening candidate compounds and drugs  
 CC for activity that promote cell survival or apoptosis. Other uses include  
 CC inducing or inhibiting apoptosis in a cell. Candidate compounds  
 CC identified and (mutant) BAD polypeptides are useful in treating  
 CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell  
 CC death, reperfusion cell death, wound healing, cancer, viral infections,  
 CC lymphoproliferative conditions, arthritis, infertility, inflammation and  
 CC autoimmune diseases. The present sequence represents a specifically  
 CC claimed shorter murine BAD mutant amino acid sequence from the present  
 CC invention.  
 XX SQ Sequence 162 AA;

Query Match 100.0%; Score 138; DB 22; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-13;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFGSFKGL 26  
 |||||  
 Db 98 NLWAAQRYGRELRRMSDEFGSFKGL 123

RESULT 7  
 AAR95168  
 ID AAR95168 standard; Protein; 204 AA.  
 XX AC AAR95168;  
 XX DT 06-JAN-1997 (first entry)  
 XX DE bcl-x(L)/bcl-2 associated death promoter protein.  
 XX KW Epitope; murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke;  
 KW polypeptide; bcl-x; cell death; regulate; BH1; BH2; apoptotic cell death;  
 KW cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS;  
 KW neurodegenerative disease; senescence; ischaemia; neoplasia.  
 XX OS Mus musculus.  
 XX SQ

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FH Key Location/Qualifiers
FT Region 147..149
FT /note= "BH1 conserved amino acids"
FT Region 191..192
FT /note= "BH2 conserved amino acids"
FT Domain 38..61
FT /note= "PEST sequence"
FT Domain 111..130
FT /note= "PEST sequence"
XX
XX WO9613614-A1.
XX
XX 09-MAY-1996.
XX
XX 31-OCT-1995; 95WO-US14246.
XX
XX 31-OCT-1994; 94US-0333565.
XX
XX (UNIW ) UNIV WASHINGTON.
XX
XX Korsmeyer SJ;
XX
XX WPI; 1996-251465/25.
XX N-PSDB; AAT29479.
XX
XX Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter -
XX useful to treat neoplasia and apoptosis and to identify agents
XX inhibiting its binding to bcl-2 or bcl-x(L) to form heteromultimers
XX
XX Claim 3; Fig 1; 130pp; English.
XX
XX This sequence represents the murine bcl-x(L)/bcl-2 associated death
XX promoter (Bad) gene. Bad is a 22.1 kD protein which interacts with
XX bcl-2 and bcl-x proteins and regulates cell death. It has homology
XX to the bcl-2-related family clustered in the BH1 and BH2 domain. Bad
XX has been found to hybridise to bcl-x(L) and bcl-2 in yeast two-hybrid
XX assays and in vivo in mammalian cells. Overexpressed Bad counters the
XX death inhibitory activity of bcl-x(L), but is much less effective at
XX countering the death inhibitory activity of bcl-2. Bad expression can
XX accelerate apoptotic cell death induced by cytokine deprivation in an
XX IL-3 dependent cell line expressing bcl-x(L), and its also counters the
XX death repressor activity of bcl-x(L). Bad competes with Bax for binding
XX to bcl-x(L). Bad may be used to identify agents which inhibit its
XX binding to bcl-2 or bcl-x(L) to form heterodimers. Such agents may be
XX used to treat neurodegenerative diseases, immunodeficiency diseases,
XX e.g. AIDS, senescence or ischaemia.
XX
XX Sequence 204 AA;
XX
XX Query Match 100.0%; Score 138; DB 17; Length 204;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-13;
XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 NLWAAQRYGRELRRMSDEFGSFKGL 26
XX |||||
XX DB 140 NLWAAQRYGRELRRMSDEFGSFKGL 165
XX
XX RESULT 8
XX AAW61315
XX ID AAW61315 standard; Protein; 204 AA.
XX
XX AC AAW61315;
XX
XX DT 07-OCT-1998 (first entry)
XX
XX DE Murine BCL-XL/BCL-2 associated cell death regulator.
XX
XX KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
XX serine substituted mutant; apoptosis; cancer; viral infection.
XX
XX OS Mus sp.
XX
XX PN WO9817682-A1.

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PN WO9817682-A1.
XX
XX 30-APR-1998.
XX
XX 17-OCT-1997; 97WO-US19175.
XX
XX 18-OCT-1996; 96US-0733505.
XX
XX (UNIW ) UNIV WASHINGTON.
XX
XX Korsmeyer SJ;
XX
XX WPI; 1998-261422/23.
XX N-PSDB; AAV27833.
XX
XX New mutant BAD polypeptide with phosphorylatable serine replaced -
XX useful for, e.g. treating reduced apoptosis such as in cancer or
XX viral infection
XX
XX Claim 1; Fig 10; 95pp; English.
XX
XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
XX death regulator) proteins, having an amino acid other than Ser at
XX position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
XX present sequence is the murine BAD protein. Also described are: (1)
XX fragments of mutant BAD protein able to decrease cell viability; (2)
XX fusion proteins of mutant BAD with a heterologous polypeptide that
XX increases intracellular delivery. Mutant BAD proteins are used to treat
XX or prevent diseases associated with reduced apoptosis, e.g. cancer,
XX viral infection, lymphoproliferation, arthritis, infertility,
XX inflammation and autoimmune disease. Polynucleotide sequences encoding
XX mutant BAD proteins can be used similarly by gene therapy or to produce
XX transgenic animals for use as disease models or in drug screening. BAD
XX proteins phosphorylated at specified Ser are used to screen for enhancers
XX and inhibitors of serine-phosphatase. Inhibitors are potentially useful
XX in treatment of excessive apoptosis such as AIDS, neurodegeneration,
XX aging or ischaemic cell death. The apoptotic status of cells is
XX determined by measuring relative amounts of phosphorylated and non-
XX phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
XX greater death-promoting activity than wild-type BAD which can become
XX phosphorylated on the specified Ser, forming a product that does not
XX heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
XX proteins in the cytosol, thus promoting cell survival. The mutants with
XX Ser substituted cannot bind 14-3-3.
XX
XX Sequence 204 AA;
XX
XX Query Match 100.0%; Score 138; DB 19; Length 204;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-13;
XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 NLWAAQRYGRELRRMSDEFGSFKGL 26
XX |||||
XX DB 140 NLWAAQRYGRELRRMSDEFGSFKGL 165
XX
XX RESULT 9
XX AAW61316
XX ID AAW61316 standard; Protein; 204 AA.
XX
XX AC AAW61316;
XX
XX DT 07-OCT-1998 (first entry)
XX
XX DE Mutant BCL-XL/BCL-2 associated cell death regulator #1.
XX
XX KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
XX serine substituted mutant; apoptosis; cancer; viral infection.
XX
XX OS Mus sp.
XX
XX OS Synthetic.
XX
XX PN WO9817682-A1.

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XX PD 30-APR-1998.
XX PF 17-OCT-1997; 97WO-US19175.
XX PR 18-OCT-1996; 96US-0733505.
XX PA (UNIW ) UNIV WASHINGTON.
XX PI Korsmeyer SJ;
XX PI
XX DR WPI; 1998-261422/23.
XX DR N-PSDB; AAV27834.
XX PT New mutant BAD polypeptide with phosphorylatable serine replaced -
XX PT useful for, e.g. treating reduced apoptosis such as in cancer or
XX PT viral infection
XX PS
XX PS Claim 7; Page 59; 95pp; English.
XX CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
XX CC death regulator) proteins, having an amino acid other than Ser at
XX CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
XX CC present sequence represents a mutant BAD protein. Also described are: (1)
XX CC fragments of mutant BAD protein able to decrease cell viability; (2)
XX CC fusion proteins of mutant BAD with a heterologous polypeptide that
XX CC increases intracellular delivery. Mutant BAD proteins are used to treat
XX CC or prevent diseases associated with reduced apoptosis, e.g. cancer,
XX CC viral infection, lymphoproliferation, arthritis, infertility,
XX CC inflammation and autoimmune disease. Polynucleotide sequences encoding
XX CC mutant BAD proteins can be used similarly by gene therapy or to produce
XX CC transgenic animals for use as disease models or in drug screening. BAD
XX CC proteins phosphorylated at specified Ser are used to screen for enhancers
XX CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
XX CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
XX CC aging or ischaemic cell death. The apoptotic status of cells is
XX CC determined by measuring relative amounts of phosphorylated and non-
XX CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
XX CC greater death-promoting activity than wild-type BAD which can become
XX CC phosphorylated on the specified Ser, forming a product that does not
XX CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
XX CC proteins in the cytosol, thus promoting cell survival. The mutants with
XX CC Ser substituted cannot bind 14-3-3.
XX SQ Sequence 204 AA;
Query Match 100.0%; Score 138; DB 19; Length 204;
Best Local Similarity 100.0%; Pred. No. 1.9e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NLWAAQRYGRELRRMSDEFGSFKGL 26
Db 140 NLWAAQRYGRELRRMSDEFGSFKGL 165
RESULT 10
AAW61317
ID AAW61317 standard; Protein; 204 AA.
XX AC AAW61317;
XX DT 07-OCT-1998 (first entry)
XX DE Mutant BCL-XL/BCL-2 associated cell death regulator #2.
XX KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
XX KW serine substituted mutant; apoptosis; cancer; viral infection.
XX OS Mus sp.
XX OS Synthetic.
XX PN W09817682-A1.
XX PD 30-APR-1998.

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PD 30-APR-1998.
XX PF 17-OCT-1997; 97WO-US19175.
XX PR 18-OCT-1996; 96US-0733505.
XX PA (UNIW ) UNIV WASHINGTON.
XX PI Korsmeyer SJ;
XX PI
XX DR WPI; 1998-261422/23.
XX DR N-PSDB; AAV27835.
XX PT New mutant BAD polypeptide with phosphorylatable serine replaced -
XX PT useful for, e.g. treating reduced apoptosis such as in cancer or
XX PT viral infection
XX PS
XX PS Claim 7; Page 60; 95pp; English.
XX CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
XX CC death regulator) proteins, having an amino acid other than Ser at
XX CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
XX CC present sequence represents a mutant BAD protein. Also described are: (1)
XX CC fragments of mutant BAD protein able to decrease cell viability; (2)
XX CC fusion proteins of mutant BAD with a heterologous polypeptide that
XX CC increases intracellular delivery. Mutant BAD proteins are used to treat
XX CC or prevent diseases associated with reduced apoptosis, e.g. cancer,
XX CC viral infection, lymphoproliferation, arthritis, infertility,
XX CC inflammation and autoimmune disease. Polynucleotide sequences encoding
XX CC mutant BAD proteins can be used similarly by gene therapy or to produce
XX CC transgenic animals for use as disease models or in drug screening. BAD
XX CC proteins phosphorylated at specified Ser are used to screen for enhancers
XX CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
XX CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
XX CC aging or ischaemic cell death. The apoptotic status of cells is
XX CC determined by measuring relative amounts of phosphorylated and non-
XX CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
XX CC greater death-promoting activity than wild-type BAD which can become
XX CC phosphorylated on the specified Ser, forming a product that does not
XX CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
XX CC proteins in the cytosol, thus promoting cell survival. The mutants with
XX CC Ser substituted cannot bind 14-3-3.
XX SQ Sequence 204 AA;
Query Match 100.0%; Score 138; DB 19; Length 204;
Best Local Similarity 100.0%; Pred. No. 1.9e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NLWAAQRYGRELRRMSDEFGSFKGL 26
Db 140 NLWAAQRYGRELRRMSDEFGSFKGL 165
RESULT 11
AAW61318
ID AAW61318 standard; Protein; 204 AA.
XX AC AAW61318;
XX DT 07-OCT-1998 (first entry)
XX DE Mutant BCL-XL/BCL-2 associated cell death regulator #3.
XX KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
XX KW serine substituted mutant; apoptosis; cancer; viral infection.
XX OS Mus sp.
XX OS Synthetic.
XX PN W09817682-A1.
XX PD 30-APR-1998.

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XX PF 17-OCT-1997; 97WO-US19175.
XX PF
XX PR 18-OCT-1996; 96US-0733505.
XX PR
XX PA (UNIW ) UNIV WASHINGTON.
XX PA
XX PI Kormsmeier SJ;
XX PI
XX DR WPI; 1998-261422/23.
XX DR N-PSDB; AAV27836.
XX
XX PT New mutant BAD polypeptide with phosphorylatable serine replaced -
XX PT useful for, e.g. treating reduced apoptosis such as in cancer or
XX PT viral infection
XX PT
XX PS Claim 7; Page 60-61; 95pp; English.
XX
XX CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
XX CC death regulator) proteins, having an amino acid other than Ser at
XX CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
XX CC present sequence represents a mutant BAD protein. Also described are: (1)
XX CC fragments of mutant BAD protein able to decrease cell viability; (2)
XX CC fusion proteins of mutant BAD with a heterologous polypeptide that
XX CC increases intracellular delivery. Mutant BAD proteins are used to treat
XX CC or prevent diseases associated with reduced apoptosis, e.g. cancer,
XX CC viral infection, lymphoproliferation, arthritis, infertility,
XX CC inflammation and autoimmune disease. Polynucleotide sequences encoding
XX CC mutant BAD proteins can be used similarly by gene therapy or to produce
XX CC transgenic animals for use as disease models or in drug screening. BAD
XX CC proteins phosphorylated at specified Ser are used to screen for enhancers
XX CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
XX CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
XX CC aging or ischaemic cell death. The apoptotic status of cells is
XX CC determined by measuring relative amounts of phosphorylated and non-
XX CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
XX CC greater death-promoting activity than wild-type BAD which can become
XX CC phosphorylated on the specified Ser, forming a product that does not
XX CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
XX CC proteins in the cytosol, thus promoting cell survival. The mutants with
XX CC Ser substituted cannot bind 14-3-3.
XX
XX SQ Sequence 204 AA;

Query Match 100.0%; Score 138; DB 19; Length 204;
Best Local Similarity 100.0%; Pred. No. 1.9e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDFEGSFKGL 26
   |||||
Db 140 NLWAAQRYGRELRRMSDFEGSFKGL 165

RESULT 12
AAW58832
ID AAW58832 standard; protein; 204 AA.
XX
XX AC AAW58832;
XX
XX DT 23-JUL-1998 (first entry)
XX
XX DE Murine BAD protein.
XX
XX KW BAD protein; Bcl-XL/Bcl-2 associated cell death regulator; 14-3-3;
XX KW serine phosphorylation; post-translational modification; apoptosis;
XX KW signal transduction regulator; phosphoserine phosphatase; senescence;
XX KW immunodeficiency disease; neurodegenerative disease; infertility;
XX KW cancer; viral infection; lymphoproliferative condition; arthritis;
XX KW inflammation; autoimmune diseases.
XX
XX OS Mus sp.
XX PF
XX PN WO9809643-A1.

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XX 12-MAR-1998.
XX
XX PF 09-SEP-1997; 97WO-US15871.
XX PF
XX PR 09-SEP-1996; 96US-0707868.
XX PR
XX PA (UNIW ) UNIV WASHINGTON.
XX PA
XX PI Kormsmeier SJ;
XX PI
XX DR WPI; 1998-207049/18.
XX DR
XX PT Serine-phosphorylated Bcl-XL/Bcl-2 Associated cell Death regulator
XX PT polypeptide - useful for modulation of apoptosis associated with,
XX PT e.g. cancer and immunodeficiency diseases
XX PT
XX PS Claim 3; Fig 8; 61pp; English.
XX
XX CC This sequence represents a novel serine-phosphorylated protein, BAD
XX CC (Bcl-XL/Bcl-2 associated cell death regulator). The serine residue is
XX CC phosphorylated in a post-translational modification and allows binding
XX CC to the 14-3-3 protein which is a signal transduction regulator.
XX CC Modulators of phosphorylated BAD, which act through inhibition/activation
XX CC of a phosphoserine phosphatase, are useful for preventing/treating
XX CC increased/decreased apoptosis in a cell. The increased apoptosis may
XX CC result from immunodeficiency diseases, senescence, neurodegenerative
XX CC disease, ischaemic cell death, reperfusion cell death, infertility and
XX CC wound-healing. Decreased apoptosis may result from cancer, viral
XX CC infection, lymphoproliferative conditions, arthritis, infertility,
XX CC inflammation and autoimmune diseases. Measuring the amount of
XX CC phosphorylated compared to unphosphorylated BAD polypeptide and/or total
XX CC BAD in a cell is useful for determining the apoptotic state of a cell.
XX
XX SQ Sequence 204 AA;

Query Match 100.0%; Score 138; DB 19; Length 204;
Best Local Similarity 100.0%; Pred. No. 1.9e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDFEGSFKGL 26
   |||||
Db 140 NLWAAQRYGRELRRMSDFEGSFKGL 165

RESULT 13
AAB70369
ID AAB70369 standard; protein; 204 AA.
XX
XX AC AAB70369;
XX
XX DT 02-MAY-2001 (first entry)
XX
XX DE Longer murine BAD mutant amino acid sequence SEQ ID NO:2.
XX
XX KW Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
XX KW immunostimulant; neuroprotective; nootropic; antiischaemic; vulnery;
XX KW cyostatic; antiviral; antiarthritic; antiinflammatory; wound healing;
XX KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;
XX KW immunodeficiency disease; neurodegenerative disease; viral infection;
XX KW ischaemic cell death; reperfusion cell death; arthritis; infertility;
XX KW lymphoproliferative condition; inflammation; autoimmune disease.
XX
XX OS Mus musculus.
XX OS Synthetic.
XX
XX PN WO200110888-A1.
XX
XX PD 15-FEB-2001.
XX
XX PF 30-MAY-2000; 2000WO-US11864.
XX
XX PR 28-MAY-1999; 99US-0136783.

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XX PA (APOP-) APOPTOSIS TECHNOLOGY INC.  
XX XX Zhou X;  
XX XX WPI; 2001-138734/14.  
XX XX New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,  
XX PT useful for screening for candidate compounds which induce or inhibit  
XX PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or  
XX PT Ser113 -  
XX XX  
XX PS Claim 4; Page 148; 157pp; English.  
XX XX The present invention describes an isolated or synthetic polypeptide  
XX CC (I) comprising a less than full length amino acid sequence of a mutant  
XX CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its  
XX CC fragment, which contains amino acid substitutions at Ser118 of a human  
XX CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine  
XX CC BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,  
XX CC nootropic, antiischaemic, vulnerary, cytostatic, antiviral,  
XX CC antiarthritic, antiinflammatory and immunosuppressive activities, and  
XX CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and  
XX CC polynucleotides can be used for screening candidate compounds and drugs  
XX CC for activity that promote cell survival or apoptosis. Other uses include  
XX CC inducing or inhibiting apoptosis in a cell. Candidate compounds  
XX CC identified and (mutant) BAD polypeptides are useful in treating  
XX CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell  
XX CC death, reperfusion cell death, wound healing, cancer, viral infections,  
XX CC lymphoproliferative conditions, arthritis, infertility, inflammation and  
XX CC autoimmune diseases. The present sequence represents a specifically  
XX CC claimed longer murine BAD mutant amino acid sequence from the present  
XX CC invention.  
XX XX  
XX SQ Sequence 204 AA;  
Query Match 100.0%; Score 138; DB 22; Length 204;  
Best Local Similarity 100.0%; Pred. No. 1.9e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NLWAAQRYGRELRRMSDEFGSFKGL 26  
|||||  
DB 140 NLWAAQRYGRELRRMSDEFGSFKGL 165  
RESULT 14  
ID ABR39082 standard; Protein; 204 AA.  
XX AC ABR39082;  
XX XX 10-MAY-2003 (first entry)  
XX DE Murine BAD protein SEQ ID NO:4.  
XX XX Murine; BAD; herpes simplex virus; HSV; US3; herpes virus; apoptosis;  
KW virucide; infection.  
XX OS Mus musculus.  
XX XX WO2003012049-A2.  
XX PN 13-FEB-2003.  
XX PD 31-JUL-2002; 2002WO-US24177.  
XX PF 31-JUL-2001; 2001US-308929P.  
XX PR (UYCH-) UNIV CHICAGO.  
XX PA Munger J, Roizman B;  
XX PI WPI; 2003-248168/24.  
XX DR WPI; 2003-248168/24.

DR N-PSDB; AB281201.  
XX Inducing apoptosis in a cell infected with herpes simplex virus, HSV,  
PT by administering to the cell, a composition comprising an agent that  
PT inhibits phosphorylation of pro-apoptotic polypeptide BAD by HSV US3 -  
XX Claim 15; Page 168; 192pp; English.  
XX The present invention describes a method (M1) for inducing apoptosis in  
XX CC a cell infected with herpes simplex virus (HSV), which comprises  
XX CC administering to the cell, a composition having an agent that inhibits  
XX CC phosphorylation of pro-apoptotic polypeptide BAD by HSV US3. Also  
XX CC described is a method (M2) for treating a patient infected with HSV, by  
XX CC administering to the patient, a composition comprising a peptide  
XX CC comprising a sequence of 4-100 continuous amino acids of a 168 residue  
XX CC amino acid sequence (see ABR39081), where the peptide comprises Ser112,  
XX CC Ser135, or Ser155, or their combinations. BAD has virucide activity.  
XX CC M1 is useful for inducing apoptosis in a cell infected with HSV, where  
XX CC the cell is in a human. M2 is useful for treating a patient infected  
XX CC with HSV. The present sequence represents murine BAD, which is used in  
XX CC the exemplification of the present invention.  
XX SQ Sequence 204 AA;  
Query Match 100.0%; Score 138; DB 24; Length 204;  
Best Local Similarity 100.0%; Pred. No. 1.9e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NLWAAQRYGRELRRMSDEFGSFKGL 26  
|||||  
DB 140 NLWAAQRYGRELRRMSDEFGSFKGL 165  
RESULT 15  
AAU00220  
ID AAU00220 standard; Protein; 567 AA.  
XX AC AAU00220;  
XX XX 31-MAY-2001 (first entry)  
XX DE Bad-DTTR apoptosis-modifying fusion protein.  
XX XX Mouse; Bad-DTTR; apoptosis; cancer; spinal muscular atrophy;  
KW diphtheria toxin receptor binding domain; DTR; neoplasm; tumour;  
KW hyper-proliferation; Alzheimer's disease; neurodegenerative disorder;  
KW transient ischaemic neuronal injury; stroke; spinal cord injury;  
KW Huntington's disease.  
XX XX Chimeric - Mus sp.  
OS Chimeric - Corynebacterium diphtheriae.  
OS Chimeric - Synthetic.  
FH Key Location/Qualifiers  
FT Region 3..12 /note= "10x histidine tag"  
XX WO200112661-A2.  
XX PN 22-FEB-2001.  
XX PD 15-AUG-2000; 2000WO-US22293.  
XX PF 16-AUG-1999; 99US-0149220.  
XX PR (HARD ) HARVARD COLLEGE.  
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX XX Youle RJ, Liu X, Collier RJ;  
XX WPI; 2001-218343/22.  
XX DR N-PSDB; AAS00248.  
XX DR

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Job time : 37.7714 secs

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OM protein - protein search, using sw model

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81.144 Million cell updates/sec

Title: US-09-544-664-1

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Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	138	100.0	204	2	US-08-661-479-2
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4	138	100.0	204	2	US-08-733-505A-12
5	138	100.0	204	2	US-08-733-505A-13
6	138	100.0	204	2	US-08-733-505A-14
7	135	97.8	204	2	US-08-717-123-3
8	135	97.8	204	4	US-09-375-257-3
9	114	82.6	166	1	US-08-665-617-2
10	114	82.6	168	2	US-08-717-123-2
11	114	82.6	168	3	US-08-985-335-1
12	114	82.6	168	3	US-08-985-335-7
13	114	82.6	168	3	US-09-410-372-1
14	114	82.6	168	3	US-09-410-372-7
15	114	82.6	168	4	US-09-375-257-2
16	113	81.9	23	1	US-08-333-565-10
17	113	81.9	23	2	US-08-661-479-10
18	102	73.9	59	2	US-08-733-505A-55
19	102	73.9	59	2	US-08-733-505A-56
20	102	73.9	59	2	US-08-733-505A-57
21	102	73.9	59	2	US-08-733-505A-58
22	86	62.3	16	1	US-08-333-565-26
23	86	62.3	16	2	US-08-661-479-26
24	61	44.2	11	2	US-08-733-505A-34
25	61	44.2	11	2	US-08-706-741B-69
26	61	44.2	11	2	US-08-924-695A-69
27	51	37.0	66	2	US-08-867-087B-40

US-08-333-565-2 4 US-09-328-352-456 Sequence 4656, Ap  
Sequence 2, Application US/083333565 Sequence 19594, A  
Patent No. 5622852 3 US-09-074-579-3 Sequence 3, Appli  
31 46 33.3 946 3 US-09-388-774-3 Sequence 3, Appli  
32 46 33.3 946 4 US-09-546-153-1 Sequence 1, Appli  
33 45 33.0 906 4 US-09-252-991A-31458 Sequence 31458, A  
34 45 32.6 229 4 US-09-252-991A-23807 Sequence 23807, A  
35 45 32.6 303 4 US-09-328-352-5164 Sequence 5164, Ap  
36 45 32.6 356 4 US-09-235-103-2 Sequence 2, Appli  
37 45 32.6 356 4 US-09-235-103-4 Sequence 4, Appli  
38 45 32.6 1064 4 US-09-252-991A-17508 Sequence 17508, A  
39 44 32.2 903 4 US-09-252-991A-28775 Sequence 28775, A  
40 44 31.9 125 4 US-09-328-352-7449 Sequence 7449, Ap  
41 44 31.9 263 4 US-09-651-656-27 Sequence 27, Appl  
42 44 31.9 263 4 US-09-650-855-27 Sequence 27, Appl  
43 44 31.9 877 4 US-09-206-551-20 Sequence 20, Appl  
44 44 31.9 1125 4 US-09-252-991A-18729 Sequence 18729, A  
45 43.5 31.5 467 4 US-09-252-991A-18296 Sequence 18296, A

## ALIGNMENTS

RESULT 1  
US-08-333-565-2  
Sequence 2, Application US/083333565  
Patent No. 5622852  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, Stanley J.  
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH  
TITLE OF INVENTION: REGULATOR  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Khourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/333,565  
FILING DATE: 31-OCT-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15726A-000700  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 204 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..204  
OTHER INFORMATION: /note= "Deduced amino acid sequence  
OTHER INFORMATION: of mouse BAD."

US-08-333-565-2  
Query Match 100.0%; Score 138; DB 1; Length 204;  
Best Local Similarity 100.0%; Pred. No. 5.8e-14;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFEGSFKGL 26  
Db 140 NLWAAQRYGRELRRMSDEFEGSFKGL 165

## RESULT 2

US-08-661-479-2  
; Sequence 2, Application US/08661479  
; Patent No. 5834209  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, Stanley J.  
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH  
; TITLE OF INVENTION: REGULATOR  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/661,479  
; FILING DATE: 11-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/333,565  
; FILING DATE: 31-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 15726A-000700  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 204 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..204  
; OTHER INFORMATION: /note= "Deduced amino acid sequence  
; OTHER INFORMATION: of mouse BAd."  
US-08-661-479-2

Query Match 100.0%; Score 138; DB 2; Length 204;  
Best Local Similarity 100.0%; Pred. No. 5.8e-14;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFEGSFKGL 26  
Db 140 NLWAAQRYGRELRRMSDEFEGSFKGL 165

## RESULT 3

US-08-733-505A-1  
; Sequence 1, Application US/08733505A  
; Patent No. 5856445  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, STANLEY J.  
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF  
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HOWELL & HAERKAMP, L.C.  
; STREET: 7733 FORSYTH BLVD., SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: USA  
; ZIP: 63105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/733,505A  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 965458  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 727-5188  
; TELEFAX: (314) 727-6092  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 204 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-733-505A-1

Query Match 100.0%; Score 138; DB 2; Length 204;  
Best Local Similarity 100.0%; Pred. No. 5.8e-14;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFEGSFKGL 26  
Db 140 NLWAAQRYGRELRRMSDEFEGSFKGL 165

## RESULT 4

US-08-733-505A-12  
; Sequence 12, Application US/08733505A  
; Patent No. 5856445  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, STANLEY J.  
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF  
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAERKAMP, L.C.  
; STREET: 7733 FORSYTH BLVD., SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: USA  
; ZIP: 63105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/733,505A  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 965458  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 727-5188  
; TELEFAX: (314) 727-6092  
; INFORMATION FOR SEQ ID NO: 12:

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-733-505A-12

Query Match 100.0%; Score 138; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 5.8e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDFEGSFKGL 26
Db 140 NLWAAQRYGRELRRMSDFEGSFKGL 165

RESULT 5
US-08-733-505A-13
; Sequence 13, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08733,505A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-733-505A-13

Query Match 100.0%; Score 138; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 5.8e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDFEGSFKGL 26
Db 140 NLWAAQRYGRELRRMSDFEGSFKGL 165

RESULT 6
US-08-733-505A-14
; Sequence 14, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.

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; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08733,505A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-733-505A-14

Query Match 100.0%; Score 138; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 5.8e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDFEGSFKGL 26
Db 140 NLWAAQRYGRELRRMSDFEGSFKGL 165

RESULT 7
US-08-717-123-3
; Sequence 3, Application US/08717123
; Patent No. 5965703
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
; TITLE OF INVENTION: Acids and Methods of Use
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08717,123
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815

```

```
; REFERENCE/DOCKET NUMBER: P-ID 1929
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-717-123-3
Query Match 97.8%; Score 135; DB 2; Length 204;
Best Local Similarity 96.2%; Pred. No. 1.7e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFEGSKGL 26
Db 140 NLWAAQRYGRELRRMTDEFEGSKGL 165

RESULT 8
US-09-375-257-3
; Sequence 3, Application US/09375257
; Patent No. 6504022
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
; TITLE OF INVENTION: ACIDS AND METHODS OF USE
; FILE REFERENCE: 480140.428D1
; CURRENT APPLICATION NUMBER: US/09/375,257
; CURRENT FILING DATE: 1999-08-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-375-257-3

Query Match 97.8%; Score 135; DB 4; Length 204;
Best Local Similarity 96.2%; Pred. No. 1.7e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFEGSKGL 26
Db 140 NLWAAQRYGRELRRMTDEFEGSKGL 165

RESULT 9
US-08-665-617-2
; Sequence 2, Application US/08665617
; Patent No. 5663316
; GENERAL INFORMATION:
; APPLICANT: Xudong, Yin
; TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,617
; FILING DATE:
; CLASSIFICATION: 530
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; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: CL-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-665-617-2
Query Match 82.6%; Score 114; DB 1; Length 166;
Best Local Similarity 91.7%; Pred. No. 2.5e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFEGSKF 24
Db 101 NLWAAQRYGRELRRMSDEFVDSFK 124

RESULT 10
US-08-717-123-2
; Sequence 2, Application US/08717123
; Patent No. 5965703
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, Encoding Nucleic
; TITLE OF INVENTION: Acids and Methods of Use
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/717,123
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 1929
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-717-123-2
Query Match 82.6%; Score 114; DB 2; Length 168;
Best Local Similarity 91.7%; Pred. No. 2.6e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFEGSKF 24
Db 103 NLWAAQRYGRELRRMSDEFVDSFK 126
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```

RESULT 11
US-08-985-335-1
; Sequence 1, Application US/08985335
; Patent No. 6080847
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,335
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0421 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SYNORAB01
; CLONE: 358673
US-08-985-335-1

Query Match 82.6%; Score 114; DB 3; Length 168;
Best Local Similarity 91.7%; Pred. No. 2.6e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFGSK 24
| | | | | | | | | | | | | | | | | | | |
Db 103 NLWAAQRYGRELRRMSDEFGSK 126

RESULT 12
US-08-985-335-7
; Sequence 7, Application US/08985335
; Patent No. 6080847
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION
; NUMBER OF SEQUENCES: 9

```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,335
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0421 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1683637
US-08-985-335-7

Query Match 82.6%; Score 114; DB 3; Length 168;
Best Local Similarity 91.7%; Pred. No. 2.6e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFGSK 24
| | | | | | | | | | | | | | | | | | | |
Db 103 NLWAAQRYGRELRRMSDEFGSK 126

RESULT 13
US-09-410-372-1
; Sequence 1, Application US/09410372
; Patent No. 6281334
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/410,372
; FILING DATE:

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;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/985,335  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Billings, Lucy J.  
;; REGISTRATION NUMBER: 36,749  
;; REFERENCE/DOCKET NUMBER: PF-0421 US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 650-855-0555  
;; TELEFAX: 650-845-4166  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 168 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; IMMEDIATE SOURCE:  
;; LIBRARY: SYNORAB01  
;; CLONE: 358673  
US-09-410-372-1

Query Match 82.6%; Score 114; DB 3; Length 168;  
Best Local Similarity 91.7%; Pred. No. 2.6e-10;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFGSFK 24  
|||||  
DB 103 NLWAAQRYGRELRRMSDEFGSFK 126

RESULT 14  
US-09-410-372-7  
; Sequence 7, Application US/09410372  
; Patent No. 6281334  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Yue, Henry  
; APPLICANT: Lal, Preeti  
; APPLICANT: Shah, Purvi  
; APPLICANT: Corley, Neil C.  
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL  
; TITLE OF INVENTION: PROLIFERATION  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Dr.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/410,372  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/985,335  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0421 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 168 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single

;; TOPOLOGY: linear  
;; IMMEDIATE SOURCE:  
;; LIBRARY: GenBank  
;; CLONE: 1683637  
US-09-410-372-7

Query Match 82.6%; Score 114; DB 3; Length 168;  
Best Local Similarity 91.7%; Pred. No. 2.6e-10;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFGSFK 24  
|||||  
DB 103 NLWAAQRYGRELRRMSDEFGSFK 126

RESULT 15  
US-09-375-257-2  
; Sequence 2, Application US/09375257  
; Patent No. 6504022  
; GENERAL INFORMATION:  
; APPLICANT: Horne, William A.  
; APPLICANT: Oltersdorf, Tilman  
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC  
; TITLE OF INVENTION: ACIDS AND METHODS OF USE  
; FILE REFERENCE: 480140.428D1  
; CURRENT APPLICATION NUMBER: US/09/375,257  
; CURRENT FILING DATE: 1999-08-16  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 168  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-375-257-2

Query Match 82.6%; Score 114; DB 4; Length 168;  
Best Local Similarity 91.7%; Pred. No. 2.6e-10;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFGSFK 24  
|||||  
DB 103 NLWAAQRYGRELRRMSDEFGSFK 126

Search completed: September 15, 2003, 17:45:05  
Job time : 14.5571 secs

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: September 15, 2003, 17:25:56 ; Search time 20.6143 Seconds  
(without alignments)  
184.034 Million cell updates/sec

Title: US-09-544-664-1

Perfect score: 138

Sequence: 1 NLWAAQRYGRELRRMSDEFEGSKGL 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 541936 seqs, 145912426 residues

Total number of hits satisfying chosen parameters: 541936

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	135	97.8	204	9	US-09-922-378-3
2	135	97.8	204	14	US-10-066-179-3
3	114	82.6	25	15	US-10-059-261-258
4	114	82.6	168	9	US-09-922-378-2
5	114	82.6	168	9	US-09-894-657-1
6	114	82.6	168	9	US-09-894-657-7
7	114	82.6	168	14	US-10-066-179-2
8	71	51.4	15	15	US-10-174-105A-147
9	50	36.2	215	15	US-10-156-761-9145
10	47	34.1	35	15	US-10-092-750-1
11	47	34.1	138	15	US-10-092-750-241
12	46	33.3	682	12	US-10-238-075-1077
13	46	33.3	946	9	US-09-828-423-3
14	44	31.9	272	15	US-10-156-761-11541
15	44	31.9	436	9	US-09-815-242-5704

16	44	31.9	699	14	US-10-008-355-8	Sequence 8, Appli
17	44	31.9	705	9	US-09-815-242-12463	Sequence 12463, A
18	44	31.9	712	14	US-10-008-355-2	Sequence 2, Appli
19	44	31.9	877	12	US-10-369-294-20	Sequence 20, Appli
20	43	31.2	213	9	US-09-843-846-18	Sequence 18, Appli
21	43	31.2	232	10	US-09-881-752A-238	Sequence 238, App
22	43	31.2	270	11	US-09-934-455-162	Sequence 162, App
23	43	31.2	380	9	US-09-149-045-2	Sequence 2, Appli
24	43	31.2	380	15	US-10-166-359-2	Sequence 2, Appli
25	43	31.2	380	15	US-10-166-113-2	Sequence 2, Appli
26	43	31.2	380	15	US-10-166-372-2	Sequence 2, Appli
27	43	31.2	380	15	US-10-166-372-2	Sequence 2, Appli
28	43	31.2	380	15	US-10-184-725-3	Sequence 3, Appli
29	43	31.2	380	15	US-10-251-385-62	Sequence 62, Appli
30	43	31.2	380	15	US-10-251-385-198	Sequence 198, App
31	43	31.2	380	15	US-10-225-567A-233	Sequence 233, App
32	43	31.2	543	15	US-10-156-761-13485	Sequence 13485, A
33	43	31.2	571	9	US-09-815-242-11813	Sequence 11813, A
34	43	31.2	582	10	US-09-331-631A-22	Sequence 22, Appli
35	43	31.2	640	9	US-09-989-722-501	Sequence 501, App
36	43	31.2	640	9	US-09-989-723-501	Sequence 501, App
37	43	31.2	640	9	US-09-989-279-501	Sequence 501, App
38	43	31.2	640	9	US-09-989-727-501	Sequence 501, App
39	43	31.2	640	10	US-09-989-731-501	Sequence 501, App
40	43	31.2	640	10	US-09-989-732-501	Sequence 501, App
41	43	31.2	640	10	US-09-991-073-501	Sequence 501, App
42	43	31.2	640	10	US-09-909-320-292	Sequence 292, App
43	43	31.2	640	10	US-09-990-442-501	Sequence 501, App
44	43	31.2	640	10	US-09-991-163-501	Sequence 501, App
45	43	31.2	640	10	US-09-993-604-501	Sequence 501, App

#### ALIGNMENTS

RESULT 1  
US-09-922-378-3  
; Sequence 3, Application US/09922378  
; Patent No. US20020037869A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, William A.  
; APPLICANT: Oltersdorf, Tilman  
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC  
; TITLE OF INVENTION: ACIDS AND METHODS OF USE  
; FILE REFERENCE: 480140.428D3  
; CURRENT APPLICATION NUMBER: US/09/922,378  
; CURRENT FILING DATE: 2001-08-03  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 204  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-922-378-3

Query Match 97.8%; Score 135; DB 9; Length 204;  
Best Local Similarity 96.2%; Pred. No. 3.3e-12;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLWAAQRYGRELRRMSDEFEGSKGL 26  
|||||  
Db 140 NLWAAQRYGRELRRMTDEFEGSKGL 165

RESULT 2  
US-10-066-179-3  
; Sequence 3, Application US/10066179  
; Publication No. US20020115631A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, William A.  
; APPLICANT: Oltersdorf, Tilman  
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC  
; TITLE OF INVENTION: ACIDS AND METHODS OF USE

; FILE REFERENCE: 480140.428C1  
; CURRENT APPLICATION NUMBER: US/10/066,179  
; CURRENT FILING DATE: 2002-02-01  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 204  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-066-179-3

Query Match 97.8%; Score 135; DB 14; Length 204;  
Best Local Similarity 96.2%; Pred. No. 3.3e-12;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFEGSFKGL 26  
|||||  
Db 140 NLWAAQRYGRELRRMTDEFEGSFKGL 165

## RESULT 3

US-10-059-261-258  
; Sequence 258, Application US/10059261  
; Publication No. US20030077826A1  
; GENERAL INFORMATION:  
; APPLICANT: EDELMAN, LENA  
; APPLICANT: JACOTOT, ETIENNE DANIEL FRANCOIS  
; APPLICANT: BRIAND, JEAN-PAUL  
; TITLE OF INVENTION: CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET  
; TITLE OF INVENTION: SPECIFIC CELLS AND A MODULE REGULATING THE APOPTOGENIC  
; TITLE OF INVENTION: FUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX  
; TITLE OF INVENTION: (PTPC)  
; FILE REFERENCE: 03495.0216  
; CURRENT APPLICATION NUMBER: US/10/059,261  
; CURRENT FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: 60/265,594  
; PRIOR FILING DATE: 2001-02-02  
; NUMBER OF SEQ ID NOS: 325  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 258  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: TOX peptide  
US-10-059-261-258

Query Match 82.6%; Score 114; DB 15; Length 25;  
Best Local Similarity 91.7%; Pred. No. 4.8e-10;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFEGSFK 24  
|||||  
Db 1 NLWAAQRYGRELRRMSDEFVDSFK 24

## RESULT 4

US-09-922-378-2  
; Sequence 2, Application US/09922378  
; Patent No. US20020037869A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, William A.  
; APPLICANT: Oltersdorf, Tilman  
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC  
; TITLE OF INVENTION: ACIDS AND METHODS OF USE  
; FILE REFERENCE: 480140.428D3  
; CURRENT APPLICATION NUMBER: US/09/922,378  
; CURRENT FILING DATE: 2001-08-03  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 168  
; TYPE: PRT

; ORGANISM: Homo sapiens  
US-09-922-378-2

Query Match 82.6%; Score 114; DB 9; Length 168;  
Best Local Similarity 91.7%; Pred. No. 3.4e-09;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFEGSFK 24  
|||||  
Db 103 NLWAAQRYGRELRRMSDEFVDSFK 126

## RESULT 5

US-09-894-657-1  
; Sequence 1, Application US/09894657  
; Patent No. US20020098569A1  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; Yue, Henry  
; Lal, Preeti  
; Shah, Purvi  
; Corley, Neil C.  
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Dr.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/894,657  
; FILING DATE: 28-Jun-2001  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/410,372  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0421 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 168 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: SYNORAB01  
; CLONE: 358673  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-894-657-1

Query Match 82.6%; Score 114; DB 9; Length 168;  
Best Local Similarity 91.7%; Pred. No. 3.4e-09;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFEGSFK 24  
|||||  
Db 103 NLWAAQRYGRELRRMSDEFVDSFK 126

## RESULT 6

US-09-894-657-7

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; Sequence 7, Application US/09894657
; Patent No. US20020098569A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; Yue, Henry
; Lal, Preeti
; Shah, Purvi
; Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; PROLIFERATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/894,657
; FILING DATE: 28-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/410,372
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0421 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1683637
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-894-657-7
Query Match      82.6%; Score 114; DB 9; Length 168;
Best Local Similarity 91.7%; Pred. No. 3.4e-09;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 NLWAAQRYGRELRRMSDEFEFSFK 24
Db      103 NLWAAQRYGRELRRMSDEFEVDSEFK 126

RESULT 7
US-10-066-179-2
; Sequence 2, Application US/10066179
; Publication No. US20020115631A1
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; Applicant: Oltersdorf, Tilman
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
; TITLE OF INVENTION: ACIDS AND METHODS OF USE
; FILE REFERENCE: 480140.428C1
; CURRENT APPLICATION NUMBER: US/10/066,179
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 168

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-066-179-2
Query Match      82.6%; Score 114; DB 14; Length 168;
Best Local Similarity 91.7%; Pred. No. 3.4e-09;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 NLWAAQRYGRELRRMSDEFEFSFK 24
Db      103 NLWAAQRYGRELRRMSDEFEVDSEFK 126

RESULT 8
US-10-174-105A-147
; Sequence 147, Application US/10174105A
; Publication No. US20030068652A1
; GENERAL INFORMATION:
; APPLICANT: Cell Signaling Technology, Inc.
; APPLICANT: ZHANG, Hui
; APPLICANT: COMB, Michael J.
; APPLICANT: TAN, Yi
; TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPECIFIC
; TITLE OF INVENTION: CONTEXT-INDEPENDENT ANTIBODIES COUPLED WITH DATABASE SEARCHING
; FILE REFERENCE: CST-138 CIP3
; CURRENT APPLICATION NUMBER: US/10/174,105A
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 09/148,712
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 09/535,364
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 147
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; NAME/KEY: MOD_RES
; LOCATION: (8)..(8)
; OTHER INFORMATION: PHOSPHORYLATION; serine at position 8 is phosphorylated
US-10-174-105A-147
Query Match      51.4%; Score 71; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00061;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 GRELRMSDEFEFS 22
Db      1 GRELRMSDEFEFS 14

RESULT 9
US-10-156-761-9145
; Sequence 9145, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
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; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9145
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9145

Query Match
Best Local Similarity 36.2%; Score 50; DB 15; Length 215;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 6 QRYGRELRRMSDEFG 21
Db 108 ERWGDLRRMRDEADG 123

RESULT 10
US-10-092-750-1
; Sequence 1, Application US/10092750
; Publication No. US2003032157A1
; GENERAL INFORMATION:
; APPLICANT: Hammond, Philip W.
; APPLICANT: Alpin, Julia
; TITLE OF INVENTION: Polypeptides Interactive with BCL-X1
; FILE REFERENCE: 50036/050002
; CURRENT APPLICATION NUMBER: US/10/092,750
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 60/274,526
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-750-1

Query Match
Best Local Similarity 34.1%; Score 47; DB 15; Length 35;
Matches 10; Conservative 3; Mismatches 5; Indels 4; Gaps 1;

QY 2 LWAAQRYGRELRRMSDEFGSF 23
Db 15 IWIAQ----ELRRIGDEFNAY 32

RESULT 11
US-10-092-750-241
; Sequence 241, Application US/10092750
; Publication No. US2003032157A1
; GENERAL INFORMATION:
; APPLICANT: Hammond, Philip W.
; APPLICANT: Alpin, Julia
; TITLE OF INVENTION: Polypeptides Interactive with BCL-X1
; FILE REFERENCE: 50036/050002
; CURRENT APPLICATION NUMBER: US/10/092,750
; CURRENT FILING DATE: 2002-03-07
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/274,526
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 241
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-750-241

Query Match
Best Local Similarity 34.1%; Score 47; DB 15; Length 138;
Matches 10; Conservative 3; Mismatches 5; Indels 4; Gaps 1;

QY 2 LWAAQRYGRELRRMSDEFGSF 23
Db 86 IWIAQ----ELRRIGDEFNAY 103

RESULT 12
US-10-238-075-1077
; Sequence 1077, Application US/10238075
; Publication No. US20030148324A1
; GENERAL INFORMATION:
; APPLICANT: I.N.S.E.R.M.
; TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are iso
; FILE REFERENCE: BLANDINE
; CURRENT APPLICATION NUMBER: US/10/238,075
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 0003145
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1077
; LENGTH: 682
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-238-075-1077

Query Match
Best Local Similarity 33.3%; Score 46; DB 12; Length 682;
Matches 10; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 2 LWAAQRYGRELRRMSDEFGSPKGL 26
Db 610 IWAAQRNGAKVPRVRNGFTSMDIGL 634

RESULT 13
US-09-828-423-3
; Sequence 3, Application US/09828423
; Patent No. US20020099178A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; Guegler, Karl J.
; Patterson, Chandra
; TITLE OF INVENTION: GROWTH-ASSOCIATED TRYPSIN-TYPE
; INHIBITOR HEAVY CHAIN PRECURSOR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Word Perfect 6.1/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/828,423
; FILING DATE: 05-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/388,774
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrione, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0505 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
```

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RESULT 15
US-09-815-242-5704
; Sequence 5704, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 15, 2003, 17:18:16 ; Search time 11.7 Seconds  
(without alignments)  
213.708 Million cell updates/sec

Title: US-09-544-664-1  
Perfect score: 138  
Sequence: 1 NLWAAQRYGRELRRMSDEFGSFKGL 26

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616882 residues  
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	138	100.0	204	2 A55671	bad protein - mouse
2	54	39.1	946	2 JC5575	inter-alpha-trypsi
3	53	38.4	223	2 D70760	hypothetical prote
4	53	38.4	946	2 S54354	inter-alpha-inhibi
5	52	37.7	370	2 S38185	2-dehydro-3-deoxy-
6	51	37.0	232	2 A42095	floral homeotic pr
7	50	36.2	374	2 C84338	spermidine/putresc
8	50	36.2	516	2 A96753	probable threonine
9	49	35.5	453	2 E83517	conserved hypothet
10	48.5	35.1	134	2 S40376	Ig kappa chain - h
11	48.5	35.1	314	2 T02975	annexin P35 - maiz
12	48	34.8	206	2 C36365	transforming prote
13	48	34.8	220	2 F72289	oxidoreductase, so
14	48	34.8	526	2 T08545	threonine synthase
15	47	34.1	597	2 G82308	oxaloacetate decar
16	47	34.1	967	2 F82668	oxoglutarate dehyd
17	47	34.1	5138	2 B96695	hypothetical prote
18	46.5	33.7	314	2 T02961	annexin p33 - maiz
19	46.5	33.7	435	2 A44308	Antho-Ramide prec
20	46.5	33.7	1140	2 T09486	hypothetical prote
21	46	33.3	399	2 T35440	probable polyamine
22	46	33.3	946	1 IYHU2	inter-alpha-trypsi
23	46	33.3	1164	2 T24806	hypothetical prote
24	46	33.3	1378	2 A81393	DNA-directed RNA p
25	45.5	33.0	261	2 G69510	conserved hypothet
26	45.5	33.0	287	2 S43852	neuropeptide Pol-R
27	45.5	33.0	334	2 A39172	Antho-RFamide neur
28	45.5	33.0	562	2 C71473	hypothetical prote
29	45.5	33.0	905	2 G63314	NADH dehydrogenase

## ALIGNMENTS

## RESULT 1

A55671

bad protein - mouse

C:Species: Mus musculus (house mouse)

C>Date: 03-Mar-1995 #sequence\_revision 03-Mar-1995 #text\_change 05-Nov-1999

C:Accession: A55671

R;Yang, E.; Zha, J.; Jockel, J.; Boise, L.H.; Thompson, C.B.; Korsmeyer, S.J.  
Cell 80, 285-291, 1995

A:Title: Bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promotes

A:Reference number: A55671; MUID:95136361; PMID:7834748

A:Accession: A55671

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-204 <YAN>

A:Cross-references: GB:L37296; NID:g639778; PIDN:AAA64465.1; PID:g639779

C:Keywords: heterodimer

Query Match

Best Local Similarity 100.0%; Score 138; DB 2; Length 204;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 NLWAAQRYGRELRRMSDEFGSFKGL 26

|||||

140 NLWAAQRYGRELRRMSDEFGSFKGL 165

DB

RESULT 2

JC5575

inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster

C:Species: Mesocricetus auratus (golden hamster)

C>Date: 23-Sep-1997 #sequence\_revision 23-Sep-1997 #text\_change 20-Jun-2000

C:Accession: JC5575; PC4485

R;Nakatani, T.; Suzuki, Y.; Yamamoto, T.; Sinozawa, H.  
J. Biochem. 122, 71-82, 1997

A:Title: Molecular cloning and sequencing of cDNAs encoding three heavy-chain precursors

in inhibitor heavy chain family.

A:Reference number: JC5575; MUID:97420688; PMID:9276673

A:Accession: JC5575

A:Molecule type: mRNA

A:Residues: 1-946 <NAK>

A:Cross-references: DBJ:D89286; NID:g1694689; PIDN:BAAL3939.1; PID:g1694690

A:Experimental source: liver

A:Accession: PC4485

A:Molecule type: protein

A:Residues: 55-64/140-146/151-156/424-447/500-528/577-605 <NA2>

C:Comment: In the plasma three inter-alpha-trypsin inhibitor heavy chains 1, 2 and 3

that the complexes play important role for pancreatic cancer.

C:Superfamily: inter-alpha-trypsin inhibitor complex component II

F;261-264,717-916/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 39.1%; Score 54; DB 2; Length 946;

Matches 34.6%; Pred. No. 8.8;

Matches 9; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFGSKGL 26  
 DB 212 NWVIELQGMFLHVPDTFEGHFGV 237

RESULT 3  
 D70760  
 hypothetical protein Rv2014 - Mycobacterium tuberculosis (strain H37RV)  
 C:Species: Mycobacterium tuberculosis  
 C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999  
 C:Accession: D70760

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
 A:Reference number: A70500; MUID:98295987; PMID:9634230  
 A:Accession: D70760  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-223 <COL>  
 A:Cross-references: GB:274025; GB:AL123456; NID:g3261586; PIDN:CAA98415.1; PID:ei299911;  
 A:Experimental source: strain H37RV  
 C:Genetics:  
 A:Gene: Rv2014

Query Match 38.4%; Score 53; DB 2; Length 223;  
 Best Local Similarity 58.8%; Pred. No. 2.8;  
 Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSD 17  
 DB 165 NLWADRYNRAIGHD 161

RESULT 4  
 S54354  
 inter-alpha-inhibitor H2 chain - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 20-Aug-1999  
 C:Accession: S54354  
 R;Chan, P.; Risler, J.L.; Raquenez, G.; Sallier, J.P.  
 Biochem. J. 306, 505-512, 1995

A:Title: The three heavy-chain precursors for the inter-alpha-inhibitor family in mouse:  
 A:Reference number: S54353; MUID:95194326; PMID:7534067  
 A:Accession: S54354  
 A:Status: preliminary; nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-946 <CHA>  
 A:Cross-references: EMBL:X70392; NID:g695633; PIDN:CAA49842.1; PID:g695634  
 C:Superfamily: inter-alpha-trypsin inhibitor complex component II

Query Match 38.4%; Score 53; DB 2; Length 946;  
 Best Local Similarity 34.6%; Pred. No. 12;  
 Matches 9; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFGSKGL 26  
 DB 212 NWVIELQGMFLHVPDTFEGHFGV 237

RESULT 5  
 S38185  
 2-dehydro-3-deoxy-phosphoheptonate aldolase (EC 4.1.2.15) ARO4 - yeast (Saccharomyces ce  
 N;Alternate names: 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase; DAHP synthase;  
 C:Species: Saccharomyces cerevisiae  
 C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 03-Jun-2002  
 C:Accession: S38185; S46126; S46130; JN0322; B48651  
 R;Doignon, F.; Biteau, N.; Aigle, M.; Crouzet, M.  
 Yeast 9, 1131-1137, 1993

A:Title: The complete sequence of a 6794 bp segment located on the right arm of chrom  
 A:Reference number: S38185; MUID:94078675; PMID:8256522  
 A:Accession: S38185  
 A:Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-370 <DOI>  
 A:Cross-references: GB:L20296; NID:g311101; PIDN:AAA65607.1; PID:g311102  
 R;Aljinovic, G.; Pohl, F.M.; Pohl, T.M.  
 submitted to the Protein Sequence Database, August 1994  
 A:Reference number: S45906  
 A:Accession: S46126  
 A:Molecule type: DNA  
 A:Residues: 1-370 <ALJ>  
 A:Cross-references: EMBL:Z36118; NID:g536664; PIDN:CAA85212.1; PID:g536665; MIPS:YBR  
 R;Aigle, M.; Bacllet, M.C.; Barthe, C.; Biteau, N.; Crouzet, M.; Doignon, F.  
 submitted to the Protein Sequence Database, August 1994  
 A:Reference number: S45940  
 A:Accession: S46130  
 A:Molecule type: DNA  
 A:Residues: 1-370 <AIG>  
 A:Cross-references: EMBL:Z36118; NID:g536664; PIDN:CAA85212.1; PID:g536665; MIPS:YBR  
 R;Ruenzler, M.; Paravicini, G.; Egli, C.M.; Paravicini, G.; Braus, G.H.  
 Gene 113, 67-74, 1992  
 A:Title: Cloning, primary structure and regulation of the ARO4 gene, encoding the ty  
 A:Reference number: JN0322; MUID:92225349; PMID:1345717  
 A:Accession: JN0322  
 A:Molecule type: DNA  
 A:Residues: 1-204,208-370 <KOE>  
 A:Cross-references: EMBL:X61107  
 R;Ruenzler, M.; Balmelli, T.; Egli, C.M.; Paravicini, G.; Braus, G.H.  
 J. Bacteriol. 175, 5548-5558, 1993  
 A:Title: Cloning, primary structure, and regulation of the HIS7 gene encoding a bifur  
 A:Reference number: A48651; MUID:93374850; PMID:8366040  
 A:Accession: B48651  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 352-370 <KU2>  
 A:Cross-references: GB:X61107  
 C:Comment: This enzyme catalyzes the condensation of phosphoenolpyruvate and D-erythr  
 C:Genetics:  
 A:Gene: SGD:ARO4  
 A:Cross-references: SGD:S0000453; MIPS:YBR249c  
 A:Map position: 2R  
 C:Function:  
 A:Description: aldehyde-lyase; carbon-carbon lyase  
 A:Pathway: aromatic amino acid biosynthesis; shikimate pathway  
 A:Note: first step in shikimate pathway  
 C:Superfamily: phospho-2-dehydro-3-deoxyheptonate aldolase  
 C:Keywords: aldehyde-lyase; aromatic amino acid biosynthesis; carbon-carbon lyase; cy

Query Match 37.7%; Score 52; DB 2; Length 370;  
 Best Local Similarity 47.6%; Pred. No. 6.7;  
 Matches 10; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFG 21  
 DB 80 DLAAQYALRLKLSDELKG 100

RESULT 6  
 A42095  
 floral homeotic protein APETALA3 (AP3) - Arabidopsis thaliana  
 N;Alternate names: homeotic protein APETALA3; MADS-box regulatory protein AP3  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jul-2000  
 C:Accession: A42095; S52633; T47593  
 R;Jack, T.; Brockman, L.L.; Meyerowitz, E.M.  
 Cell 68, 683-697, 1992  
 A:Title: The homeotic gene APETALA3 of Arabidopsis thaliana encodes a MADS box and is  
 A:Reference number: A42095; MUID:92154682; PMID:1346756  
 A:Accession: A42095  
 A:Status: preliminary  
 A:Molecule type: mRNA

A;Residues: 1-232 <JAC>  
A;Cross-references: GB:M86357; NID:gl166607; PIDN:AAA32740.1; PID:gl156608  
A;Experimental source: petals, stamens  
A;Note: sequence extracted from NCBI backbone (NCBIN:82520, NCBIP:82521)  
R;Okamoto, H.; Yano, A.; Shiraiishi, H.; Okada, K.; Shimura, Y.  
Plant Mol. Biol. 26, 465-472, 1994  
A;Title: Genetic complementation of a floral homeotic mutation, apetala3, with an Arabidopsis gene  
A;Reference number: S52633; MUID:95036018; PMID:7948893  
A;Accession: S52633  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-63 <OKA>  
A;Cross-references: GB:D21125  
R;Bloeker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat M.Mewes,  
submitted to the Protein Sequence Database, March 2000  
A;Reference number: Z24469  
A;Accession: T47593  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-232 <BLO>  
A;Cross-references: EMEL:AL132971  
A;Experimental source: cultivar Columbia; BAC clone T12E18  
C;Genetics:  
A;Map position: 3  
A;Introns: 63/2; 85/3; 106/2; 139/3; 153/3; 168/3  
A;Note: T12E18.30  
C;Superfamily: transcription factor squa; serum response factor DNA-binding domain homolog  
C;Keywords: DNA binding; nucleus; transcription regulation  
F;2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 37.0%; Score 51; DB 2; Length 232;  
Best Local Similarity 44.4%; Pred. No. 5.8;  
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;  
Db 6 QRYG-----RELRRMSDEFEGSK 24  
||| :|||: ||| :||  
107 QRLGCLDELDIQELRLDEMENTFK 133

RESULT 7  
C84338  
spermidine/putrescine ABC transporter [imported] - Halobacterium sp. NRC-1  
C;Species: Halobacterium sp. NRC-1  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C;Accession: C84338  
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.  
Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo  
Jung, K.H.; Alam, M.; Freitas, T.  
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li  
A;Title: Genome sequence of Halobacterium species NRC-1.  
A;Reference number: A84160; MUID:20504483; PMID:11016950  
A;Accession: C84338  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-374 <STO>  
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C;Genetics:  
A;Gene: potA2

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Best Local Similarity 76.9%; Pred. No. 13;  
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Db 11 ELRRMSDEFEGSF 23  
197 ELRRLSDAVEGSF 209

RESULT 8  
A96753  
probable threonine synthase [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)

A;Residues: 1-232 <JAC>  
A;Cross-references: GB:M86357; NID:gl166607; PIDN:AAA32740.1; PID:gl156608  
A;Experimental source: petals, stamens  
A;Note: sequence extracted from NCBI backbone (NCBIN:82520, NCBIP:82521)  
R;Okamoto, H.; Yano, A.; Shiraiishi, H.; Okada, K.; Shimura, Y.  
Plant Mol. Biol. 26, 465-472, 1994  
A;Title: Genetic complementation of a floral homeotic mutation, apetala3, with an Arabidopsis gene  
A;Reference number: S52633; MUID:95036018; PMID:7948893  
A;Accession: S52633  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-63 <OKA>  
A;Cross-references: GB:D21125  
R;Bloeker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat M.Mewes,  
submitted to the Protein Sequence Database, March 2000  
A;Reference number: Z24469  
A;Accession: T47593  
A;Status: preliminary  
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A;Cross-references: EMEL:AL132971  
A;Experimental source: cultivar Columbia; BAC clone T12E18  
C;Genetics:  
A;Map position: 3  
A;Introns: 63/2; 85/3; 106/2; 139/3; 153/3; 168/3  
A;Note: T12E18.30  
C;Superfamily: transcription factor squa; serum response factor DNA-binding domain homolog  
C;Keywords: DNA binding; nucleus; transcription regulation  
F;2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 37.0%; Score 51; DB 2; Length 232;  
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Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;  
Db 6 QRYG-----RELRRMSDEFEGSK 24  
||| :|||: ||| :||  
107 QRLGCLDELDIQELRLDEMENTFK 133

RESULT 7  
C84338  
spermidine/putrescine ABC transporter [imported] - Halobacterium sp. NRC-1  
C;Species: Halobacterium sp. NRC-1  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C;Accession: C84338  
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.  
Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo  
Jung, K.H.; Alam, M.; Freitas, T.  
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li  
A;Title: Genome sequence of Halobacterium species NRC-1.  
A;Reference number: A84160; MUID:20504483; PMID:11016950  
A;Accession: C84338  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-374 <STO>  
A;Cross-references: GB:AE004437; NID:gl0581314; PIDN:AAG20071.1; GSPDB:GN00138  
C;Genetics:  
A;Gene: potA2

Query Match 36.2%; Score 50; DB 2; Length 374;  
Best Local Similarity 76.9%; Pred. No. 13;  
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Db 11 ELRRMSDEFEGSF 23  
197 ELRRLSDAVEGSF 209

RESULT 8  
A96753  
probable threonine synthase [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C;Accession: A96753  
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar,  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mafti, R.; Marzia  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; MUID:21016719; PMID:11130712  
A;Accession: A96753  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-516 <STO>  
A;Cross-references: GB:AE005173; NID:g5903070; PIDN:AAD55628.1; GSPDB:GN00141  
C;Genetics:  
A;Gene: F3N23.1  
A;Map position: 1

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Best Local Similarity 35.3%; Pred. No. 18;  
Matches 12; Conservative 7; Mismatches 7; Indels 8; Gaps 1;  
Db 1 NLFWAQRYGRELRRMSD-----EFEGSFKGL 26  
||| :|||: ||| :||  
163 NLFWAERFGKYLQMDLWVRHQCISHTGSRKDL 196

RESULT 9  
E83517  
conserved hypothetical protein PA1031 [imported] - Pseudomonas aeruginosa (strain PAO  
C;Species: Pseudomonas aeruginosa  
C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C;Accession: E83517  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa  
A;Reference number: A82950; MUID:20437337; PMID:10984043  
A;Accession: E83517  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-453 <STO>  
A;Cross-references: GB:AE004535; GB:AE004091; NID:g9946936; PIDN:AAG04420.1; GSPDB:GN  
A;Experimental source: strain PA01  
C;Genetics:  
A;Gene: PA1031

Query Match 35.5%; Score 49; DB 2; Length 453;  
Best Local Similarity 55.6%; Pred. No. 23;  
Matches 10; Conservative 4; Mismatches 2; Indels 2; Gaps 1;  
Db 3 WAAQRYGR--ELRRMSDE 18  
||| :|||: ||| :||  
65 WASERQGRFEELRLRLASE 82

RESULT 10  
S40376  
Ig kappa chain - human  
C;Species: Homo sapiens (man)  
C;Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C;Accession: S40376  
R;Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A;Reference number: S40312; MUID:94080891; PMID:8258341  
A;Accession: S40376  
A;Status: preliminary; translation not shown

QY 10 RELRRMSDEFFEGSFKG 25

Search completed: September 15, 2003, 17:27:00  
Job time : 12.7 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 15, 2003, 17:16:55; Search time 6.12857 Seconds  
(without alignments)  
199.507 Million cell updates/sec

Title: US-09-544-664-1  
Perfect score: 138  
Sequence: 1 NLWAAQRYGELRRMSDEFGSKGL 26

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	138	100.0	204	1 BAD_MOUSE	Q61337 mus musculus
2	138	100.0	205	1 BAD_RAT	Q35147 rattus norv
3	114	82.6	168	1 BAD_HUMAN	Q92934 homo sapien
4	54	39.1	946	1 ITH2_MESAU	P97279 mesocricetu
5	53	38.4	946	1 ITH2_MOUSE	Q61703 mus musculus
6	52	37.7	370	1 ARCG_YEAST	P32449 saccharomyc
7	51	37.0	232	1 AP3_ARATH	P35632 arabidopsis
8	50	36.2	851	1 CE05_MOUSE	Q8X2H3 mus musculus
9	49.5	35.9	506	1 MATK_LEDPA	O62992 ledum palus
10	49.5	35.9	506	1 MATK_RHOFR	O62984 rhododendro
11	49.5	35.9	506	1 MATK_RHOTS	O62991 rhododendro
12	49	35.5	453	1 RMUC_PSEAE	Q914U3 pseudomonas
13	48	34.8	205	1 RAS3_RHTRA	P22280 rhizomucor
14	48	34.8	220	1 6PGL_THEMA	Q9X0N8 thermotoga
15	48	34.8	519	1 THRC_SOLITU	Q9MT28 solanum tub
16	48	34.8	526	1 THRC_ARATH	Q9S7B5 arabidopsis
17	47	34.1	198	1 BIM_HUMAN	Q43521 homo sapien
18	46.5	33.7	429	1 FMR2_ANTEL	Q16994 anthopleura
19	46.5	33.7	435	1 FMR1_ANTEL	P10419 anthopleura
20	46	33.3	946	1 ITH2_HUMAN	P19823 homo sapien
21	46	33.3	1378	1 RPOB_CAMJE	Q46124 campylobact
22	45.5	33.0	287	1 PRFA_POLPE	P21259 polyorchis
23	45.5	33.0	334	1 FMR4_CALPA	Q01133 calliactis
24	45.5	33.0	507	1 MATK_LOIPR	Q47169 loiseleuria
25	45	32.6	328	1 SNE4_KLULA	Q9P869 kluyveromyc
26	45	32.6	590	1 DCOA_SALTY	Q03030 salmonella
27	45	32.6	595	1 DCOA_KLEPN	P13187 klebsiella
28	45	32.6	653	1 HT2A_HUMAN	Q13049 homo sapien
29	45	32.6	865	1 ENV_SIVAT	P05886 simian immu
30	45	32.6	1535	1 LML1_CABEL	P18823 caenorhabdi
31	44.5	32.2	907	1 NUOG_ECOLI	P33602 escherichia
32	44.5	32.2	907	1 NUOG_SALTY	P33900 salmonella
33	44	31.9	196	1 BIM_MOUSE	O54918 mus musculus

RESULT 1  
BAD\_MOUSE  
ID BAD\_MOUSE STANDARD; PRT; 204 AA.  
AC Q61337;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bcl2-antagonist of cell death (BAB) (Bcl-2 binding component  
DE 6) (Bcl-xL/Bcl-2 associated death promoter).  
GN BAD OR BCC6.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain, and Thymus; MEDLINE=7834748;  
RX MEDLINE=95136361; PubMed=7834748;  
RA Yang E., Zha J., Jockel J., Boise L.H., Thompson C.B., Korsmeyer S.J.;  
RT "Bad, a heterodimeric partner for Bcl-xL and Bcl-2, displaces Bax and  
RT promotes cell death.";  
RL Cell 80:285-291(1995).  
RN [2]  
RP PHOSPHORYLATION, AND MUTAGENESIS OF SER-112 AND SER-136.  
RX MEDLINE=98022383; PubMed=9381178;  
RA Del Peso L., Gonzalez-Garcia M., Page C., Herrera R., Nunez G.;  
RT "Interleukin-3-induced phosphorylation of BAD through the protein  
RT kinase Akt.";  
RL Science 278:687-689(1997).  
RN [3]  
RP MUTAGENESIS OF SERINE RESIDUES.  
RX MEDLINE=20403302; PubMed=10949026;  
RA Datta S.R., Katsov A., Hu L., Petros A., Fesik S.W., Yaffe M.B.,  
RT Greenberg M.E.;  
RT "14-3-3 proteins and survival kinases cooperate to inactivate BAD by  
RT BH3 domain phosphorylation.";  
RL Mol. Cell 6:41-51(2000).  
CC -!- FUNCTION: Promotes cell death. Successfully competes for the  
CC binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level  
CC of heterodimerization of these proteins with BAX. Can reverse the  
CC death repressor activity of Bcl-x(L), but not that of Bcl-2.  
CC Appears to act as a link between growth factor receptor signaling  
CC and the apoptotic pathways.  
CC -!- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-  
CC x(L), Bcl-2 and Bcl-w. Also binds protein S100A10 (By similarity).  
CC The Ser-112/Ser-136 phosphorylated form binds 14-3-3 proteins.  
CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon  
CC phosphorylation, locates to the cytoplasm.  
CC -!- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND  
CC BAX for their pro-apoptotic activity and for their interaction  
CC with anti-apoptotic members of the Bcl-2 family.  
CC -!- PTM: Phosphorylated on Ser-112 in response to survival stimuli.  
CC Subsequent phosphorylation on Ser-136 promotes heterodimerization  
CC with 14-3-3 proteins. This interaction then facilitates the  
CC phosphorylation at Ser-155, a site within the BH3 domain, leading  
CC to the release of Bcl-x(L) and the promotion of cell survival.

34 44 31.9 196 1 BIM\_RAT  
35 44 31.9 262 1 END8\_ECO57  
36 44 31.9 262 1 END8\_ECOLI  
37 44 31.9 262 1 END8\_SALTY  
38 44 31.9 262 1 END8\_SALTY  
39 44 31.9 768 1 ENV\_SIVAT  
40 44 31.9 877 1 ENV\_SIVAG  
41 44 31.9 915 1 CE05\_HUMAN  
42 44 31.9 5596 1 MDN1\_HUMAN  
43 44 31.9 8797 1 SNE1\_HUMAN  
44 43.5 31.5 217 1 UREF\_SYNY3  
45 43.5 31.5 1014 1 UVRA\_STRCO

## ALIGNMENTS

O88498 rattus norv  
Q8x9c6 escherichia  
P50465 escherichia  
Q828d2 salmonella  
Q8zqu6 salmonella  
P27757 simian immu  
P27977 simian immu  
Q9nyf5 homo sapien  
Q9nu22 homo sapien  
Q8nf91 homo sapien  
P73327 synechocyst  
Q9z507 streptomyce

CC Ser-136 is the major site of AKT/PKB phosphorylation, Ser-155 the  
 CC major site of protein kinase A (CApk) phosphorylation.  
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.  
 CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; L37296; AAA64465.1; -;  
 CC PIR; A55671; A55671.  
 CC HSP; Q92934; LGSJ.  
 CC MGD; MGI:1096330; Bad.  
 CC InterPro; IPR000712; Bcl2\_BH.  
 CC PROSITE; PS01259; BH3; FALSE\_NEG.  
 CC Apoptosis; Phosphorylation.  
 CC DOMAIN 147 161 BH3.  
 CC MOD\_RES 112 112 PHOSPHORYLATION (BY PKA AND PKB).  
 CC MOD\_RES 136 136 PHOSPHORYLATION (BY PKA AND PKB).  
 CC MOD\_RES 155 155 PHOSPHORYLATION (BY PKA AND PKB).  
 CC MUTAGEN 112 112 S->A: NO PHOSPHORYLATION.  
 CC MUTAGEN 136 136 S->A: NO PHOSPHORYLATION.  
 CC MUTAGEN 155 155 S->A: NO PHOSPHORYLATION; INTERACTS WITH  
 CC BCL-X(L).  
 CC SEQUENCE 204 AA; 22080 MW; 6C2BA910205053F7 CRC64;  
 CC  
 CC Query Match 100.0%; Score 138; DB 1; Length 204;  
 CC Best Local Similarity 100.0%; Pred. No. 1.5e-13;  
 CC Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 1 NLNAAQRYGRELRRMSDEFGSEKGL 26  
 CC |||||  
 CC Db 140 NLNAAQRYGRELRRMSDEFGSEKGL 165  
 CC  
 CC RESULT 2  
 CC ID BAD\_RAT STANDARD; PRT; 205 AA.  
 CC AC Q35147; Q70256; Q9JHX1;  
 CC DT 16-OCT-2001 (Rel. 40, Created)  
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 CC DE Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component  
 CC 6) (Bcl-XL/Bcl-2 associated death promoter).  
 CC GN Rat.  
 CC OS Rattus norvegicus (Rat).  
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 CC OX NCBI\_TaxID=10116;  
 CC RN [1]  
 CC RP SEQUENCE FROM N.A., AND MUTAGENESIS OF SER-113 AND SER-137.  
 CC RC TISSUE=Ovary;  
 CC RX MEDLINE=98034386; PubMed=9359453;  
 CC RA Hsu S.Y., Kaipia A., Zhu L., Hsueh A.J.W.;  
 CC RT "Interference of BAD (Bcl-XL/Bcl-2-associated death promoter)-induced  
 CC RT apoptosis in mammalian cells by 14-3-3 isoforms and P11";  
 CC RL Mol. Endocrinol. 11:1858-1867(1997).  
 CC RN [2]  
 CC RP SEQUENCE FROM N.A.  
 CC RC TISSUE=Brain;  
 CC RX MEDLINE=98194755; PubMed=9535132;  
 CC RA D'Agata V., Magro G., Travali S., Musco S., Cavallaro S.;  
 CC RT "cloning and expression of the programmed cell death regulator BAD in  
 CC RT the rat brain";  
 CC RL Neurosci. Lett. 243:137-140(1998).  
 CC RN [3]  
 CC RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).  
 CC RC TISSUE=Brain;  
 CC RX MEDLINE=21109372; PubMed=11161472;  
 CC

RA Hamner S., Arumae U., Yu L.-Y., Sun Y.-F., Saarna M., Lindholm D.;  
 RT "Functional characterization of two splice variants of rat BAD and  
 RT their interaction with Bcl-w in sympathetic neurons";  
 RL Mol. Cell. Neurosci. 17:97-106(2001).  
 CC -!- FUNCTION: Promotes cell death. Successfully competes for the  
 CC binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level  
 CC of heterodimerization of these proteins with BAX. Can reverse the  
 CC death repressor activity of Bcl-x(L), but not that of Bcl-2 (By  
 CC similarity). Appears to act as a link between growth factor  
 CC receptor signaling and the apoptotic pathways.  
 CC -!- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-  
 CC x(L), Bcl-2 and Bcl-w. Also binds protein S100A10. The Ser-  
 CC 113/Ser-137 phosphorylated form binds 14-3-3 proteins.  
 CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon  
 CC phosphorylation, locates to the cytoplasm (By similarity).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=2;  
 CC Name=Alpha;  
 CC IsoId=Q35147-1; Sequence=Displayed;  
 CC Name=Beta;  
 CC IsoId=Q35147-2; Sequence=VSP\_000534;  
 CC -!- TISSUE SPECIFICITY: Expressed in all tissues tested, including  
 CC brain, liver, spleen and heart. In the brain, restricted to  
 CC epithelial cells of the choroid plexus. Isoform alpha is the more  
 CC abundant form.  
 CC -!- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND  
 CC BAX for their pro-apoptotic activity and for their interaction  
 CC with anti-apoptotic members of the Bcl-2 family.  
 CC -!- PTM: Phosphorylated on Ser-113 in response to survival stimuli.  
 CC Subsequent phosphorylation on Ser-137 promotes heterodimerization  
 CC with 14-3-3 proteins. This interaction then facilitates the  
 CC phosphorylation at Ser-156, a site within the BH3 domain, leading  
 CC to the release of Bcl-x(L) and the promotion of cell survival.  
 CC Ser-137 is the major site of AKT/PKB phosphorylation, Ser-156 the  
 CC major site of protein kinase A (CApk) phosphorylation (By  
 CC similarity).  
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.  
 CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; AF003523; AAC33374.1; -;  
 CC EMBL; AF031227; AAC15100.1; -;  
 CC EMBL; AF279910; AAF91427.1; -;  
 CC EMBL; AF279911; AAF91428.1; -;  
 CC HSP; Q92934; LGSJ.  
 CC InterPro; IPR000712; Bcl2\_BH.  
 CC PROSITE; PS01259; BH3; FALSE\_NEG.  
 CC Apoptosis; Phosphorylation; Alternative splicing.  
 CC DOMAIN 148 162 BH3.  
 CC MOD\_RES 113 113 PHOSPHORYLATION (BY PKA AND PKB)  
 CC (BY SIMILARITY).  
 CC MOD\_RES 137 137 PHOSPHORYLATION (BY PKA AND PKB)  
 CC (BY SIMILARITY).  
 CC MOD\_RES 156 156 PHOSPHORYLATION (BY PKA AND PKB)  
 CC (BY SIMILARITY).  
 CC VARSPLIC 166 205 LPRKSGATGATMPQASWTRIIQSWWDRNLKGSGSTPSQ  
 CC -> EETYSVEFLPVRAIMEGWPLNSFQSPHTLPPTPP  
 CC /FTId-VSP\_000534.  
 CC S->A: NO EFFECT ON HETERODIMERIZATION  
 CC WITH 14-3-3 PROTEINS.  
 CC S->A: NO HETERODIMERIZATION WITH 14-3-3  
 CC PROTEINS. NO EFFECT ON HETERODIMERIZATION  
 CC WITH BCL2 NOR WITH PROTEIN P11.  
 CC CONFLICT 29 34 SDAGGR -> ERRGRK (IN REF. 1).  
 CC SEQUENCE 205 AA; 22228 MW; 7AFA71DAE9CF4A81 CRC64;  
 CC

Query Match 100.0%; Score 138; DB 1; Length 205;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-13;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFEGSKGL 26  
 DB 141 NLWAAQRYGRELRRMSDEFEGSKGL 166

RESULT 3  
 BAD\_HUMAN STANDARD; PRT; 168 AA.  
 AC Q92934; O14803;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component 6) (Bcl-  
 XL/Bcl-2 associated death promoter) (BCL2-like 8 protein).  
 GN BAD OR BCL6 OR BCL2L8.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Yin D.X., Li 2., Huang B., Chen S., Zhou H.;  
 RT "A human protein that interacts with Bcl-2 and have homology to mouse  
 BAD";  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A., AND PHOSPHORYLATION BY RAF-1.  
 RX MEDLINE=97083574; PubMed=8929532;  
 RA Wang H.-G., Rapp U.R., Reed J.C.;  
 RT "Bcl-2 targets the protein kinase Raf-1 to mitochondria";  
 RL Cell 87:629-638(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Takayama S., Reed J.C.;  
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A., AND DIMERIZATION.  
 RC TISSUE=Bone marrow;  
 RX MEDLINE=98049554; PubMed=9388232;  
 RA Otilie S., Diaz J.-L., Horne W., Chang J., Wang Y., Wilson G.,  
 RA Chang S., Weeks S., Fritz L.C., Oltersdorf T.;  
 RT "Dimerization properties of human BAD";  
 RL J. Biol. Chem. 272:30866-30872(1997).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [6]

RP STRUCTURE BY NMR OF 103-127.  
 RX MEDLINE=21073561; PubMed=11206074;  
 RA Petros A.M., Nettesheim D.G., Wang Y., Olejniczak E.T., Meadows R.P.,  
 RA Mack J., Swift K., Matayoshi E.D., Zhang H., Thompson C.B.,  
 RA Resik S.W.;  
 RT "Rationale for Bcl-xL/Bad peptide complex formation from structure,  
 RT mutagenesis, and biophysical studies";  
 RL Protein Sci. 9:2528-2534(2000).  
 CC -!- FUNCTION: Promotes cell death. Successfully competes for the  
 CC binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level  
 CC of heterodimerization of these proteins with BAX. Can reverse the  
 CC death repressor activity of Bcl-x(L), but not that of Bcl-2 (By  
 CC similarity). Appears to act as a link between growth factor  
 CC receptor signaling and the apoptotic pathways.  
 CC -!- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-  
 CC x(L), Bcl-2 and Bcl-w. Also binds protein Sl00A10 (By similarity).  
 CC The Ser-75/Ser-99 phosphorylated form binds 14-3-3 proteins (By  
 CC similarity).  
 CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon  
 CC phosphorylation, locates to the cytoplasm.  
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.  
 CC -!- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND  
 CC BAX for their pro-apoptotic activity and for their interaction  
 CC with anti-apoptotic members of the Bcl-2 family.  
 CC -!- PTM: Phosphorylated on Ser-75 in response to survival stimuli.  
 CC Subsequent phosphorylation on Ser-99 promotes heterodimerization  
 CC with 14-3-3 proteins. This interaction then facilitates the  
 CC phosphorylation at Ser-118, a site within the BH3 domain, leading  
 CC to the release of Bcl-x(L) and the promotion of cell survival.  
 CC Ser-99 is the major site of AKT/PKB phosphorylation, Ser-118 the  
 CC major site of protein kinase A (CAPK) phosphorylation (by  
 CC similarity).  
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.  
 CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -!- CAUTION: Ref.1 sequence differs from that shown due to frameshifts  
 CC in position 64 and 91.

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 CC -----  
 DR EMBL; U66879; AAB36516.1; ALT\_FRAME.  
 DR EMBL; AF021752; AAB72092.1; -.  
 DR EMBL; AF031523; AAB88124.1; -.  
 DR EMBL; BC001901; AAH01901.1; -.  
 DR PDB; 1G5U; 07-FEB-01.  
 DR Genew; HGNC:936; BAD.  
 DR MIM; 603167; -.  
 DR GO; GO:0005737; C:cytoplasm; NAS.  
 DR GO; GO:0005741; C:mitochondrial outer membrane; NAS.  
 DR GO; GO:0005315; P:protein binding activity; NAS.  
 DR GO; GO:0008632; P:apoptotic program; TAS.  
 DR GO; GO:0006917; P:induction of apoptosis; NAS.  
 DR InterPro; IPR000712; Bcl2 BH.  
 DR PROSITE; PS01259; BH3; FALSE\_NEG.  
 KW Apoptosis; Phosphorylation; Polymorphism; 3D-structure.  
 FT DOMAIN 110 124  
 FT MOD\_RES 75 75 PHOSPHORYLATION (BY PKA AND PKB) (BY  
 FT SIMILARITY).  
 FT MOD\_RES 99 99 PHOSPHORYLATION (BY PKA AND PKB) (BY  
 FT SIMILARITY).  
 FT MOD\_RES 118 118 PHOSPHORYLATION (BY PKA AND PKB) (BY  
 FT SIMILARITY).  
 FT VARIANT 107 107 A->S (in dbSNP:3729933).  
 FT HELIX 106 121 /FTID=VAR\_015380.  
 FT SEQUENCE 168 AA; 18392 MW; 69FD8D27DDEE3241 CRC64;  
 SQ

Query Match 82.6%; Score 114; DB 1; Length 168;

```

SMART; SM00327; VWA; 1.
DR PROSITE; PS0234; VWFA; 1.
KW Serine protease inhibitor; Repeat; Signal; Multigene family;
FT SIGNAL 1 18 POTENTIAL.
FT PROPEP 19 54 BY SIMILARITY.
FT CHAIN 55 702 INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN
H2.
FT PROPEP 703 946 BY SIMILARITY.
FT DOMAIN 308 468 VWFA.
FT CARBOHYD 118 118 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 578 578 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT BINDING 702 702 CHONDROITIN 4-SULFATE, CROSS-LINK SITE
(BY SIMILARITY).
FT CONFLICT 510 510 V -> Y (IN REF. 2).
FT CONFLICT 595 595 E -> I (IN REF. 2).
SQ SEQUENCE 946 AA; 106580 MW; CA8BF565458E7B2E CRC64;

Query Match 39.1%; Score 54; DB 1; Length 946;
Best Local Similarity 34.6%; Pred. No. 3.4;
Matches 9; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFGSKGL 26
: : : : :
Db 212 NWWIVELQGMRELHVDPTEFGHQGV 237

RESULT 5
ITH2_MOUSE
ID ITH2_MOUSE STANDARD; PRT; 946 AA.
AC Q61703;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITH heavy
DE chain H2) (Inter-alpha-inhibitor heavy chain 2).
GN ITH2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=C57BL/6N; TISSUE=Liver;
RX MEDLINE=95194326; PubMed=7534067;
RA Chan P., Risler J.-L., Reguenez G., Salier J.-P.;
RT "The three heavy-chain precursors for the inter-alpha-inhibitor
RT family in mouse: new members of the multicopper oxidase protein group
RT with differential transcription in liver and brain.";
RL Biochem. J. 306:505-512(1995).
CC -!- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
CC SIMILARITY).
CC -!- SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,
CC BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2
CC AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND
CC BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN BOTH LIVER AND BRAIN.
CC -!- PFM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
CC 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE ITH FAMILY.
CC -!- SIMILARITY: Contains 1 VWFA domain.
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CC -----
DR EMBL; X70392; CAA49842.1; -.
DR PIR; S54354; S54354.
DR MGD; MGI:96619; Itih2.
DR InterPro; IPR006587; VIT.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00092; vwa; 1.
DR SMART; SM00609; VIT; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS50334; VWF_A; 1.
KW Serine protease inhibitor; Repeat; Signal: Multigene family;
KW Glycoprotein.
FT SIGNAL 1 18 POTENTIAL.
FT PROPEP 19 54 BY SIMILARITY.
FT CHAIN 55 702 INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN
FT H2.
FT PROPEP 703 946 BY SIMILARITY.
FT DOMAIN 308 468 VWA.
FT CARBOHYD 118 118 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT BINDING 702 702 CHONDROITIN 4-SULFATE, CROSS-LINK SITE
FT (BY SIMILARITY).
SQ SEQUENCE 946 AA; 105927 MW; 40DB6716433ED9DC CRC64;

Query Match 38.4%; Score 53; DB 1; Length 946;
Best Local Similarity 34.6%; Pred. No. 4.8;
Matches 9; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRLRRMSDFEGSKGL 26
   I : I : I : I : I : I : I : I :
Db 212 NWIIPEQGMFLHVPDFEGHFGV 237

RESULT 6
AARG_YEAST STANDARD; PRT; 370 AA.
AC P32449;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited
DE (EC 4.1.2.15) (Phospho-2-keto-3-deoxyheptonate aldolase) (DAHP
DE synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase).
GN ARO4 OR YBR249C OR YBR1701.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9225349; PubMed=8256522;
RA Kuenzler M., Paravicini G., Egli C., Irniger S., Braus G.H.;
RT "Cloning, primary structure and regulation of the ARO4 gene, encoding
RT the tyrosine-inhibited 3-deoxy-D-arabino-heptulosonate-7-phosphate
RT synthase from Saccharomyces cerevisiae.";
RL Gene 113:67-74(1992).
RN [2]
RP REVISIONS TO 205-207.
RA Kuenzler M.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c;
RX MEDLINE=94078675; PubMed=8256522;
RA Daignon F., Biteau N., Aigle M., Crouzet M.;
RT "The complete sequence of a 6794 bp segment located on the right arm
RT of chromosome II of Saccharomyces cerevisiae. Finding of a putative
RT dUTPase in a yeast.";
```

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RL Yeast 9:1131-1137(1993).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c;
RA Aljinovic G., Pohl F.M., Pohl T.M.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: STEREOSPECIFIC CONDENSATION OF PHOSPHONOLPYRUVATE (PEP)
CC AND D-ERYTHROSE-4-PHOSPHATE (E4P) GIVING RISE TO 3-DEOXY-D-
CC ARABINO-HEPTULOSONATE-7-PHOSPHATE (DAHP).
CC -!- CATALYTIC ACTIVITY: 2-dehydro-3-deoxy-D-arabino-heptonate 7-
CC phosphate + phosphate = phosphoenolpyruvate + D-erythrose 4-
CC phosphate + H(2)O.
CC -!- ENZYME REGULATION: INHIBITED BY TYROSINE.
CC -!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC first step.
CC -!- INDUCTION: By amino acid starvation.
CC -!- SIMILARITY: BELONGS TO CLASS-I DAHP SYNTHETASE FAMILY.
CC -----
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CC -----
DR EMBL; X61107; CAA43419.1; -.
DR EMBL; L20296; AAA65607.1; -.
DR EMBL; Z36118; CAA85212.1; -.
DR PIR; S38185; S38185.
DR HSSP; P00886; IQR7.
DR SGD; S0000453; ARO4.
DR GO; GO:0003849; F:2-dehydro-3-deoxyphosphoheptonate aldolase . . . ; IDA.
DR InterPro; IPR006219; AroFGH.
DR InterPro; IPR006218; DAHP1/KDSA.
DR Pfam; PF00793; DAHP_synth_1; 1.
DR Prodom; PD005060; AroFGH; 1.
DR TIGRFAMs; TIGR00034; aroFGH; 1.
KW Aromatic amino acid biosynthesis; Lyase; Multigene family.
SQ SEQUENCE 370 AA; 39749 MW; 594ED48F24175979 CRC64;

Query Match 37.7%; Score 52; DB 1; Length 370;
Best Local Similarity 47.6%; Pred. No. 2.4;
Matches 10; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRLRRMSDFEG 21
   : | | | | | : | | | | | :
Db 80 DLPAQAQVEYALRLKLSDELKG 100

RESULT 7
AP3_ARATH STANDARD; PRT; 232 AA.
ID AP3_ARATH STANDARD; PRT; 232 AA.
AC P35632; Q39003; Q8LE79; Q9SQ14; Q9SQ15; Q9SQ16; Q9SQ17;
AC Q9SQ18; Q9SQ19; Q9SQ20; Q9SQ21; Q9SQ22; Q9SQ13;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Floral homeotic protein APETALA3.
GN AP3 OR AP3G54340 OR T12E18_30.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Petal;
RX MEDLINE=92154682; PubMed=1346756;
RA Jack T., Brockman L.I., Meyerowitz E.M.;
RT "The homeotic gene APETALA3 of Arabidopsis thaliana encodes a MADS
RT box and is expressed in petals and stamens.";
RL Cell 68:683-697(1992).
```

RN RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Landsberg erecta;  
 RA MEDLINE=95036018; PubMed=7948893;  
 RA Okamoto H., Yano A., Shiraishi H., Okada K., Shimura Y.;  
 RT "Genetic complementation of a floral homeotic mutation, *apetala3*,  
 with an Arabidopsis thaliana gene homologous to *DEFICIENS* of  
 RT *Antirrhinum majus*.";  
 RL Plant Mol. Biol. 26:465-472(1994).  
 RN [3]  
 RN RP SEQUENCE FROM N.A., AND VARIANTS.  
 RC STRAIN=cv. Bla-1, cv. Bretagny, cv. Bs-1, cv. Bu-0, cv. Bu-2,  
 RC cv. Chi-1, cv. Co-1, cv. Columbia, cv. Corsacalla-1, cv. Cvi-0,  
 RC cv. Gr-3, cv. J1-1, cv. Kas-1, cv. Kent, cv. Landsberg erecta,  
 RC cv. Li-3, cv. Li-8, and cv. Lisse;  
 RX MEDLINE=99126449; PubMed=9927474;  
 RA Purugganan M.D., Suddith J.I.;  
 RT "Molecular population genetics of floral homeotic loci: departures  
 from the equilibrium-neutral model at the *APETALA3* and *PISTILLATA*  
 genes of Arabidopsis thaliana.";  
 RL Genetics 151:839-848(1999).  
 RN [4]  
 RN RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=21016720; PubMed=11130713;  
 RA Salanoubat M., Lemcke K., Rieger M., Ansoorge W., Unselid M.,  
 RA Partmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,  
 RA Delsen M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,  
 RA De Simone V., Choise N., Artiguenave F., Robert C., Brottier P.,  
 RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Queflier F.,  
 RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,  
 RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,  
 RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,  
 RA Vezzi A., D'Angelo M., Pallavicini A., Toppi S., Simonati B.,  
 RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G.,  
 RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,  
 RA Navarro P., Colliado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,  
 RA Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,  
 RA De Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,  
 RA Monfort A., Argirion A., Flores M., Liguori R., Vitale D.,  
 RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,  
 RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,  
 RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,  
 RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,  
 RA Pai G., Miltischer J., Sellers P., Gill J.E., Feldblyum T.V.,  
 RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,  
 RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,  
 RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,  
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,  
 RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,  
 RA Watanabe A., Yamada M., Yasuda M., Tabata S.;  
 RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis  
 thaliana.";  
 RL Nature 408:820-822(2000).  
 RN [5]  
 RN RP SEQUENCE FROM N.A.  
 RA Prover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,  
 RA Feldmann K.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RN RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;  
 RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the  
 RT SSP consortium (Salk/stanford/PGECC).";  
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RN RP SEQUENCE OF 36-128 FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=99311297; PubMed=10382288;  
 RA Brunel D., Froger N., Pelletier G.;  
 RT "Development of amplified consensus genetic markers (ACGM) in Brassica  
 napus from Arabidopsis thaliana sequences of known biological  
 function.";  
 RL Genome 42:387-402(1999).  
 RN [8]  
 RN RP FUNCTION.  
 RX PubMed=8565821;  
 RA Krizek B.A., Meyerowitz E.M.;  
 RT "The Arabidopsis homeotic genes *APETALA3* and *PISTILLATA* are sufficient  
 to provide the B class organ identity function.";  
 RL Development 122:11-22(1996).  
 RN [9]  
 RN RP CHARACTERIZATION.  
 RX PubMed=8643482;  
 RA Riechmann J.L., Krizek B.A., Meyerowitz E.M.;  
 RT "Dimerization specificity of Arabidopsis MADS domain homeotic proteins  
*APETALA1*, *APETALA3*, *PISTILLATA*, and *AGAMOUS*.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:4793-4798(1996).  
 RN [10]  
 RN RP GENETIC REGULATION.  
 RX PubMed=11283333;  
 RA Ng M., Yanoofsky M.F.;  
 RT "Activation of the Arabidopsis B class homeotic genes by *APETALA1*.";  
 RL Plant Cell 13:739-753(2001).  
 RN [11]  
 RN RP CHARACTERIZATION.  
 RX PubMed=11206550;  
 RA Honma T., Goto K.;  
 RT "Complexes of MADS-box proteins are sufficient to convert leaves into  
 floral organs.";  
 RL Nature 409:525-529(2001).  
 CC -!- FUNCTION: Probable transcription factor involved in the genetic  
 control of flower development. Is required for normal development  
 of petals and stamens in the wild-type flower. Forms an  
 heterodimer with *PISTILLATA* that is required for autoregulation of  
 both *AP3* and *PI* genes. *AP3/PI* heterodimer interacts with *APETALA1*  
 or *SEPALLATA3* to form a ternary complex that could be responsible  
 for the regulation of the genes involved in the flower  
 development.  
 CC -!- SUBUNIT: Forms an heterodimer with *PISTILLATA*, capable of binding  
 to CARG-box sequences. *AP3/PI* heterodimer binds *AP1* or *SEP3* to  
 form complexes.  
 CC -!- SUBCELLULAR LOCATION: Nuclear.  
 CC -!- TISSUE SPECIFICITY: Expressed in petals and stamens.  
 CC -!- INDUCTION: Positively regulated by the meristem identity proteins  
*APETALA1* and *LEAFY* with the cooperation of UFO.  
 CC -!- MISCELLANEOUS: Mutations in *AP3* cause transformation of petals  
 into sepals and stamens into carpels.  
 CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION  
 FACTORS.  
 CC -!- SIMILARITY: Contains 1 k-box dimerization domain.  
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 CC -----  
 DR EMBL; M86357; AAA32740.1; -  
 DR EMBL; D21125; BAA04665.1; -  
 DR EMBL; AF115798; AAD51887.1; -  
 DR EMBL; AF115799; AAD51888.1; -  
 DR EMBL; AF115800; AAD51889.1; -  
 DR EMBL; AF115801; AAD51890.1; -  
 DR EMBL; AF115802; AAD51891.1; -  
 DR EMBL; AF115803; AAD51892.1; -  
 DR EMBL; AF115804; AAD51893.1; -  
 DR EMBL; AF115805; AAD51894.1; -  
 DR EMBL; AF115806; AAD51895.1; -  
 DR EMBL; AF115807; AAD51896.1; -  
 DR EMBL; AF115808; AAD51897.1; -  
 DR EMBL; AF115809; AAD51898.1; -

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DR EMBL; AF115810; AAD51899.1; -.
DR EMBL; AF115811; AAD51900.1; -.
DR EMBL; AF115812; AAD51901.1; -.
DR EMBL; AF115813; AAD51902.1; -.
DR EMBL; AF115814; AAD51903.1; -.
DR EMBL; AL132971; CAB81799.1; -.
DR EMBL; AY087369; AAM64919.1; -.
DR EMBL; AY070397; AAL49893.1; -.
DR EMBL; AY142590; AAN13159.1; -.
DR EMBL; AF056541; AAD41557.1; -.
DR PIR; A42095; A42095.
DR HSP; P11746; 1MM.
DR TRANSFAC; T01776; -.
DR InterPro; IPR002487; TF_Xbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS00666; MADS_BOX_2; 1.
KW Flowering; Transcription regulation; Activator; Developmental protein;
KW Nuclear protein; DNA-binding; Coiled coil; Polymorphism.
FT DOMAIN 3 57 MADS.
FT DOMAIN 93 165 K-BOX.
FT DOMAIN 75 164 COILED COIL (POTENTIAL).
FT VARIANT 31 31 K -> R (in strain cv. Lisse).
FT VARIANT 47 47 M -> T (in strain cv. Bretagne).
FT VARIANT 61 61 N -> D (in strain cv. Corsacalla-1).
FT VARIANT 73 73 T -> S (in strain cv. Li-8).
FT VARIANT 109 109 L -> V (in strain cv. Kas-1).
FT VARIANT 115 115 E -> K (in strains cv. Chi-1 and cv. Gr-3).
Query Match 37.0%; Score 51; DB 1; Length 232;
Best Local Similarity 44.4%; Pred. No. 2.1;
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;

QY 6 QRYG-----RELRLMSDEFGSFK 24
||| :|||: |||: |||
Db 107 QRLGCLDELDIQELRLDEMENTFK 133

RESULT 8
CE05_MOUSE
ID CE05_MOUSE STANDARD; PRT; 851 AA.
AC Q8K2H3;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein C5orf5 homolog.
GN C5ORF5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SIMILARITY: Belongs to the FAM13 family.
CC -!- SIMILARITY: Contains 1 Rho-GAP domain.
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CC EMBL; BC031465; AAH31465.1; -.
DR InterPro; IPR000198; RhoGAP.
DR Pfam; PF00620; RhoGAP; 1.
DR SMART; SM00324; RhoGAP; 1.
DR PROSITE; PS50238; RHO-GAP; 1.
KW GTPase activation.
FT DOMAIN 23 212 RHO-GAP.
FT DOMAIN 189 256 GLU-RICH.
SQ SEQUENCE 851 AA; 97054 MW; C2B26669FB6DB2CE CRC64;
Query Match 36.2%; Score 50; DB 1; Length 851;
Best Local Similarity 45.5%; Pred. No. 12;
Matches 10; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 2 LWAAQRYGRELRMSDEFGSF 23
||| :|||: |||: |||
Db 784 LWKARAEKKLRKMLREFEAR 805

RESULT 9
MATK_LEDPA
ID MATK_LEDPA STANDARD; PRT; 506 AA.
AC O62992;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Maturase K (Intron maturase).
GN MATK.
OS Ledum palustre (Wild rosemary).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
OX NCBI_TaxID=75583;
RN [1]
RP SEQUENCE FROM N.A.
RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
RA Yukawa T.;
RT "Investigation of sectional relationships in the genus
RT Rhododendron (Ericaceae) based on matk sequences.";
RL Shokubutsu Kenkyu Zasshi 73:143-154(1998).
CC -!- FUNCTION: Probably assists in splicing chloroplast group II
CC introns (By similarity).
CC -!- SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK
CC SUBFAMILY.
-----
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CC EMBL; AB012751; BAA25872.1; -.

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DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_maturas2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW mRNA processing; Chloroplast.
SQ SEQUENCE 506 AA; 60412 MW; CFEA926307DAC85E CRC64;

Query Match      35.9%; Score 49.5; DB 1; Length 506;
Best Local Similarity 36.7%; Pred. No. 8.2;
Matches 11; Conservative 5; Mismatches 7; Indels 7; Gaps 1;

QY 2 LWAA-----QRYGRELRLMSDEFEFGSK 24
DB 393 VWAALSDSDIIFRGRYRNLSHYSGSLK 422

RESULT 10
MATK_RHOF
ID MATK_RHOF STANDARD; PRT; 506 AA.
AC 062984;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Maturase K (Intron maturase).
GN MATK.
OS Rhododendron ferrugineum (Alpenrose).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Ericales; Ericaceae; Rhododendron.
OX NCBI_TaxID=49622;
RN [1]
RP SEQUENCE FROM N.A.
RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
RA Yukawa T.;
RT "Investigation of sectional relationships in the genus
RT Rhododendron (Ericaceae) based on matk sequences.";
RL Shokubutsu Kenkyu Zasshi 73:143-154(1998).
CC -!- FUNCTION: Probably assists in splicing chloroplast group II
CC introns (By similarity).
CC -!- SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK
CC SUBFAMILY.
CC -----
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CC -----
DR EMBL; AB012741; BAA25862.1; -.
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_maturas2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW mRNA processing; Chloroplast.
SQ SEQUENCE 506 AA; 60534 MW; ADA4B25E92436E8 CRC64;

Query Match      35.9%; Score 49.5; DB 1; Length 506;
Best Local Similarity 36.7%; Pred. No. 8.2;
Matches 11; Conservative 5; Mismatches 7; Indels 7; Gaps 1;

QY 2 LWAA-----QRYGRELRLMSDEFEFGSK 24
DB 393 VWAALSDSDIIFRGRYRNLSHYSGSLK 422

RESULT 11
MATK_RHOTS
ID MATK_RHOTS STANDARD; PRT; 506 AA.
AC 062991;
DT 28-FEB-2003 (Rel. 41, Created)

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DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Maturase K (Intron maturase).
GN MATK.
OS Rhododendron tsusisophyllum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Ericales; Ericaceae; Rhododendron.
OX NCBI_TaxID=49629;
RN [1]
RP SEQUENCE FROM N.A.
RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
RA Yukawa T.;
RT "Investigation of sectional relationships in the genus
RT Rhododendron (Ericaceae) based on matk sequences.";
RL Shokubutsu Kenkyu Zasshi 73:143-154(1998).
CC -!- FUNCTION: Probably assists in splicing chloroplast group II
CC introns (By similarity).
CC -!- SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK
CC SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB012750; BAA25871.1; -.
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_maturas2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW mRNA processing; Chloroplast.
SQ SEQUENCE 506 AA; 60569 MW; AEEL2FF8809C223E CRC64;

Query Match      35.9%; Score 49.5; DB 1; Length 506;
Best Local Similarity 36.7%; Pred. No. 8.2;
Matches 11; Conservative 5; Mismatches 7; Indels 7; Gaps 1;

QY 2 LWAA-----QRYGRELRLMSDEFEFGSK 24
DB 393 VWAALSDSDIIFRGRYRNLSHYSGSLK 422

RESULT 12
RMUC_PSEAE
ID RMUC_PSEAE STANDARD; PRT; 453 AA.
AC Q914U3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA recombination protein rmuc homolog.
GN RMUC OR PA1031.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Huftagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RN Nature 406:959-964(2000).

```



Matches 8; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 4 AAORYGRELREMSDEEGSFKGL 26  
|::| |::| |::| |::| : : :  
Db 111 ACEKYEREIRSATQDFDLAILGM 133

## RESULT 15

THRC\_SOLTU STANDARD; PRT; 519 AA.  
AC Q9MT28;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Threonine synthase, chloroplast precursor (EC 4.2.3.1) (TS).  
OS Solanum tuberosum (Potato).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; lamiids; Solanales; Solanaceae; Solanum.  
OX NCBI\_TaxID=4113;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=leaf;  
RX PubMed=10940468;  
RA Casazza A.P., Basner A., Hoefgen R., Hesse H.;  
RT "Expression of threonine synthase from Solanum tuberosum L. is not  
RT metabolically regulated by photosynthesis-related signals or by  
RT nitrogenous compounds";  
RL Plant Sci. 157:43-50(2000).  
CC -! CATALYTIC ACTIVITY: O-phospho-L-homoserine + H(2)O = L-threonine +  
CC phosphate.  
CC -! COFACTOR: Pyridoxal phosphate (By similarity).  
CC -! ENZYME REGULATION: Allosterically activated by S-adenosyl-  
CC methionine (SAM) (By similarity).  
CC -! PATHWAY: Threonine biosynthesis; last step.  
CC -! SUBUNIT: Homodimer (By similarity).  
CC -! SUBCELLULAR LOCATION: Chloroplast (By similarity).  
CC -! SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.  
-----  
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-----  
DR EMBL; AF082894; AAF74984.1; -.  
DR HSSP; Q9S7B5; IESX.  
DR InterPro; IPR001926; B6\_enzyme\_beta.  
DR InterPro; IPR000634; S/T\_dehydratase.  
DR InterPro; IPR004450; Thr\_synthase.  
DR Pfam; PF00291; PALP; 1.  
DR TIGRFAMs; TIGR00260; thrc; 1.  
DR PROSITE; PS00165; DEHYDRATASE\_SER\_THR; 1.  
KW Threonine biosynthesis; Lyase; Pyridoxal phosphate; Allosteric enzyme;  
KW Chloroplast; Transit peptide.  
FT TRANSIT 1 40 CHLOROPLAST (BY SIMILARITY).  
FT CHAIN 41 519 THREONINE SYNTHASE.  
FT BINDING 196 196 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
SQ SEQUENCE 519 AA; 57412 MW; 114C0979CD231464 CRC64;

Query Match 34.8%; Score 48; DB 1; Length 519;  
Best Local Similarity 35.3%; Pred. No. 14;  
Matches 12; Conservative 6; Mismatches 8; Indels 8; Gaps 1;

QY 1 NLWAAQRYGRELREMSD-----EFGSFKGL 26  
|::| |::| |::| |::| : : :  
Db 165 NLFWAERFGKQLGMDTLWVKHCGISHGTSFKDL 198

Search completed: September 15, 2003, 17:22:59  
Job time : 7.12857 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 15, 2003, 17:17:31 ; Search time 28.2286 Seconds  
(without alignments)  
237.680 Million cell updates/sec

Title: US-09-544-664-1  
Perfect score: 138  
Sequence: 1 NLWAAQRYGRELRLMSDEFEGSFYKGL 26

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	87	63.0	146	13 Q9I9N2	Q9I9N2 brachydanio
2	53	38.4	196	16 Q8VJS3	Q8VJS3 mycobacteri
3	53	38.4	223	16 Q10843	Q10843 mycobacteri
4	53	38.4	946	11 Q8K016	Q8K016 mus musculu
5	52	37.7	471	17 Q8ZY71	Q8ZY71 pyrobaculum
6	51	37.0	231	10 Q9SEGO	Q9SEGO arabidopsis
7	51	37.0	232	10 Q9SQ20	Q9SQ20 arabidopsis
8	51	37.0	232	10 Q9SQ22	Q9SQ22 arabidopsis
9	51	37.0	232	10 Q9SQ17	Q9SQ17 arabidopsis
10	51	37.0	232	10 Q9SQ19	Q9SQ19 arabidopsis
11	51	37.0	232	10 Q9SQ21	Q9SQ21 arabidopsis
12	51	37.0	232	10 Q8LB79	Q8LB79 arabidopsis
13	51	37.0	232	10 Q9SQ16	Q9SQ16 arabidopsis
14	51	37.0	232	10 Q9SQ15	Q9SQ15 arabidopsis
15	51	37.0	232	10 Q9SQ18	Q9SQ18 arabidopsis
16	51	37.0	232	10 Q9SQ18	Q9SQ18 arabidopsis

17 50.5 36.6 904 2 Q9KGW3  
18 50.5 36.6 909 16 Q8E134  
19 50 36.2 168 11 Q8K316  
20 50 36.2 283 15 Q37056  
21 50 36.2 374 17 Q9HN29  
22 50 36.2 516 10 Q9SSP5  
23 50 36.2 851 11 Q8K2H3  
24 49.5 35.9 153 5 Q9UB33  
25 49.5 35.9 401 5 Q97407  
26 49.5 35.9 505 8 Q47148  
27 49.5 35.9 506 8 Q47149  
28 49.5 35.9 506 8 Q47171  
29 49.5 35.9 506 8 Q63960  
30 49.5 35.9 506 8 Q62982  
31 49.5 35.9 506 8 Q62975  
32 49.5 35.9 506 8 Q62972  
33 49.5 35.9 506 8 Q62989  
34 49.5 35.9 506 8 Q62978  
35 49.5 35.9 506 8 Q47155  
36 49.5 35.9 506 8 Q47152  
37 49.5 35.9 506 8 Q47173  
38 49.5 35.9 506 8 Q62990  
39 49.5 35.9 506 8 Q62974  
40 49.5 35.9 506 8 Q62993  
41 49.5 35.9 506 8 Q47170  
42 49.5 35.9 506 8 Q47174  
43 49.5 35.9 506 8 Q62983  
44 49.5 35.9 506 8 Q62980  
45 49.5 35.9 506 8 Q62981

## ALIGNMENTS

RESULT 1  
Q9I9N2 PRELIMINARY; PRT; 146 AA.  
ID Q9I9N2  
AC Q9I9N2;  
DT 01-OCT-2000 (TRENBLrel. 15, Created)  
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)  
DE Bad.  
GN BAD.  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20373792; PubMed=10917738;  
RA Inohara N., Nunez G.;  
RT "Genes with homology to mammalian apoptosis regulators identified in zebrafish."  
RL Cell Death Differ. 7:509-510(2000).  
DR EMBL; AF231017; AAF66962.2; -;  
DR HSSP; Q92934; 1G5J.  
DR ZFIN; ZDB-GENE-000616-1; bad.  
SQ SEQUENCE 146 AA; 16546 MW; 28A5650BB5107ECB CRC64;

Query Match 63.0%; Score 87; DB 13; Length 146;  
Best Local Similarity 65.2%; Pred. No. 5.3e-05;  
Matches 15; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 LWAAQRYGRELRLMSDEFEGSFYK 24  
|||||:|||||:  
Db 89 LWAAQRYGRELRLMSDEFEGSFYK 111

RESULT 2  
Q8VJS3 PRELIMINARY; PRT; 196 AA.  
ID Q8VJS3  
AC Q8VJS3;



```

Query Match          37.7%; Score 52; DB 17; Length 471;
Best Local Similarity 41.7%; Pred. No. 29;
Matches 10; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 3 WAAQRYGRELRLMSDEFGSKGL 26
DB 404 WQHSGNGRELRLAEETAGERAL 427

RESULT 6
Q9SEGO PRELIMINARY; PRT; 231 AA.
AC Q9SEGO;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Apetala3 (Fragment).
OS Arabidopsis lyrata.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=59689;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99404148; PubMed=10474900;
RA Layton-Rauh A.L., Buckler E.S. IV, Purugganan M.D.;
RT "Patterns of molecular evolution among paralogous floral homeotic
  genes.";
RL Mol. Biol. Evol. 16:1037-1045(1999).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
  FACTORS.
DR EMBL; AF143380; AAF25590.1; -.
DR HSSP; P11746; 1MNM.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00666; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription; Transcription regulation.
FT NON_TER 231 231
SQ SEQUENCE 231 AA; 27176 MW; A67CAE1EBDB8F7AA CRC64;

Query Match          37.0%; Score 51; DB 10; Length 231;
Best Local Similarity 44.4%; Pred. No. 18;
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;

QY 6 QRYG-----RELRLMSDEFGSK 24
DB 107 QRLGECDELDIQELRLLEDEMENTFK 133

RESULT 7
Q9SQ20 PRELIMINARY; PRT; 232 AA.
AC Q9SQ20;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Floral homeotic protein AP3.
GN APETALA3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Corscalla;
RX MEDLINE=99126449; PubMed=9927474;
RA Purugganan M.D., Suddith J.I.;
RT "Molecular population genetics of floral homeotic loci. Departures
  from the equilibrium-neutral model at the APETALA3 and PISTILLATA
  genes of Arabidopsis thaliana.";
RL Genetics 151:839-848(1999).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
  FACTORS.
DR EMBL; AF115801; AAD51890.1; -.
DR HSSP; P11746; 1MNM.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SQ SEQUENCE 232 AA; 27267 MW; 42A852D697E22A65 CRC64;

Query Match          37.0%; Score 51; DB 10; Length 232;
Best Local Similarity 44.4%; Pred. No. 18;
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;

QY 6 QRYG-----RELRLMSDEFGSK 24
DB 107 QRLGECDELDIQELRLLEDEMENTFK 133

RESULT 8
Q9SQ22 PRELIMINARY; PRT; 232 AA.
AC Q9SQ22;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Floral homeotic protein AP3.
GN APETALA3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Li-8;
RX MEDLINE=99126449; PubMed=9927474;
RA Purugganan M.D., Suddith J.I.;
RT "Molecular population genetics of floral homeotic loci. Departures
  from the equilibrium-neutral model at the APETALA3 and PISTILLATA
  genes of Arabidopsis thaliana.";
RL Genetics 151:839-848(1999).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
  FACTORS.
DR EMBL; AF115801; AAD51890.1; -.
DR HSSP; P11746; 1MNM.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SQ SEQUENCE 232 AA; 27342 MW; BDFDCB59B73F4601 CRC64;

Query Match          37.0%; Score 51; DB 10; Length 232;
Best Local Similarity 44.4%; Pred. No. 18;
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;

QY 6 QRYG-----RELRLMSDEFGSK 24
DB 107 QRLGECDELDIQELRLLEDEMENTFK 133

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Db      107 QRLGECLELDIQELRLLEDEMENTFK 133
          ||| | :|||: || | :||
          107 QRLGECLELDIQELRLLEDEMENTFK 133

RESULT 9
Q9SQ17 ID Q9SQ17 PRELIMINARY; PRT; 232 AA.
AC Q9SQ17;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Floral homeotic protein AP3.
GN APETALA3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Lisse;
RX MEDLINE=99126449; PubMed=9927474;
RA Purugganan M.D., Suddith J.I.;
RT "Molecular population genetics of floral homeotic loci. Departures
RT from the equilibrium-neutral model at the APETALA3 and PISTILLATA
RT genes of Arabidopsis thaliana.";
RL Genetics 151:839-848(1999).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
DR EMBL; AF115809; AAD51898.1; -.
DR HSSP; P11746; IMNM.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; SM00432; MADS; 1.
DR SMART; PR00404; MADSDOMAIN.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS00350; MADS_BOX_2; 1.
DR PROSITE; PS00666; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SQ SEQUENCE 232 AA; 27284 MW; 04FCFC55B73C7729 CRC64;

Query Match 37.0%; Score 51; DB 10; Length 232;
Best Local Similarity 44.4%; Pred. No. 18;
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;

QY 6 QRYG-----RELRRMSDEFEGSFK 24
||| | :|||: || | :||
Db 107 QRLGECLELDIQELRLLEDEMENTFK 133

RESULT 10
Q9SQ19 ID Q9SQ19 PRELIMINARY; PRT; 232 AA.
AC Q9SQ19;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Floral homeotic protein AP3.
GN APETALA3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Bretagny;
RX MEDLINE=99126449; PubMed=9927474;
RA Purugganan M.D., Suddith J.I.;
RT "Molecular population genetics of floral homeotic loci. Departures
RT from the equilibrium-neutral model at the APETALA3 and PISTILLATA

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RT genes of Arabidopsis thaliana.";
RL Genetics 151:839-848(1999).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
DR EMBL; AF115807; AAD51896.1; -.
DR HSSP; P11746; IMNM.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; SM00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SQ SEQUENCE 232 AA; 27311 MW; 71AE593FB8A67EC3 CRC64;

Query Match 37.0%; Score 51; DB 10; Length 232;
Best Local Similarity 44.4%; Pred. No. 18;
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;

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Db 107 QRLGECLELDIQELRLLEDEMENTFK 133

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AC Q9SQ21;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Floral homeotic protein AP3.
GN APETALA3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Kent;
RX MEDLINE=99126449; PubMed=9927474;
RA Purugganan M.D., Suddith J.I.;
RT "Molecular population genetics of floral homeotic loci. Departures
RT from the equilibrium-neutral model at the APETALA3 and PISTILLATA
RT genes of Arabidopsis thaliana.";
RL Genetics 151:839-848(1999).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
DR EMBL; AF115805; AAD51894.1; -.
DR HSSP; P11746; IMNM.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SQ SEQUENCE 232 AA; 27286 MW; 66976305B88B63E3 CRC64;

Query Match 37.0%; Score 51; DB 10; Length 232;
Best Local Similarity 44.4%; Pred. No. 18;
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;

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||| | :|||: || | :||
Db 107 QRLGECLELDIQELRLLEDEMENTFK 133

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DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)  
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)  
DE Floral homeotic protein APETALA3 (AP3).  
OS Arabidopsis thaliana (Mouse-ear cross).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
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OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Haas B.J., Volfovsky N., Town C.D., Troupkhan M., Alexandrov N.,  
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;  
RT "Full-length messenger RNA sequences greatly improve genome  
RT annotation.";  
RL Genome Biol. 0:0-0(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Brover V., Troupkhan M., Alexandrov N., Lu Y.-P., Flavell R.,  
RA Feldmann K.;  
RT "Full-length cDNA from Arabidopsis thaliana.";  
RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION  
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DR InterPro; IPR002100; TF\_MADSbox.  
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DR Pfam; PF00319; SRF-TF; 1.  
DR PRINTS; PR00404; MADSDOMAIN.  
DR SMART; SM00432; MADS; 1.  
DR PROSITE; PS00350; MADS\_BOX\_1; 1.  
DR PROSITE; PS50066; MADS\_BOX\_2; 1.  
DR DNA-binding; Nuclear protein; Transcription; Transcription regulation.  
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SQ SEQUENCE 232 AA; 27339 MW; CC90703F959CFAD5 CRC64;  
Query Match 37.0%; Score 51; DB 10; Length 232;  
Best Local Similarity 44.4%; Pred. No. 18;  
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;  
Qy 6 QRYG-----RELRRMSDEFECSFK 24  
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Db 107 QRLGECLELDIQELRLLEDEMENTFK 133  
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AC Q9SQ16;  
DT 01-MAY-2000 (TREMELrel. 13, Created)  
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)  
DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)  
DE Floral homeotic protein AP3.  
GN APETALA3.  
OS Arabidopsis thaliana (Mouse-ear cross).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=cv. Lisse;  
RX MEDLINE=99126449; PubMed=9927474;  
RA Purugganan M.D., Suddith J.I.;  
RT "Molecular population genetics of floral homeotic loci. Departures  
RT from the equilibrium-neutral model at the APETALA3 and PISTILLATA  
genes of Arabidopsis thaliana.";  
RL Genetics 151:839-848(1999).  
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION  
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DR HSSP; P11746; LMNM.  
DR InterPro; IPR002487; TF\_Kbox.  
DR InterPro; IPR002100; TF\_MADSbox.  
DR Pfam; PF01486; K-box; 1.  
DR Pfam; PF00319; SRF-TF; 1.  
DR PRINTS; PR00404; MADSDOMAIN.  
DR SMART; SM00432; MADS; 1.  
DR PROSITE; PS00350; MADS\_BOX\_1; 1.  
DR PROSITE; PS50066; MADS\_BOX\_2; 1.  
KW DNA-binding; Nuclear protein; Transcription; Transcription regulation.  
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Query Match 37.0%; Score 51; DB 10; Length 232;  
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Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;  
Qy 6 QRYG-----RELRRMSDEFECSFK 24  
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Db 107 QRVGECLELDIQELRLLEDEMENTFK 133

Genetics 151:839-848(1999).  
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DR Pfam; PF01486; K-box; 1.  
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DR PRINTS; PR00404; MADSDOMAIN.  
DR SMART; SM00432; MADS; 1.  
DR PROSITE; PS00350; MADS\_BOX\_1; 1.  
DR PROSITE; PS50066; MADS\_BOX\_2; 1.  
KW DNA-binding; Nuclear protein; Transcription; Transcription regulation.  
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Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;  
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Db 107 QRLGECLELDIQELRLLEDEMENTFK 133  
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AC Q9SQ15;  
DT 01-MAY-2000 (TREMELrel. 13, Created)  
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)  
DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)  
DE Floral homeotic protein AP3.  
GN APETALA3.  
OS Arabidopsis thaliana (Mouse-ear cross).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=cv. Kas-1;  
RX MEDLINE=99126449; PubMed=9927474;  
RA Purugganan M.D., Suddith J.I.;  
RT "Molecular population genetics of floral homeotic loci. Departures  
RT from the equilibrium-neutral model at the APETALA3 and PISTILLATA  
genes of Arabidopsis thaliana.";  
RL Genetics 151:839-848(1999).  
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DR SMART; SM00432; MADS; 1.  
DR PROSITE; PS00350; MADS\_BOX\_1; 1.  
DR PROSITE; PS50066; MADS\_BOX\_2; 1.  
KW DNA-binding; Nuclear protein; Transcription; Transcription regulation.  
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Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;  
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Db 107 QRVGECLELDIQELRLLEDEMENTFK 133

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DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Floral homeotic protein AP3.
GN APETALA3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. GR-3, and cv. CHI-1;
RX MEDLINE=99126449; PubMed=927474;
RA Purgganan M.D., Suddith J.I.;
RT "Molecular population genetics of floral homeotic loci. Departures
RT from the equilibrium-neutral model at the APETALA3 and PISTILLATA
RT genes of Arabidopsis thaliana.";
RL Genetics 151:839-848(1999).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
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DR EMBL; AF115798; AAD51887.1; -.
DR HSSP; P11746; 1MNM.
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DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
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KW DNA-binding; Nuclear protein; Transcription; Transcription regulation.
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Query Match 37.0%; Score 51; DB 10; Length 232;
Best Local Similarity 44.4%; Pred. No. 18;
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;

QY 6 QRYG-----RELRLMSDEFEQSFK 24
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Db 107 QRLGCLDKLDIQELRLRLEDEMENTFK 133

Search completed: September 15, 2003, 17:25:45
Job time : 30.2286 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 23, 2003, 09:43:16 : Search time 86 Seconds  
(without alignments)  
49,833 Million cell updates/sec

Title: US-09-544-664B-2

Perfect score: 142

Sequence: 1 NLWAAQYEGRELRLMSDFVDSFKKGL (27)

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	137	96.5	166	18 AAW32476	BBC6 protein for r
2	137	96.5	168	19 AAW55779	Human Bcl-xL/Bcl-2
3	137	96.5	168	21 AAB13512	Human cell prolif
4	137	96.5	168	22 AAB70368	Human BAD mutant a
5	137	96.5	168	22 AAB48287	Human BAD protein.
6	137	96.5	168	22 AAG67688	Amino acid sequenc
7	137	96.5	168	24 ABR39081	Human BAD protein
8	137	96.5	207	23 ABP41630	Human ovarian anti
9	127	89.4	25	23 ABP56161	PTPC-interacting T

10	127	89.4	25	23	ABG78484	Mutant Bcl2 compet
11	127	89.4	25	23	AAU78610	Human Bad peptide
12	124	87.3	25	23	ABG78490	Mutant Bcl2 compet
13	124	87.3	25	23	AAU78617	Human Bad peptide
14	123	86.6	25	23	ABG78488	Mutant Bcl2 compet
15	123	86.6	25	23	ABG78489	Mutant Bcl2 compet
16	123	86.6	25	23	AAU78615	Human Bad peptide
17	123	86.6	25	23	AAU78616	Human Bad peptide
18	122	85.9	24	23	AAU78627	Human Bad peptide
19	122	85.9	25	23	ABG78486	Mutant Bcl2 compet
20	122	85.9	25	23	ABG78493	Mutant Bcl2 compet
21	122	85.9	25	23	ABG78497	Mutant Bcl2 compet
22	122	85.9	25	23	AAU78612	Human Bad peptide
23	122	85.9	25	23	AAU78620	Human Bad peptide
24	122	85.9	25	23	AAU78624	Human Bad peptide
25	121	85.2	25	23	ABG78485	Mutant Bcl2 compet
26	121	85.2	25	23	ABG78492	Mutant Bcl2 compet
27	121	85.2	25	23	AAU78611	Human Bad peptide
28	121	85.2	25	23	AAU78619	Human Bad peptide
29	119	83.8	25	23	ABG78491	Mutant Bcl2 compet
30	119	83.8	25	23	ABG78498	Mutant Bcl2 compet
31	119	83.8	25	23	AAU78618	Human Bad peptide
32	119	83.8	25	23	AAU78625	Human Bad peptide
33	117	82.4	23	23	AAU78628	Human Bad peptide
34	116	81.7	26	21	AAU96321	Mammalian Bad Bcl-
35	116	81.7	26	22	AAU70371	BAD BH3 consensus
36	113	79.6	25	23	ABG78487	Mutant Bcl2 compet
37	113	79.6	25	23	AAU78613	Human Bad peptide
38	112	78.9	25	23	ABG78495	Mutant Bcl2 compet
39	112	78.9	25	23	AAU78629	Human Bad peptide
40	111	78.2	22	23	AAU78622	Human Bad peptide
41	110	77.5	25	23	ABG78496	Mutant Bcl2 compet
42	110	77.5	25	23	AAU78623	Human Bad peptide
43	109	76.8	26	21	AAU37001	Bcl2 polypeptide B
44	109	76.8	26	21	AAU37002	Bcl2 polypeptide B
45	109	76.8	27	21	AAU37003	Bcl2 polypeptide B

ALIGNMENTS

RESULT 1  
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ID AAW32476 standard; Protein; 166 AA.  
XX  
AC AAW32476;  
XX  
DT 15-JAN-1998 (first entry)  
XX  
DE BBC6 protein for regulating cell death.  
KW BBC6 gene; cell death; cell cycle; Bcl2; human.  
XX  
OS Homo sapiens.  
XX  
PN US5663316-A.  
XX  
PD 02-SEP-1997.  
XX  
PF 18-JUN-1996; 96US-0665617.  
XX  
PR 18-JUN-1996; 96US-0665617.  
XX  
PA (CLON-) CLONTECH LAB INC.  
XX  
PI Xudong Y;  
XX  
DR WPI; 1997-447980/41.  
XX  
DR N-PSDB; AAT91561.  
XX  
PT Isolated BBC6 gene - encodes a protein that regulates cell death  
PT through interaction with Bcl-2  
XX

PS Claim 1; Column 11-12; 7pp; English.

XX The present sequence represents a protein of 166 amino acids. The  
CC sequence is disclosed as being a protein called Bcl-2 which regulates  
CC cell death through interaction with Bcl-2. The DNA may be used for the  
CC production of the recombinant protein, which can be used in unspecified  
CC therapeutic or diagnostic procedures, as a molecular weight marker, and  
CC to raise antibodies that can be used in unspecified diagnostic or  
CC therapeutic applications and to reduce or eliminate the biological  
CC activity of the Bcl-2 protein in vivo.

XX SQ Sequence 166 AA;

Query Match 96.5%; Score 137; DB-18; Length 166;  
Best Local Similarity 96.3%; Pred. No. 1.1e-12;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDFVDSFKKGL 27  
|||||  
Db 101 NLWAAQRYGRELRRMSDFVDSFKKGL 127

RESULT 2

AAW55779  
ID AAW55779 standard; Protein; 168 AA.

XX AAW55779;

XX 17-JUL-1998 (first entry)

XX Human Bcl-xL/Bcl-2 associated death promoting polypeptide.

XX Human; Bcl-xL/Bcl-2 associated death promoting polypeptide; Bad;  
KW programmed cell death; apoptosis.

XX Homo sapiens.

XX WO9812328-A2.

XX 26-MAR-1998.

XX 18-SEP-1997; 97WO-US16991.

XX 20-SEP-1996; 96US-0717123.

XX (IDUN-) IDUN PHARM INC.

XX Horne WA, Oltersdorf T;

XX WPI; 1998-217267/19.

XX N-PSDB; AAV25877.

XX Bad gene mediating apoptosis - used to develop products for treating  
PT e.g. neurodegenerative disease, cancers or autoimmune disease

XX Claim 8; Fig 1; 41pp; English.

XX The present sequence is the human Bcl-xL/Bcl-2 associated  
CC death promoting polypeptide, Bad, the binding of which to Bcl-xL  
CC results in the induction of programmed cell death, i.e. apoptosis.  
CC Bad can be used in screening assays for compounds to treat or  
CC prevent diseases characterised by apoptotic cell death, such as  
CC neurodegenerative disorders, e.g. Alzheimer's and Parkinson's  
CC disease, amyotrophic lateral sclerosis, retinitis pigmentosa and  
CC cerebellar degeneration, and myelodysplastic syndromes, e.g.  
CC aplastic anaemia and ischaemic injury including myocardial  
CC infarction, stroke and reperfusion injury. Assays can also be  
CC used to obtain apoptosis enhancing compounds to treat or prevent  
CC diseases characterised by the loss of apoptotic cell death, such as  
CC cancers, e.g. lymphoma and hormone dependent tumours, autoimmune  
CC diseases, e.g. systemic lupus erythematosus and immune-mediated  
CC glomerulonephritis and viral infections, e.g. herpesvirus,  
CC poxvirus or adenovirus infection. Bad can also be used for

CC detection and diagnosis.

XX SQ Sequence 168 AA;

Query Match 96.5%; Score 137; DB-18; Length 168;  
Best Local Similarity 96.3%; Pred. No. 1.1e-12;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDFVDSFKKGL 27  
|||||  
Db 103 NLWAAQRYGRELRRMSDFVDSFKKGL 129

RESULT 3

AAB13512  
ID AAB13512 standard; protein; 168 AA.

XX AAB13512;

XX 02-NOV-2000 (first entry)

XX Human cell proliferation protein APOP-1.

XX Human; cell proliferation; APOP-1; cancer; inflammation; infection;  
KW trauma; neurodegenerative disease; ischaemic injury; wasting disease.

XX Homo sapiens.

XX US6080847-A.

XX 27-JUN-2000.

XX 04-DEC-1997; 97US-0985335.

XX 04-DEC-1997; 97US-0985335.

XX (INCY-) INCYTE PHARM INC.

XX Corley NC, Hillman JL, Yue H, Lal P, Shah P;

XX WPI; 2000-451230/39.

XX N-PSDB; AAA63332.

XX Novel polynucleotide and polypeptide sequences of proteins associated  
PT with cell proliferation for diagnosis, prevention and treatment of e.g.  
PT cancer, acquired immunodeficiency syndrome, and Parkinson's disease -

XX Example 8; Fig 1; 58pp; English.

XX The present sequence is the human APOP-1 protein. This protein, which  
CC shares structural and chemical homology with Bcl-2, is involved in cell  
CC proliferation. Its coding sequence was isolated by screening a synovial  
CC tissue cDNA library using a computer search for amino acid sequence  
CC alignments. The gene and protein can be used in the treatment of various  
CC cancers, disorders with associated inflammation such as Addison's  
CC disease, adult respiratory distress syndrome, allergies, anaemia, asthma,  
CC atherosclerosis, Crohn's disease, ulcerative colitis, diabetes mellitus,  
CC emphysema, glomerulonephritis, gout, Graves' disease, irritable bowel  
CC syndrome, lupus erythematosus, multiple sclerosis, myasthenia gravis,  
CC myocardial or pericardial inflammation, osteoporosis, rheumatoid  
CC arthritis, Sjogren's syndrome and autoimmune thyroiditis, complications  
CC of cancer, haemodialysis and extracorporeal circulation, infections,  
CC trauma, disorders with associated apoptosis including AIDS and other  
CC infectious and genetic immunodeficiencies, neurodegenerative diseases  
CC such as Alzheimer's disease and Parkinson's disease, ischaemic injuries  
CC such as myocardial infarction, and wasting diseases including cachexia.

XX SQ Sequence 168 AA;

Query Match 96.5%; Score 137; DB-18; Length 168;  
Best Local Similarity 96.3%; Pred. No. 1.1e-12;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLWAAQYGRELRMSDEFVDSFKKGL 27  
 DB 103 NLWAAQYGRELRMSDEFVDSFKKGL 129

## RESULT 4

AAB70368  
 ID AAB70368 standard; protein; 168 AA.

XX AC AAB70368;

DT 02-MAY-2001 (first entry)

DE Human BAD mutant amino acid sequence SEQ ID NO:1.

KW Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;  
 KW immunostimulant; neuroprotective; nootropic; antiischaemic; vulnery;  
 KW cytosolic; antiviral; antiarthritic; antiinflammatory; wound healing;  
 KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;  
 KW immunodeficiency disease; neurodegenerative disease; viral infection;  
 KW ischaemic cell death; reperfusion cell death; arthritis; infertility;  
 KW lymphoproliferative condition; inflammation; autoimmune disease.

XX OS Homo sapiens.

OS Synthetic.

XX PN WO200110888-A1.

XX PD 15-FEB-2001.

PF 30-MAY-2000; 2000WO-US11864.

PR 28-MAY-1999; 99US-0136783.

XX PA (APOP-) APOPTOSIS TECHNOLOGY INC.

XX PI Zhou X;

XX DR WPI; 2001-138734/14.

XX PT New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,  
 PT useful for screening for candidate compounds which induce or inhibit  
 PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or  
 PT Ser113 -

PS Claim 1; Page 147; 157pp; English.

XX The present invention describes an isolated or synthetic polypeptide  
 CC (I) comprising a less than full length amino acid sequence of a mutant  
 CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its  
 CC fragment, which contains amino acid substitutions at Ser118 of a human  
 CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine  
 CC BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,  
 CC nootropic, antiischaemic, vulnery, cytosolic, antiviral,  
 CC antiarthritic, antiinflammatory and immunosuppressive activities, and  
 CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and  
 CC polynucleotides can be used for screening candidate compounds and drugs  
 CC for activity that promote cell survival or apoptosis. Other uses include  
 CC inducing or inhibiting apoptosis in a cell. Candidate compounds  
 CC identified and (mutant) BAD polypeptides are useful in treating  
 CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell  
 CC death, reperfusion cell death, wound healing, cancer, viral infections,  
 CC lymphoproliferative conditions, arthritis, infertility, inflammation and  
 CC autoimmune diseases. The present sequence represents a specifically  
 CC claimed human BAD mutant amino acid sequence from the present invention.

XX SQ Sequence 168 AA;

Query Match 96.5%; Score 137; DB 22; Length 168;  
 Best Local Similarity 96.3%; Pred. No. 1.1e-12;  
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLWAAQYGRELRMSDEFVDSFKKGL 27

DB 103 NLWAAQYGRELRMSDEFVDSFKKGL 129

## RESULT 5

AAB48287  
 ID AAB48287 standard; protein; 168 AA.

XX AC AAB48287;

DT 02-APR-2001 (first entry)

DE Human Bad protein.

KW S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; 2F;  
 KW CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;  
 KW Bad; Bcl-2; tumour; cytosolic.

XX OS Homo sapiens.

XX PN WO200075184-A1.

XX PD 14-DEC-2000.

XX PF 05-JUN-2000; 2000WO-US15449.

XX PR 04-JUN-1999; 99US-0137494.

XX PA (UYVA) UNIV YALE.

XX PI Zhang H, Tsvetkov LM, Kondo T;

XX DR WPI; 2001-061703/07.

XX DR N-PSDB; AAC84599.

XX PT Modulating polypeptide levels in a cell, diagnosing and treating tumor,  
 PT involves altering levels of proteins such as S-phase kinase associated  
 PT proteins 1, 2 and cullin/CDC53 proteins -

XX PS Claim 5; Page 102-103; 162pp; English.

XX The invention relates to methods of altering the polypeptide levels in a  
 CC cell, using proteins selected from S-phase kinase associated proteins 1  
 CC and 2 (SKP1, SKP2), SKP2-like proteins (2F) and CUL-1 (a member of the  
 CC cullin/CDC53 family of proteins). The method is useful for altering the  
 CC level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2  
 CC polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for  
 CC detecting tumours, and in monitoring tumor treatment in a mammal. Agents  
 CC that modulate interactions between SKP and target proteins are useful for  
 CC treating tumours.

XX SQ Sequence 168 AA;

Query Match 96.5%; Score 137; DB 22; Length 168;  
 Best Local Similarity 96.3%; Pred. No. 1.1e-12;  
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLWAAQYGRELRMSDEFVDSFKKGL 27

DB 103 NLWAAQYGRELRMSDEFVDSFKKGL 129

## RESULT 6

AAG67688

ID AAG67688 standard; Protein; 168 AA.

XX AC AAG67688;

DT 26-NOV-2001 (first entry)

XX DE Amino acid sequence of protein associated with cell proliferation-1.

KW Human; cell proliferation; APOP-1; APOP-2; APOP-3; apoptosis; cancer;

KW brain cancer; breast cancer; Alzheimer's disease; Parkinson's disease;  
KW inflammation; allergy; gout; osteoarthritis; bronchitis.  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FT Modified-site 10..13 /note= "potential casein kinase II phosphorylation site"  
FT Modified-site 16..19 /note= "potential casein kinase II phosphorylation site"  
FT Modified-site 34..36 /note= "potential protein kinase C phosphorylation site"  
FT Modified-site 80..83 /note= "potential casein kinase II phosphorylation site"  
FT Modified-site 115..118 /note= "potential CAMP- and cGMP-dependent protein kinase phosphorylation site"  
FT Modified-site 124..126 /note= "potential protein kinase C phosphorylation site"  
FT Modified-site 153..156 /note= "potential casein kinase II phosphorylation site"  
XX  
PN US6281334-B1.  
XX  
PD 28-AUG-2001.  
XX  
XX 30-SEP-1999; 99US-0410372.  
XX  
PR 04-DEC-1997; 97US-0985335.  
XX  
XX (INCY-) INCYTE GENOMICS INC.  
XX  
PI Hillman JL, Yue H, Lal P, Shah P, Corley NC;  
XX  
XX WPI: 2001-569961/64.  
DR N-PSDB; AAH78430.  
XX  
XX New polypeptides associated with cell proliferation, useful for preventing or treating cancer (e.g. brain cancer), a disorder associated with an increase in apoptosis (e.g. Alzheimer's disease) or inflammation (e.g. gout) -  
XX  
XX Example; Fig 1A-C; 59pp; English.  
XX  
PS The present sequence represents a human protein which is associated with cell proliferation, designated APOP-1. The specification also describes APOP-2 and APOP-3. The APOP polypeptides are useful for diagnosing, preventing or treating disorders associated with abnormal cell proliferation and apoptosis. The polypeptides and composition are particularly useful for treating or preventing cancer (e.g. brain or breast cancer), a disorder associated with an increase in apoptosis (e.g. Alzheimer's disease or Parkinson's disease) or inflammation (e.g. allergies, gout, osteoarthritis or bronchitis).  
XX  
SQ Sequence 168 AA;  
Query Match 96.5%; Score 137; DB 22; Length 168;  
Best Local Similarity 96.3%; Pred. No. 1.1e-12;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 NLWAAQRYGRELRRMSDEFVDSFKKGL 27  
DB 103 NLWAAQRYGRELRRMSDEFVDSFKKGL 129  
RESULT 7  
ABR39081  
ID ABR39081 standard; Protein; 168 AA.  
XX  
XX ABR39081;  
XX  
DT 10-MAY-2003 (first entry)  
XX

DE Human BAD protein SEQ ID NO:2.  
XX  
KW Human; BAD; herpes simplex virus; HSV; US3; herpes virus; apoptosis; virucide; infection.  
XX  
XX Homo sapiens.  
XX  
PN WO2003012049-A2.  
XX  
PD 13-FEB-2003.  
XX  
PF 31-JUL-2002; 2002WO-US24177.  
XX  
XX 31-JUL-2001; 2001US-308929P.  
PR (UYCH-) UNIV CHICAGO.  
XX  
XX Munger J, Roizman B;  
XX WPI: 2003-248168/24.  
DR N-PSDB; ABZ81200.  
XX  
XX Inducing apoptosis in a cell infected with herpes simplex virus, HSV, by administering to the cell, a composition comprising an agent that inhibits phosphorylation of pro-apoptotic polypeptide BAD by HSV US3 -  
XX  
PS Claim 15; Page 166-167; 192pp; English.  
XX  
XX The present invention describes a method (M1) for inducing apoptosis in a cell infected with herpes simplex virus (HSV), which comprises administering to the cell, a composition having an agent that inhibits phosphorylation of pro-apoptotic polypeptide BAD by HSV US3. Also described is a method (M2) for treating a patient infected with HSV, by administering to the patient, a composition comprising a peptide comprising a sequence of 4-100 continuous amino acids of a 168 residue amino acid sequence (see ABR39081), where the peptide comprises ser112, ser135, or ser155, or their combinations. BAD has virucide activity. M1 is useful for inducing apoptosis in a cell infected with HSV, where the cell is in a human. M2 is useful for treating a patient infected with HSV. The present sequence represents human BAD, which is used in the exemplification of the present invention.  
XX  
SQ Sequence 168 AA;  
Query Match 96.5%; Score 137; DB 24; Length 168;  
Best Local Similarity 96.3%; Pred. No. 1.1e-12;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 NLWAAQRYGRELRRMSDEFVDSFKKGL 27  
DB 103 NLWAAQRYGRELRRMSDEFVDSFKKGL 129  
RESULT 8  
ABP41630  
ID ABP41630 standard; Protein; 201 AA.  
XX  
XX ABP41630;  
XX  
DT 22-AUG-2002 (first entry)  
XX  
XX Human ovarian antigen HCE4K28, SEQ ID NO:2762.  
XX  
KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;  
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;  
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;  
KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;  
KW inflammatory condition; immune disorder; blood disorder;  
KW cardiovascular disorder; respiratory disorder; neurological disorder;  
KW gastrointestinal disorder; urinary system disorder; drug screening;  
KW gene therapy; chromosome mapping; forensic analysis;  
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive.

XX OS Homo sapiens.  
XX PN WO200200677-A1.  
XX PD 03-JAN-2002.  
XX PF 07-JUN-2001; 2001WO-US18569.  
XX PR 07-JUN-2000; 2000US-209467P.  
XX PA (HUMA-) HUMAN GENOME SCI INC.  
XX PI Birse CE, Rosen CA;  
XX WPI; 2002-147878/19.  
XX DR N-PSDB; ABQ54707.  
XX  
PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,  
PT useful in the prevention, treatment and diagnosis of cancer (e.g.  
PT ovarian cancer), immune disorders, cardiovascular disorders and  
PT neurological diseases -  
XX  
PS Claim 11; SEQ ID No 2762; 2922pp; English.  
XX  
CC The invention relates to 2175 novel human ovarian antigens (ABP41054-  
CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also  
CC encompasses polypeptides 90% identical and polynucleotides 95% identical  
CC to the sequences of the invention. The invention additionally relates to  
CC recombinant vectors and host cells comprising human ovarian antigen  
CC polynucleotides, antibodies against human ovarian antigens, and the use  
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,  
CC treating, prognosing or preventing various ovary and/or breast-related  
CC disorders. Such conditions include ovarian cancer and breast cancer, and  
CC metastatic tumours of ovarian or breast origin, reproductive system  
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,  
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine  
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic  
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and  
CC vaginitis), immune disorders (e.g., congenital and acquired  
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),  
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,  
CC respiratory disorders, neurological disorders, gastrointestinal disorders  
CC and urinary system disorders. Ovarian antigen polypeptides and  
CC polynucleotides may also be used in screening for compounds which  
CC modulate ovarian antigen expression or activity. The polynucleotides may  
CC further be used for gene therapy, chromosome mapping, in the  
CC identification of individuals and in forensic analysis, and the  
CC polypeptides may be used as food additives or to prepare antibodies  
CC useful in disease diagnosis, drug targeting and phenotyping. The present  
CC sequence represents a human ovarian antigen of the invention.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published\_pct\_sequences.  
XX SQ Sequence 201 AA;  
Query Match 96.5%; Score 137; DB 23; Length 201;  
Best Local Similarity 96.3%; Pred. No. 1.3e-12;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 NLWAAQRYGRELRRMSDEFVDSFKKGL 27  
DB 111 NLWAAQRYGRELRRMSDEFVDSFKKGL 137  
RESULT 9  
ABP56161  
ID ABP56161 standard; peptide; 25 AA.  
XX  
AC ABP56161;  
XX  
DT 28-MAR-2003 (first entry)

XX PTPC-interacting TOX peptide #27.  
XX DE  
XX KW Mitochondrial membrane permeabilisation; mitochondrion; PTPC;  
KW permeability transition pore complex; virucide; neuroprotective;  
KW vasotropic; cytostatic; infection; cell death regulation; apoptosis;  
KW mitochondrial permeability transition pore complex modulator; cancer;  
KW apoptogenic; ischaemia; neurodegenerative disease; fulminant hepatitis.  
XX Synthetic.  
XX OS  
XX PN WO200261105-A2.  
XX PD 08-AUG-2002.  
XX PF 01-FEB-2002; 2002WO-EP01633.  
XX PR 02-FEB-2001; 2001US-265594P.  
XX PA (INSP INST PASTEUR.  
XX PA (CNRS CENT NAT RECH SCI  
XX Edelman L, Jacotot E, Briand J;  
XX WPI; 2002-619260/66.  
XX  
PT New chimeric bifunctional molecules that target specific cells and  
PT regulate the apoptosis function of the permeability transition pore  
PT complex of the mitochondria, useful for treating or preventing e.g.  
PT cancer or ischemia -  
XX  
PS Claim 9; Page 11; 76pp; English.  
XX  
CC The present invention describes a chimeric bifunctional molecule (I)  
CC comprising at least a first functional molecule covalently linked to a  
CC second functional molecule, which is able to modulate the activity of  
CC the permeability transition pore complex (PTPC) of the mitochondria.  
CC (I) has the function of specifically targeting and entering a tissue  
CC cell population. The second functional molecule has the function of  
CC specifically targeting, and inducing the opening or the closing of the PTPC  
CC cells by apoptosis by regulating the opening or the closing of the PTPC  
CC of the mitochondria or its fragment. (I) has virucide, neuroprotective,  
CC vasotropic and cytostatic activities, and can be used as a mitochondrial  
CC permeability transition pore complex (PTPC) modulator. (I) is useful for  
CC treating or preventing a pathological infection or disease. (I) is also  
CC useful for regulating cell death regulatory molecules, specifically the  
CC apoptogenic function of the PTPC, for treating e.g. cancer, ischaemia,  
CC neurodegenerative diseases, fulminant hepatitis or viral infections.  
CC The present sequence represents a PTPC-interacting TOX peptide which is  
CC given in the exemplification of the present invention.  
XX SQ Sequence 25 AA;  
Query Match 89.4%; Score 127; DB 23; Length 25;  
Best Local Similarity 96.0%; Pred. No. 4.2e-12;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 NLWAAQRYGRELRRMSDEFVDSFKK 25  
DB 1 NLWAAQRYGRELRRMSDEFVDSFKK 25  
RESULT 10  
ABG78484  
ID ABG78484 standard; Peptide; 25 AA.  
XX  
AC ABG78484;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Mutant Bcl2 competitive binding assay peptide #1.  
XX Human; Bcl2; BclXl; programmed cell death; apoptosis; mutant; mutin.

XX OS Homo sapiens.  
 OS Synthetic.  
 XX WO200240530-A2.  
 XX 23-MAY-2002.  
 XX 15-NOV-2001; 2001WO-US45693.  
 XX 20-NOV-2000; 2000US-0716395.  
 XX (ABBO ) ABBOTT LAB.  
 XX Fesik SW, Petros AM, Yoon H, Nettesheim DG;  
 XX WPI; 2002-490141/52.  
 XX New mutant Bcl-2 proteins derived from a wild type human Bcl-2 protein,  
 PT useful in biological assays to identify substances that block the  
 PT ability of Bcl-2 to inhibit programmed cell death or apoptosis -  
 XX Example 2; Page 17; 36pp; English.  
 XX This invention relates to a novel mutant protein which is derived from  
 CC a wild type human Bcl-2 protein. The mutant is created by replacing a  
 CC sequence of amino acid residues comprising a flexible loop from the wild  
 CC type Bcl-2 protein with an amino acid sequence comprising at least two  
 CC acidic amino acids. The mutant Bcl-2 protein comprises a 166 residue  
 CC shown in the specification. The invention also comprises an assay for  
 CC identifying substances that bind to the Bcl-2 protein. The protein  
 CC sequences of the invention are useful in biological assays to identify  
 CC substances that block the ability of Bcl-2 to inhibit programmed cell  
 CC death or apoptosis. The present sequence represents a human Bcl2  
 CC peptide of the invention.  
 XX SQ Sequence 25 AA;  
 Query Match 89.4%; Score 127; DB 23; Length 25;  
 Best Local Similarity 96.0%; Pred. No. 4.2e-12;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 NLWAAQYEGRELRRMSDEFVDSFKK 25  
 ||||| ||||| ||||| ||||| |||||  
 Db 1 NLWAAQRYGRELRRMSDEFVDSFKK 25  
 RESULT 11  
 AAU78610  
 ID AAU78610 standard; Peptide; 25 AA.  
 XX AAU78610;  
 XX 18-JUN-2002 (first entry)  
 XX Human Bad peptide #10 which binds to a member of the Bcl-2 family.  
 DE Human; Bad; Bcl-2; apoptosis; cancer; inducer; degenerative disease;  
 KW ischemic injury; suppressor; BH3 domain.  
 XX Homo sapiens.  
 XX WO200220568-A2.  
 XX 14-MAR-2002.  
 XX 04-SEP-2001; 2001WO-US27410.  
 XX 06-SEP-2000; 2000US-0656399.  
 XX (ABBO ) ABBOTT LAB.  
 XX Fesik SW, Meadows RP, Joseph MK, Olejniczak ET, Petros AM;

PI Nettesheim DG, Swift KM, Matayoshi E, Zhang H;  
 XX WPI; 2002-292254/33.  
 XX New derivatives of Bad peptide, useful for identifying compounds that  
 PT bind to Bcl-2 proteins, potential agents for treating cancer and  
 PT degenerative disease -  
 XX Claim 18; Page 18; 31pp; English.  
 XX The present invention relates to new peptides that are derived from a  
 CC wild-type human Bad peptide and are able to bind to a member of the  
 CC Bcl-2 protein family. The peptides are useful, when labelled, in  
 CC competitive/displacement assays for identifying substances that bind to  
 CC members of the Bcl-2 family and may induce or suppress apoptosis so are  
 CC potentially useful for treating cancer (inducers) or degenerative  
 CC diseases or ischemic injury (suppressors). The peptides of the invention  
 CC have high helix propensity, maintain the contacts of the wild-type Bad  
 CC peptide and, compared with the Bad peptide, may have better physical  
 CC properties, particularly solubility. The present sequence represents one  
 CC of a collection of Bad peptides (AAU78601-AAU78631) that were derived  
 CC from the BH3 domain of the human wild-type Bad peptide.  
 XX SQ Sequence 25 AA;  
 Query Match 89.4%; Score 127; DB 23; Length 25;  
 Best Local Similarity 96.0%; Pred. No. 4.2e-12;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 NLWAAQYEGRELRRMSDEFVDSFKK 25  
 ||||| ||||| ||||| ||||| |||||  
 Db 1 NLWAAQRYGRELRRMSDEFVDSFKK 25  
 RESULT 12  
 ABG78490  
 ID ABG78490 standard; Peptide; 25 AA.  
 XX ABG78490;  
 AC ABG78490;  
 XX 15-NOV-2002 (first entry)  
 XX Mutant Bcl2 competitive binding assay peptide #7.  
 DE Human; Bcl2; BclX1; programmed cell death; apoptosis; mutant; mutein.  
 KW Homo sapiens.  
 OS Synthetic.  
 XX WO200240530-A2.  
 XX 23-MAY-2002.  
 XX 15-NOV-2001; 2001WO-US45693.  
 XX 20-NOV-2000; 2000US-0716395.  
 XX (ABBO ) ABBOTT LAB.  
 XX Fesik SW, Petros AM, Yoon H, Nettesheim DG;  
 XX WPI; 2002-490141/52.  
 XX New mutant Bcl-2 proteins derived from a wild type human Bcl-2 protein,  
 PT useful in biological assays to identify substances that block the  
 PT ability of Bcl-2 to inhibit programmed cell death or apoptosis -  
 XX Example 2; Page 17; 36pp; English.  
 XX This invention relates to a novel mutant protein which is derived from  
 CC a wild type human Bcl-2 protein. The mutant is created by replacing a  
 CC sequence of amino acid residues comprising a flexible loop from the wild  
 CC type Bcl-2 protein with an amino acid sequence comprising at least two  
 CC acidic amino acids. The mutant Bcl-2 protein comprises a 166 residue  
 CC shown in the specification. The invention also comprises an assay for  
 CC identifying substances that bind to the Bcl-2 protein. The protein  
 CC sequences of the invention are useful in biological assays to identify  
 CC substances that block the ability of Bcl-2 to inhibit programmed cell  
 CC death or apoptosis. The present sequence represents a human Bcl2  
 CC peptide of the invention.  
 XX SQ Sequence 25 AA;  
 Query Match 89.4%; Score 127; DB 23; Length 25;  
 Best Local Similarity 96.0%; Pred. No. 4.2e-12;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 NLWAAQYEGRELRRMSDEFVDSFKK 25  
 ||||| ||||| ||||| ||||| |||||  
 Db 1 NLWAAQRYGRELRRMSDEFVDSFKK 25

CC acidic amino acids. The mutant Bcl-2 protein comprises a 166 residue  
 CC shown in the specification. The invention also comprises an assay for  
 CC identifying substances that bind to the Bcl-2 protein. The protein  
 CC sequences of the invention are useful in biological assays to identify  
 CC substances that block the ability of Bcl-2 to inhibit programmed cell  
 CC death or apoptosis. The present sequence represents a human Bcl2  
 CC peptide of the invention.  
 XX  
 SQ Sequence 25 AA;

Query Match 87.3%; Score 124; DB 23; Length 25;  
 Best Local Similarity 92.0%; Pred. No. 1.2e-11;  
 Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRLMSDEFVDSFKK 25  
 DB 1 NLWAAQRYGRELRLMSDEFVDAFKK 25

RESULT 13  
 AAU78617  
 ID AAU78617 standard; Peptide; 25 AA.  
 AC AAU78617;  
 XX  
 DT 18-JUN-2002 (first entry)  
 XX  
 DE Human Bad peptide #17 which binds to a member of the Bcl-2 family.  
 XX  
 KW Human; Bad; Bcl-2; apoptosis; cancer; inducer; degenerative disease;  
 KW ischemic injury; suppressor; BH3 domain.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200220568-A2.  
 XX  
 PD 14-MAR-2002.  
 XX  
 PF 04-SEP-2001; 2001WO-US27410.  
 XX  
 PR 06-SEP-2000; 2000US-0656399.  
 XX  
 PA (ABBO ) ABBOTT LAB.  
 XX  
 PI Fesik SW, Meadows RP, Joseph MK, Olejniczak ET, Petros AM;  
 PI Nettesheim DG, Swift KM, Matayoshi E, Zhang H;  
 DR WPI; 2002-292254/33.  
 XX  
 PT New derivatives of Bad peptide, useful for identifying compounds that  
 PT bind to Bcl-2 proteins, potential agents for treating cancer and  
 PT degenerative disease -  
 XX  
 PS Example 1; Page 14; 3lpp; English.  
 XX

The present invention relates to new peptides that are derived from a  
 CC wild-type human Bad peptide and are able to bind to a member of the  
 CC Bcl-2 protein family. The peptides are useful, when labelled, in  
 CC competitive/displacement assays for identifying substances that bind to  
 CC members of the Bcl-2 family and may induce or suppress apoptosis so are  
 CC potentially useful for treating cancer (inducers) or degenerative  
 CC diseases or ischemic injury (suppressors). The peptides of the invention  
 CC have high helix propensity, maintain the contacts of the wild-type Bad  
 CC peptide and, compared with the Bad peptide, may have better physical  
 CC properties, particularly solubility. The present sequence represents one  
 CC of a collection of Bad peptides (AAU78601-AAU78631) that were derived  
 CC from the BH3 domain of the human wild-type Bad peptide.  
 XX  
 SQ Sequence 25 AA;

Query Match 87.3%; Score 124; DB 23; Length 25;  
 Best Local Similarity 92.0%; Pred. No. 1.2e-11;  
 Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRLMSDEFVDSFKK 25  
 DB 1 NLWAAQRYGRELRLMSDEFVDAFKK 25

RESULT 14  
 ABG78488  
 ID ABG78488 standard; Peptide; 25 AA.  
 AC ABG78488;  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX  
 DE Mutant Bcl2 competitive binding assay peptide #5.  
 XX  
 KW Human; Bcl2; BclX1; programmed cell death; apoptosis; mutant; muten.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200240530-A2.  
 XX  
 PD 23-MAY-2002.  
 XX  
 PF 15-NOV-2001; 2001WO-US45693.  
 XX  
 PR 20-NOV-2000; 2000US-0716395.  
 XX  
 PA (ABBO ) ABBOTT LAB.  
 XX  
 PI Fesik SW, Petros AM, Yoon H, Nettesheim DG;  
 XX WPI; 2002-490141/52.  
 XX

New mutant Bcl-2 proteins derived from a wild type human Bcl-2 protein,  
 useful in biological assays to identify substances that block the  
 ability of Bcl-2 to inhibit programmed cell death or apoptosis -  
 XX  
 PS Example 2; Page 17; 36pp; English.  
 XX

This invention relates to a novel mutant protein which is derived from  
 CC a wild type human Bcl-2 protein. The mutant is created by replacing a  
 CC sequence of amino acid residues comprising a flexible loop from the wild  
 CC type Bcl-2 protein with an amino acid sequence comprising at least two  
 CC acidic amino acids. The mutant Bcl-2 protein comprises a 166 residue  
 CC shown in the specification. The invention also comprises an assay for  
 CC identifying substances that bind to the Bcl-2 protein. The protein  
 CC sequences of the invention are useful in biological assays to identify  
 CC substances that block the ability of Bcl-2 to inhibit programmed cell  
 CC death or apoptosis. The present sequence represents a human Bcl2  
 CC peptide of the invention.  
 XX  
 SQ Sequence 25 AA;

Query Match 86.6%; Score 123; DB 23; Length 25;  
 Best Local Similarity 92.0%; Pred. No. 1.7e-11;  
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRLMSDEFVDSFKK 25  
 DB 1 NLWGAQRYGRELRLMSDEFVDSFKK 25

RESULT 15  
 ABG78489  
 ID ABG78489 standard; Peptide; 25 AA.  
 AC ABG78489;  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX  
 DE Mutant Bcl2 competitive binding assay peptide #6.

XX	Human; Bcl2; Bclx1; programmed cell death; apoptosis; mutant; mteuin.
KW	
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	WO200240530-A2.
XX	
PD	23-MAY-2002.
XX	
XX	15-NOV-2001; 2001WO-US45693.
PF	
XX	
PR	20-NOV-2000; 2000US-0716395.
XX	
XX	(ABBO ) ABBOTT LAB.
FA	
XX	
PI	Fesik SW, Petros AM, Yoon H, Nettessheim DG;
XX	
DR	WPI; 2002-490141/52.
XX	
PT	New mutant Bcl-2 proteins derived from a wild type human Bcl-2 protein,
PT	useful in biological assays to identify substances that block the
PT	ability of Bcl-2 to inhibit programmed cell death or apoptosis
XX	
PS	Example 2; Page 17; 36pp; English.
XX	
CC	This invention relates to a novel mutant protein which is derived from
CC	a wild type human Bcl-2 protein. The mutant is created by replacing a
CC	sequence of amino acid residues comprising a flexible loop from the wild
CC	type Bcl-2 protein with an amino acid sequence comprising at least two
CC	acidic amino acids. The mutant Bcl-2 protein comprises a 165 residue
CC	shown in the specification. The invention also comprises an assay for
CC	identifying substances that bind to the Bcl-2 protein. The protein
CC	sequences of the invention are useful in biological assays to identify
CC	substances that block the ability of Bcl-2 to inhibit programmed cell
CC	death or apoptosis. The present sequence represents a human Bcl2
CC	peptide of the invention.
XX	
SQ	Sequence 25 AA;
	Query Match 86.6%; Score 123; DB 23; Length 25;
	Best Local Similarity 92.0%; Pred. No. 1.7e-11;
	Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1 NLWAAQYEGRELRRMSDEFYDSFKK 25
Db	1 NLWAGQRYGRELRRMSDEFYDSFKK 25

Search completed: September 23, 2003, 09:47:13  
Job time : 87 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 23, 2003, 09:43:16 ; Search time 30 Seconds  
(without alignments)  
38.080 Million cell updates/sec

Title: US-09-544-664B-2

Perfect score: 142

Sequence: 1 NLWAAQYGRRLRRMSDEFVDFKGL 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	137	96.5	166	1	US-08-665-617-2
2	137	96.5	168	2	US-08-717-123-2
3	137	96.5	168	3	US-08-985-335-1
4	137	96.5	168	3	US-08-985-335-7
5	137	96.5	168	3	US-09-410-372-1
6	137	96.5	168	3	US-09-410-372-7
7	137	96.5	168	4	US-09-375-257-2
8	109	76.8	204	1	US-08-333-565-2
9	109	76.8	204	2	US-08-661-479-2
10	109	76.8	204	2	US-08-733-505A-1
11	109	76.8	204	2	US-08-733-505A-12
12	109	76.8	204	2	US-08-733-505A-13
13	109	76.8	204	2	US-08-733-505A-14
14	106	74.6	204	2	US-08-717-123-3
15	106	74.6	204	4	US-09-375-257-3
16	97	68.3	23	1	US-08-333-565-10
17	97	68.3	23	2	US-08-661-479-10
18	97	68.3	59	2	US-08-733-505A-55
19	97	68.3	59	2	US-08-733-505A-56
20	97	68.3	59	2	US-08-733-505A-57
21	97	68.3	59	2	US-08-733-505A-58
22	81	57.0	16	1	US-08-333-565-26
23	81	57.0	16	2	US-08-661-479-26
24	56	39.4	11	2	US-08-733-505A-34
25	56	39.4	11	2	US-08-706-741B-69
26	56	39.4	11	2	US-08-924-695A-69
27	51	35.9	1125	4	US-09-252-991A-18729

ALIGNMENTS

RESULT 1

US-08-665-617-2  
; Sequence 2, Application US/08665617  
; Patent No. 5663316  
; GENERAL INFORMATION:  
; APPLICANT: Xudong, Yin  
; TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/665,617  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: CL-8  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (352) 375-8100  
; TELEFAX: (352) 372-5800  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 166 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-665-617-2

Query Match 96.5%; Score 137; DB 1; Length 166;  
Best Local Similarity 96.3%; Pred. No. 530-14;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLWAAQYGRRLRRMSDEFVDFKGL 27

Db 101 NLWAAQYGRRLRRMSDEFVDFKGL 127

RESULT 2

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US-08-717-123-2
; Sequence 2, Application US/08717123
; Patent No. 5965703
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oitersdorf, Tilman
; TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
; TITLE OF INVENTION: Acids and Methods of Use
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/717,123
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 1929
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-717-123-2

Query Match          96.5%; Score 137; DB 2; Length 168;
Best Local Similarity 96.3%; Pred. No. 5.4e-14;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLWAAQYGRRLRMSDFVDSFKKGL 27
Db 103 NLWAAQYGRRLRMSDFVDSFKKGL 129

RESULT 3
US-08-985-335-1
; Sequence 1, Application US/08985335
; Patent No. 6080847
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,335
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0421 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 7:
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SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,335
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0421 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SYNORAB01
; CLONE: 358673
US-08-985-335-1

Query Match          96.5%; Score 137; DB 3; Length 168;
Best Local Similarity 96.3%; Pred. No. 5.4e-14;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLWAAQYGRRLRMSDFVDSFKKGL 27
Db 103 NLWAAQYGRRLRMSDFVDSFKKGL 129

RESULT 4
US-08-985-335-7
; Sequence 7, Application US/08985335
; Patent No. 6080847
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,335
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0421 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 7:
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SEQUENCE CHARACTERISTICS:  
LENGTH: 168 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 1683637  
US-08-985-335-7

Query Match 96.5%; Score 137; DB 3; Length 168;  
Best Local Similarity 96.3%; Pred. No. 5.4e-14;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLWAAQYGRRLRMSDFVDSFKKGL 27  
|||||  
Db 103 NLWAAQYGRRLRMSDFVDSFKKGL 129

## RESULT 5

US-09-410-372-1  
; Sequence 1, Application US/09410372  
; Patent No. 6281334

## GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.  
APPLICANT: Yue, Henry  
APPLICANT: Lal, Preeti  
APPLICANT: Shah, Purvi  
APPLICANT: Corley, Neil C.  
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL  
TITLE OF INVENTION: PROLIFERATION  
NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA

COUNTRY: USA  
ZIP: 94304

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/410,372

FILING DATE:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/985,335

FILING DATE:

## ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0421 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:

LENGTH: 168 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

## IMMEDIATE SOURCE:

LIBRARY: SYNORAB01  
CLONE: 358673

US-09-410-372-1

Query Match 96.5%; Score 137; DB 3; Length 168;  
Best Local Similarity 96.3%; Pred. No. 5.4e-14;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLWAAQYGRRLRMSDFVDSFKKGL 27

Db 103 NLWAAQYGRRLRMSDFVDSFKKGL 129  
|||||

## RESULT 6

US-09-410-372-7  
; Sequence 7, Application US/09410372  
; Patent No. 6281334

## GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.  
APPLICANT: Yue, Henry  
APPLICANT: Lal, Preeti  
APPLICANT: Shah, Purvi  
APPLICANT: Corley, Neil C.  
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL  
TITLE OF INVENTION: PROLIFERATION  
NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/410,372

FILING DATE:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/985,335

FILING DATE:

## ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0421 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:  
LENGTH: 168 amino acids  
TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

## IMMEDIATE SOURCE:

LIBRARY: GenBank  
CLONE: 1683637

US-09-410-372-7

Query Match 96.5%; Score 137; DB 3; Length 168;  
Best Local Similarity 96.3%; Pred. No. 5.4e-14;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLWAAQYGRRLRMSDFVDSFKKGL 27  
|||||

Db 103 NLWAAQYGRRLRMSDFVDSFKKGL 129  
|||||

## RESULT 7

US-09-375-257-2  
; Sequence 2, Application US/09375257  
; Patent No. 6504022

## GENERAL INFORMATION:

APPLICANT: Horne, William A.  
APPLICANT: Oltersdorf, Tilman  
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC  
TITLE OF INVENTION: ACIDS AND METHODS OF USE  
FILE REFERENCE: 480140.428D1  
CURRENT APPLICATION NUMBER: US/09/375,257

; CURRENT FILING DATE: 1999-08-16  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 168  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-375-257-2

Query Match 96.5%; Score 137; DB 4; Length 168;  
Best Local Similarity 96.3%; Pred. No. 5.4e-14;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFVDSFKKGL 27  
||||| ||||||| ||||||| |||  
Db 103 NLWAAQRYGRELRRMSDEFVDSFKKGL 129

RESULT 8  
US-08-333-565-2  
; Sequence 2, Application US/08333565  
; Patent No. 5622852  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, Stanley J.  
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH  
; TITLE OF INVENTION: REGULATOR  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/333,565  
FILING DATE: 31-OCT-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15726A-000700  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 204 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..204  
OTHER INFORMATION: /note= "Deduced amino acid sequence  
OTHER INFORMATION: of mouse BAD."  
US-08-333-565-2

Query Match 76.8%; Score 109; DB 1; Length 204;  
Best Local Similarity 87.5%; Pred. No. 1.7e-09;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFVDSFK 24  
||||| ||||||| ||||||| |||  
Db 140 NLWAAQRYGRELRRMSDEFEGSK 163

RESULT 9  
US-08-661-479-2  
; Sequence 2, Application US/08661479  
; Patent No. 5834209  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, Stanley J.  
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH  
; TITLE OF INVENTION: REGULATOR  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/661,479  
FILING DATE: 11-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/333,565  
FILING DATE: 31-OCT-1994

ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15726A-000700  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 204 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:

NAME/KEY: Protein  
LOCATION: 1..204  
OTHER INFORMATION: /note= "Deduced amino acid sequence  
OTHER INFORMATION: of mouse BAD."  
US-08-661-479-2

Query Match 76.8%; Score 109; DB 2; Length 204;  
Best Local Similarity 87.5%; Pred. No. 1.7e-09;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFVDSFK 24  
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Db 140 NLWAAQRYGRELRRMSDEFEGSK 163

RESULT 10  
US-08-733-505A-1  
; Sequence 1, Application US/08733505A  
; Patent No. 5856445  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, Stanley J.  
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF  
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAERKAMP, L.C.  
; STREET: 7733 FORSYTH BLVD., SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: USA

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;
;   ZIP: 63105
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/733,505A
;   FILING DATE:
;   CLASSIFICATION: 530
;   ATTORNEY/AGENT INFORMATION:
;   NAME: HOLLAND, DONALD R.
;   REGISTRATION NUMBER: 35,197
;   REFERENCE/DOCKET NUMBER: 965458
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (314) 727-5188
;   TELEFAX: (314) 727-6092
;   INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 204 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   US-08-733-505A-1
;
;   Query Match          76.8%; Score 109; DB 2; Length 204;
;   Best Local Similarity 87.5%; Pred. No. 1.7e-09;
;   Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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; QY 1 NLWAAQYGRRLRMSDEFVDSFK 24
;   ||||| ||||| ||||| ||||| |||
; Db 140 NLWAAQYGRRLRMSDEFVDSFK 163
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; RESULT 11
; US-08-733-505A-12
; Sequence 12, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,505A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
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;   MOLECULE TYPE: peptide
;   US-08-733-505A-12
;
;   Query Match          76.8%; Score 109; DB 2; Length 204;
;   Best Local Similarity 87.5%; Pred. No. 1.7e-09;
;   Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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; QY 1 NLWAAQYGRRLRMSDEFVDSFK 24
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; Db 140 NLWAAQYGRRLRMSDEFVDSFK 163
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; RESULT 12
; US-08-733-505A-13
; Sequence 13, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,505A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-733-505A-13
;
;   Query Match          76.8%; Score 109; DB 2; Length 204;
;   Best Local Similarity 87.5%; Pred. No. 1.7e-09;
;   Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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; QY 1 NLWAAQYGRRLRMSDEFVDSFK 24
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; Db 140 NLWAAQYGRRLRMSDEFVDSFK 163
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; RESULT 13
; US-08-733-505A-14
; Sequence 14, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAERKAMP, L.C.
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; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,505A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-733-505A-14

Query Match 75.8%; Score 109; DB 2; Length 204;
Best Local Similarity 87.5%; Pred. No. 1.7e-09;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 NLWAAQYRGRELRRMSDEFVDSFK 24
Db 140 NLWAAQYRGRELRRMSDEFEGSFK 163

RESULT 14
US-08-717-123-3
; Sequence 3, Application US/08/717123
; Patent No. 5965703
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
; TITLE OF INVENTION: Acids and Methods of Use
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/717,123
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 1929
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-717-123-3

Query Match 74.6%; Score 106; DB 2; Length 204;
Best Local Similarity 83.3%; Pred. No. 5e-09;
Matches 20; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NLWAAQYRGRELRRMSDEFVDSFK 24
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RESULT 15
US-09-375-257-3
; Sequence 3, Application US/09375257
; Patent No. 6504022
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
; TITLE OF INVENTION: ACIDS AND METHODS OF USE
; FILE REFERENCE: 480140.428D1
; CURRENT APPLICATION NUMBER: US/09/375,257
; CURRENT FILING DATE: 1999-08-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-375-257-3

Query Match 74.6%; Score 106; DB 4; Length 204;
Best Local Similarity 83.3%; Pred. No. 5e-09;
Matches 20; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NLWAAQYRGRELRRMSDEFVDSFK 24
Db 140 NLWAAQYRGRELRRMTDEFEGSFK 163

Search completed: September 23, 2003, 09:45:40
Job time : 32 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 23, 2003, 09:47:20 : Search time 389 Seconds  
(without alignments)  
10.335 Million cell updates/sec

Title: US-09-544-664B-2

Perfect score: 142

Sequence: 1 NLWAAQYGRRLRMSDFVDSFKKGL 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 55269 seqs, 148893369 residues

Total number of hits satisfying chosen parameters: 556269

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	137	96.5	168	9	US-09-922-378-2
2	137	96.5	168	9	US-09-894-657-1
3	137	96.5	168	9	US-09-894-657-7
4	137	96.5	168	12	US-10-209-967-2
5	137	96.5	168	14	US-10-066-179-2
6	127	89.4	23	15	US-10-059-261-258
7	109	76.8	204	12	US-10-209-967-4
8	106	74.6	204	9	US-09-922-378-3
9	106	74.6	204	14	US-10-066-179-3
10	57	40.1	15	15	US-10-174-105A-147
11	48	33.8	373	12	US-10-168-780-2
12	47	33.1	350	11	US-09-940-244-394
13	46.5	32.7	1053	9	US-09-841-132-583
14	46.5	32.7	1053	14	US-10-007-693-97
15	46	32.4	35	15	US-10-092-750-1

16	46	32.4	113	9	US-09-815-242-13424	Sequence 13424, A
17	46	32.4	138	15	US-10-092-750-241	Sequence 241, App
18	46	32.4	359	15	US-10-136-444-8	Sequence 8, Appli
19	46	32.4	558	12	US-10-342-224-110	Sequence 110, App
20	46	32.4	1270	15	US-10-223-070-8	Sequence 8, Appli
21	45	31.7	404	15	US-10-156-761-10995	Sequence 10995, A
22	45	31.7	441	15	US-10-156-761-13669	Sequence 13669, A
23	45	31.7	454	15	US-10-166-087-46	Sequence 46, Appl
24	45	31.7	541	15	US-10-234-432-37	Sequence 37, Appl
25	45	31.7	662	15	US-10-234-432-75	Sequence 75, Appl
26	45	31.7	678	15	US-10-234-432-38	Sequence 38, Appl
27	45	31.7	901	9	US-09-815-242-11148	Sequence 11148, A
28	44	31.0	272	15	US-10-156-761-11541	Sequence 11541, A
29	44	31.0	362	9	US-09-815-242-10793	Sequence 10793, A
30	44	31.0	414	10	US-09-854-286-18	Sequence 18, Appl
31	44	31.0	426	12	US-10-137-870-218	Sequence 218, App
32	44	31.0	426	12	US-10-140-018-218	Sequence 218, App
33	44	31.0	426	12	US-10-140-021-218	Sequence 218, App
34	44	31.0	426	12	US-10-140-274-218	Sequence 218, App
35	44	31.0	426	12	US-10-140-471-218	Sequence 218, App
36	44	31.0	426	12	US-10-140-807-218	Sequence 218, App
37	44	31.0	426	12	US-10-140-922-218	Sequence 218, App
38	44	31.0	426	12	US-10-140-924-218	Sequence 218, App
39	44	31.0	426	12	US-10-140-926-218	Sequence 218, App
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41	44	31.0	426	12	US-10-141-702-218	Sequence 218, App
42	44	31.0	426	12	US-10-141-704-218	Sequence 218, App
43	44	31.0	426	12	US-10-142-421-218	Sequence 218, App
44	44	31.0	426	12	US-10-142-432-218	Sequence 218, App
45	44	31.0	426	12	US-10-142-767-218	Sequence 218, App

#### ALIGNMENTS

RESULT 1  
US-09-922-378-2  
; Sequence 2, Application US/09922378  
; Patent No. US20020037859A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, William A.  
; APPLICANT: Oltersdorf, Tilman  
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC  
; TITLE OF INVENTION: ACIDS AND METHODS OF USE  
; FILE REFERENCE: 480140.428D3  
; CURRENT APPLICATION NUMBER: US/09/922,378  
; CURRENT FILING DATE: 2001-08-03  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 168  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-922-378-2

Query Match 96.5%; Score 137; DB: 9; Length 168;  
Best Local Similarity 96.3%; Pred. NO. 1-2e-12;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLWAAQYGRRLRMSDFVDSFKKGL-27  
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Db 103 NLWAAQYGRRLRMSDFVDSFKKGL 129

RESULT 2  
US-09-894-657-1  
; Sequence 1, Application US/09894657  
; Patent No. US20020098569A1  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; yue, Henry  
; Lal, Preeti  
; Shah, Purvi

Corley, Neil C.  
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL  
PROLIFERATION  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/894,657  
FILING DATE: 28-Jun-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/410,372  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0421 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 168 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: SYNORAB01  
CLONE: 358673  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-894-657-1  
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Best Local Similarity 96.3%; Pred. No. 1-2e-12;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 NLWAAQYRGRELRRMSDEFVDSFKKGL 27  
Db 103 NLWAAQYRGRELRRMSDEFVDSFKKGL 129  
RESULT 3  
US-09-894-657-7  
Sequence 7, Application US/09894657  
Patent No. US20020098569A1  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
Yue, Henry  
Lal, Preeti  
Shah, Purvi  
Corley, Neil C.  
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL  
PROLIFERATION  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/894,657  
FILING DATE: 28-Jun-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/410,372  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0421 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 168 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 1683637  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-09-894-657-7  
Query Match 96.5%; Score 137; DB 9; Length 168;  
Best Local Similarity 96.3%; Pred. No. 1-2e-12;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 NLWAAQYRGRELRRMSDEFVDSFKKGL 27  
Db 103 NLWAAQYRGRELRRMSDEFVDSFKKGL 129  
RESULT 4  
US-10-209-967-2  
Sequence 2, Application US/10209967  
Publication No. US20030171279A1  
GENERAL INFORMATION:  
APPLICANT: MUNGER, JOSHUA  
APPLICANT: ROIZMAN, BERNARD  
TITLE OF INVENTION: METHODS AND COMPOSITION CONCERNING HERPESVIRUS US3 AND  
TITLE OF INVENTION: BAD-INVOLVED APOPTOSIS  
FILE REFERENCE: ARCD.380US  
CURRENT APPLICATION NUMBER: US/10/209,967  
CURRENT FILING DATE: 2002-07-31  
PRIOR APPLICATION NUMBER: 60/308,929  
PRIOR FILING DATE: 2001-07-31  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 168  
TYPE: PRT  
ORGANISM: Human BAD  
US-10-209-967-2  
Query Match 96.5%; Score 137; DB-12; Length 168;  
Best Local Similarity 96.3%; Pred. No. 1-2e-12;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 NLWAAQYRGRELRRMSDEFVDSFKKGL 27  
Db 103 NLWAAQYRGRELRRMSDEFVDSFKKGL 129  
RESULT 5  
US-10-066-179-2  
Sequence 2, Application US/10066179  
Publication No. US20020115631A1  
GENERAL INFORMATION:  
APPLICANT: Horne, William A.

; APPLICANT: Oltersdorf, Tilman  
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC  
; FILE REFERENCE: 480140.428C1  
; CURRENT APPLICATION NUMBER: US/10/066,179  
; CURRENT FILING DATE: 2002-02-01  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 168  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-066-179-2

Query Match 96.5%; Score 137; DB 14; Length 168;  
Best Local Similarity 96.3%; Pred. No. 1.2e-12;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLWAAQYRGRELRRMSDEFVDSFKKGL 27  
||||| ||||||||| ||||||||| |||  
Db 103 NLWAAQYRGRELRRMSDEFVDSFKKGL 129

## RESULT 6

US-10-059-261-258  
; Sequence 258, Application US/10059261  
; Publication No. US20030077826A1  
; GENERAL INFORMATION:  
; APPLICANT: EDELMAN, LENA  
; APPLICANT: JACOTOT, ETIENNE DANIEL FRANCOIS  
; APPLICANT: BRIAND, JEAN-PAUL  
; TITLE OF INVENTION: CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET  
; TITLE OF INVENTION: SPECIFIC CELLS AND A MODULE REGULATING THE APOPTOTIC  
; TITLE OF INVENTION: FUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX  
; TITLE OF INVENTION: (PTPC)  
; FILE REFERENCE: 03495.0216  
; CURRENT APPLICATION NUMBER: US/10/059,261  
; CURRENT FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: 60/265,594  
; PRIOR FILING DATE: 2001-02-02  
; NUMBER OF SEQ ID NOS: 325  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 258  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: TOX peptide  
US-10-059-261-258

Query Match 89.4%; Score 127; DB 15; Length 25;  
Best Local Similarity 96.0%; Pred. No. 4.6e-12;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLWAAQYRGRELRRMSDEFVDSFKK 25  
||||| ||||||||| ||||||||| |||  
Db 1 NLWAAQYRGRELRRMSDEFVDSFKK 25

## RESULT 7

US-10-209-967-4  
; Sequence 4, Application US/10209967  
; Publication No. US20030171279A1  
; GENERAL INFORMATION:  
; APPLICANT: MUNGER, JOSHUA  
; APPLICANT: ROIZMAN, BERNARD  
; TITLE OF INVENTION: METHODS AND COMPOSITION CONCERNING HERPESVIRUS US3 AND  
; TITLE OF INVENTION: BAD-INVOLVED APOPTOSIS  
; FILE REFERENCE: ARGD:380US  
; CURRENT APPLICATION NUMBER: US/10/209,967  
; CURRENT FILING DATE: 2002-07-31  
; PRIOR APPLICATION NUMBER: 60/308,929  
; PRIOR FILING DATE: 2001-07-31

; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 204  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-209-967-4

Query Match 76.8%; Score 109; DB 12; Length 204;  
Best Local Similarity 87.5%; Pred. No. 2.1e-08;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 NLWAAQYRGRELRRMSDEFVDSFK 24  
||||| ||||||||| |||  
Db 140 NLWAAQYRGRELRRMSDEFEGSFK 163

## RESULT 8

US-09-922-378-3  
; Sequence 3, Application US/09922378  
; Patent No. US20020037869A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, William A.  
; APPLICANT: Oltersdorf, Tilman  
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC  
; TITLE OF INVENTION: ACIDS AND METHODS OF USE  
; FILE REFERENCE: 480140.428D3  
; CURRENT APPLICATION NUMBER: US/09/922,378  
; CURRENT FILING DATE: 2001-08-03  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 204  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-922-378-3

Query Match 74.6%; Score 106; DB 9; Length 204;  
Best Local Similarity 83.3%; Pred. No. 5.8e-08;  
Matches 20; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NLWAAQYRGRELRRMSDEFVDSFK 24  
||||| ||||||||| |||  
Db 140 NLWAAQYRGRELRRMTDEFEGSFK 163

## RESULT 9

US-10-066-179-3  
; Sequence 3, Application US/10066179  
; Publication No. US20020115631A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, William A.  
; APPLICANT: Oltersdorf, Tilman  
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC  
; TITLE OF INVENTION: ACIDS AND METHODS OF USE  
; FILE REFERENCE: 480140.428C1  
; CURRENT APPLICATION NUMBER: US/10/066,179  
; CURRENT FILING DATE: 2002-02-01  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 204  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-066-179-3

Query Match 74.6%; Score 106; DB 14; Length 204;  
Best Local Similarity 83.3%; Pred. No. 5.8e-08;  
Matches 20; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NLWAAQYRGRELRRMSDEFVDSFK 24  
||||| ||||||||| |||  
Db 140 NLWAAQYRGRELRRMTDEFEGSFK 163

RESULT 10  
US-10-174-105A-147  
; Sequence 147, Application US/10174105A  
; Publication No. US20030068652A1  
; GENERAL INFORMATION:  
; APPLICANT: ZHANG, Hui  
; APPLICANT: COMB, Michael J.  
; APPLICANT: TAN, Yi  
; TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPECIFIC,  
; TITLE OF INVENTION: CONTEXT-INDEPENDENT ANTIBODIES COUPLED WITH DATABASE SEARCHING  
; FILE REFERENCE: CST-138 CIP3  
; CURRENT APPLICATION NUMBER: US/10/174,105A  
; CURRENT FILING DATE: 2002-06-13  
; PRIOR APPLICATION NUMBER: US 09/148,712  
; PRIOR FILING DATE: 1998-09-04  
; PRIOR APPLICATION NUMBER: US 09/535,364  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 193  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 147  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptide  
; NAME/KEY: MOD\_RES  
; LOCATION: (8)..(8)  
; OTHER INFORMATION: PHOSPHORYLATION; serine at position 8 is phosphorylated  
US-10-174-105A-147

Query Match 40.1%; Score 57; DB 15; Length 15;  
Best Local Similarity 85.7%; Pred. No. 0.063; 2; Indels 0; Gaps 0;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 GRELRMSDEFVDS 22  
Db 1 GRELRMSDEFVS 14

RESULT 11  
US-10-168-780-2  
; Sequence 2, Application US/10168780  
; Publication No. US20030172405A1  
; GENERAL INFORMATION:  
; APPLICANT: TANAKA, Hiroshi  
; APPLICANT: KAYANO, Toshiaki  
; APPLICANT: YANO, Masahiro  
; APPLICANT: MATSUOKA, Makoto  
; APPLICANT: KOBAYASHI, Masatomo  
; TITLE OF INVENTION: GIBBERELLIN 3BETA-HYDROXYLASE GENES OF RICE AND USES THEREOF  
; FILE REFERENCE: SHZ-004US  
; CURRENT APPLICATION NUMBER: US/10/168,780  
; CURRENT FILING DATE: 2002-06-20  
; PRIOR APPLICATION NUMBER: PCT/JP00/09037  
; PRIOR FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: JP 11/361608  
; PRIOR FILING DATE: 1999-12-20  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 373  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-168-780-2

Query Match 33.8%; Score 48; DB 12; Length 373;  
Best Local Similarity 36.4%; Pred. No. 45;  
Matches 8; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 6 QEYGRELRMSDEFVDSFKKGL 27  
Db 162 EEFKEMRRRLADELRLFLRAL 183

RESULT 12  
US-09-940-244-394  
; Sequence 394, Application US/09940244  
; Publication No. US20030044796A1  
; GENERAL INFORMATION:  
; APPLICANT: Neri, Bruce P.  
; APPLICANT: Hall, Jeff G.  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Smith, Lloyd M.  
; TITLE OF INVENTION: Reactions on Dendrimers  
; FILE REFERENCE: FORS-06478  
; CURRENT APPLICATION NUMBER: US/09/940,244  
; CURRENT FILING DATE: 2002-05-06  
; NUMBER OF SEQ ID NOS: 422  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 394  
; LENGTH: 350  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-940-244-394

Query Match 33.1%; Score 47; DB 11; Length 350;  
Best Local Similarity 40.9%; Pred. No. 58;  
Matches 9; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 4 AAQEYGRELRMSDEFVDSFKK 25  
Db 119 AARYAQAARLTDEVEDAKK 140

RESULT 13  
US-09-841-132-583  
; Sequence 583, Application US/09841132  
; Patent No. US20020061848A1  
; GENERAL INFORMATION:  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Probst, Peter  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND  
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION  
; FILE REFERENCE: 210121.469C8  
; CURRENT APPLICATION NUMBER: US/09/841,132  
; CURRENT FILING DATE: 2001-04-23  
; NUMBER OF SEQ ID NOS: 599  
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0  
; SEQ ID NO 583  
; LENGTH: 1053  
; TYPE: PRT  
; ORGANISM: C. Trachomatis D serovar  
US-09-841-132-583

Query Match 32.7%; Score 46.5; DB 9; Length 1053;  
Best Local Similarity 40.7%; Pred. No. 2.3e+02;  
Matches 11; Conservative 7; Mismatches 6; Indels 3; Gaps 1;

QY 1 NLWAAQEYGRELRMSDEFVDSFKKGL 27  
Db 969 NLYLAQPDGKKLSNM---YLTAWKKGL 992

RESULT 14  
US-10-007-693-97  
; Sequence 97, Application US/10007693  
; Publication No. US20020146776A1  
; GENERAL INFORMATION:  
; APPLICANT: Bhatia, Ajay

Search completed: September 23, 2003, 10:03:35  
Job time : 390 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 23, 2003, 09:43:16 ; Search time 22 Seconds  
(without alignments)  
57.715 Million cell updates/sec

Title: US-09-544-664B-2  
Perfect score: 142  
Sequence: 1 NLMAAQEYGRELRMSDEFVDFPKKGL 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description
1	137	96.5	168	1	BAD_HUMAN	Q2934	homo sapien
2	109	76.8	204	1	BAD_MOUSE	Q61337	mus musculus
3	109	76.8	205	1	BAD_RAT	Q35147	rattus norv
4	51	35.9	653	1	HT2A_HUMAN	Q13049	homo sapien
5	50.5	35.6	503	1	MTBR_BPRH1	P09915	bacterioph
6	50.5	35.6	521	1	PPCK_THEFN	Q8r943	thermoanaer
7	50	35.2	370	1	AROG_YEAST	P32449	saccharomyc
8	49.5	34.9	320	1	EXD1_DROME	Q9veb3	drosofila
9	49	34.5	478	1	HKK_DEBOC	P50506	debariomyce
10	48	33.8	370	1	AROG_CANAL	P79023	candida alb
11	48	33.8	526	1	VP5_PTV2A	P30209	bluetongue
12	48	33.8	629	1	SYM_THEMEA	Q33925	thermotoga
13	47.5	33.5	537	1	PPCK_RHISN	P43086	rhizobium s
14	47.5	33.5	595	1	VGL3_BPMD2	O64206	mycobacteri
15	47	33.1	631	1	RPSD_BORBU	P52323	borrelia bu
16	47	33.1	851	1	CE05_MOUSE	Q8k2h3	mus musculus
17	46.5	32.7	181	1	IPYR_MYCPE	Q8evw9	mycoplasma
18	46.5	32.7	333	1	Y591_AQUAE	O66853	aquifex aeo
19	46.5	32.7	1047	1	R1RL_CHLMU	Q9pl93	chlamydia m
20	46.5	32.7	1047	1	R1RL_CHLMU	O84834	chlamydia t
21	46	32.4	198	1	BIM_HUMAN	O43521	homo sapien
22	46	32.4	306	1	MRAW_RICPR	Q9zcy2	ricketsia
23	46	32.4	348	1	FLS_PETHY	Q9yci2	aeropyrum p
24	46	32.4	467	1	TNAE_AERPE	P12436	bluetongue
25	46	32.4	526	1	VP5_PTVIA	P2436	saccharomyc
26	46	32.4	1513	1	STUL_YEAST	P38198	saccharomyc
27	45.5	32.0	143	1	YXAD_BACSU	P42103	bacillus su
28	45.5	32.0	527	1	PPCK_BACSU	Q9k7q7	bacillus ha
29	45.5	32.0	659	1	YYBT_BACSU	P37464	bacillus su
30	45	31.7	878	1	SYV_METJA	Q58413	methanococc
31	45	31.7	901	1	SECA_HAEIN	P43803	haemophilus
32	44.5	31.3	382	1	ISCL_ARCFU	Q30052	archaeoglob
33	44.5	31.3	1339	1	DPOA_LEIDO	O00874	leishmania

RESULT 1  
BAD\_HUMAN  
ID BAD\_HUMAN STANDARD; PRT; 168 AA.  
AC Q92934; O14803;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component 6) (Bcl-XL/Bcl-2 associated death promoter) (BCL2-like 8 protein).  
GN BAD OR BBC6 OR BCL2L8.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Yin D.X., Li Z., Huang B., Chen S., Zhou H.;  
RT "A human protein that interacts with Bcl-2 and have homology to mouse BAD";  
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A., AND PHOSPHORYLATION BY RAF-1.  
RX MEDLINE=97083574; PubMed=8929532;  
RA Wang H.-G., Rapp U.R., Reed J.C.;  
RL "Bcl-2 targets the protein kinase Raf-1 to mitochondria";  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Takayama S., Reed J.C.;  
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A., AND DIMERIZATION.  
RX TISSUE=Bone marrow;  
RX MEDLINE=98049554; PubMed=9388232;  
RA Ottillie S., Diaz J.-L., Horne W., Chang J., Wang Y., Wilson G.,  
RA Chang S., Weeks S., Fritz L.C., Oltsdorf T.;  
RL "Dimerization properties of human BAD";  
RN [5]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

## ALIGNMENTS

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [6]  
RP STRUCTURE BY NMR OF 103-127.  
RX MEDLINE=21073561; PubMed=11206074;  
RA Petros A.M., Nettesheim D.G., Wang Y., Olejniczak E.T., Meadows R.P.,  
RA Mack J., Swift K., Matayoshi E.D., Zhang H., Thompson C.B.,  
RA Fesik S.W.;  
RT "Rationale for Bcl-xL/Bad peptide complex formation from structure,  
RT mutagenesis, and biophysical studies.";  
RL Protein Sci. 9:2528-2534(2000).  
CC -!- FUNCTION: Promotes cell death. Successfully competes for the  
CC binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level  
CC of heterodimerization of these proteins with BAX. Can reverse the  
CC death repressor activity of Bcl-x(L), but not that of Bcl-2 (By  
CC similarity). Appears to act as a link between growth factor  
CC receptor signaling and the apoptotic pathways.  
CC -!- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-  
CC x(L), Bcl-2 and Bcl-w. Also binds protein S100A10 (By similarity).  
CC The Ser-75/Ser-99 phosphorylated form binds 14-3-3 proteins (By  
CC similarity).  
CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon  
CC phosphorylation, locates to the cytoplasm.  
CC -!- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.  
CC -!- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND  
CC BAX for their pro-apoptotic activity and for their interaction  
CC with anti-apoptotic members of the Bcl-2 family.  
CC -!- PTM: Phosphorylated on Ser-75 in response to survival stimuli.  
CC Subsequent phosphorylation on Ser-99 promotes heterodimerization  
CC with 14-3-3 proteins. This interaction then facilitates the  
CC phosphorylation at Ser-118, a site within the BH3 domain, leading  
CC to the release of Bcl-x(L) and the promotion of cell survival.  
CC Ser-99 is the major site of AKT/PKB phosphorylation, Ser-118 the  
CC major site of protein kinase A (CAPK) phosphorylation (by  
CC similarity).  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.  
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
CC -!- CAUTION: Ref.1 sequence differs from that shown due to frameshifts  
CC in position 64 and 91.  
-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
DR EMBL; U66879; AAB36516.1; ALT\_FRAME.  
DR EMBL; AF021792; AAB72092.1; -.  
DR EMBL; AF031523; AAB88124.1; -.  
DR EMBL; BC001901; AAB01901.1; -.  
DR PDB; 1G5J; 07-FEB-01.  
DR Genew; HGNC:936; BAD.  
DR MIM; 603167; -.  
DR GO; GO:0005737; C:cytoplasm; NAS.  
DR GO; GO:0005741; C:mitochondrial outer membrane; NAS.  
DR GO; GO:0005515; F:protein binding activity; NAS.  
DR GO; GO:0008632; P:apoptotic program; NAS.  
DR GO; GO:0006917; P:induction of apoptosis; NAS.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR PROSITE; PS01259; BH3; FALSE\_NEG.  
KW Apoptosis; Phosphorylation; Polymorphism; 3D-structure.  
FT DOMAIN 110 124 BH3.  
FT MOD\_RES 75 75 PHOSPHORYLATION (BY PKA AND PKB) (BY  
FT MOD\_RES 99 99 PHOSPHORYLATION (BY PKA AND PKB) (BY  
FT MOD\_RES 118 118 PHOSPHORYLATION (BY PKA AND PKB) (BY

FT VARIANT 107 107 SIMILARITY).  
FT A -> S (in dbSNP:3729933).  
FT /FTID=VAR\_015380.  
FT HELIX 106 121  
SQ SEQUENCE 168 AA; 18392 MW; 69FD8D27DDEE3241 CRC64;  
Query Match 96.5%; Score 137; DB-1; Length 168;  
Best Local Similarity 96.3%; Pred. No. 8.2e-13;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 NLWAAQCYGRELRRMSDEFVDSFKKGL 27  
||||| |||||||||  
DB 103 NLWAAQRYGRELRRMSDEFVDSFKKGL 129  
RESULT 2  
ID BAD\_MOUSE STANDARD; PRT; 204 AA.  
AC O61337;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component  
DE 6) (Bcl-xL/Bcl-2 associated death promoter).  
GN BAD OR BCL6.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain, and Thymus;  
RX MEDLINE=95136361; PubMed=7834748;  
RA Yang E., Zha J., Jockel J., Boise L.R., Thompson C.B., Korsmeyer S.J.;  
RT "Bad, a heterodimeric partner for Bcl-XL and Bcl-2, displaces Bax and  
RT promotes cell death.";  
RL Cell 80:285-291(1995).  
RN [2]  
RP PHOSPHORYLATION, AND MUTAGENESIS OF SER-112 AND SER-136.  
RX MEDLINE=98022383; PubMed=9381178;  
RA Del Peso L., Gonzalez-Garcia M., Page C., Herrera R., Nunez G.;  
RT "Interleukin-3-induced phosphorylation of BAD through the protein  
RT kinase Akt.";  
RL Science 278:687-689(1997).  
RN [3]  
RP MUTAGENESIS OF SERINE RESIDUES.  
RX MEDLINE=20403302; PubMed=10949026;  
RA Datta S.R., Katsov A., Hu L., Petros A., Fesik S.W., Yaffe M.B.,  
RA Greenberg M.E.;  
RT "14-3-3 proteins and survival kinases cooperate to inactivate BAD by  
RT BH3 domain phosphorylation.";  
RL Mol. Cell 6:41-51(2000).  
CC -!- FUNCTION: Promotes cell death. Successfully competes for the  
CC binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level  
CC of heterodimerization of these proteins with BAX. Can reverse the  
CC death repressor activity of Bcl-x(L), but not that of Bcl-2.  
CC Appears to act as a link between growth factor receptor signaling  
CC and the apoptotic pathways.  
CC -!- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-  
CC x(L), Bcl-2 and Bcl-w. Also binds protein S100A10 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon  
CC phosphorylation, locates to the cytoplasm.  
CC -!- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND  
CC BAX for their pro-apoptotic activity and for their interaction  
CC with anti-apoptotic members of the Bcl-2 family.  
CC -!- PTM: Phosphorylated on Ser-112 in response to survival stimuli.  
CC Subsequent phosphorylation on Ser-136 promotes heterodimerization  
CC with 14-3-3 proteins. This interaction then facilitates the  
CC phosphorylation at Ser-155, a site within the BH3 domain, leading  
CC to the release of Bcl-x(L) and the promotion of cell survival.  
CC Ser-136 is the major site of AKT/PKB phosphorylation, Ser-155 the  
CC major site of protein kinase A (CAPK) phosphorylation.

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CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC -----
CC EMBL: L37296; AAA64465.1; -.
CC PIR: A55671; A55671.
CC HSP: Q92934; IG5J.
CC MGI: 1096330; Bad.
CC InterPro: IPR000712; Bcl2_BH.
CC PROSITE: PS01259; BH3; FALSE_NEG.
CC Apoptosis; Phosphorylation.
CC DOMAIN 147 161 BH3.
CC MOD_RES 112 112 PHOSPHORYLATION (BY PKA AND PKB).
CC MOD_RES 136 136 PHOSPHORYLATION (BY PKA AND PKB).
CC MOD_RES 155 155 PHOSPHORYLATION (BY PKA AND PKB).
CC MUTAGEN 112 112 S->A: NO PHOSPHORYLATION.
CC MUTAGEN 136 136 S->A: NO PHOSPHORYLATION.
CC MUTAGEN 155 155 S->A: NO PHOSPHORYLATION; INTERACTS WITH
CC BCL-X(L).
CC SEQUENCE 204 AA; 22080 MW; 6C2BA910205053F7 CRC64;
Query Match 76.8%; Score 109; DB 1; Length 204;
Best Local Similarity 87.5%; Pred. No. 1.2e-08;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 NLWAAQYGRRLRMSDFVDSFK 24
||||| ||||| ||||| ||||| |||||
Db 140 NLWAAQRYGRRLRMSDFEGSFK 163

RESULT 3
BAD_RAT
ID BAD_RAT STANDARD; PRT; 205 AA.
AC Q35147; O70256; Q9JHX1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component
DE 6) (Bcl-xL/Bcl-2 associated death promoter).
DE BAD.
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF SER-113 AND SER-137.
RC TISSUE=Ovary;
RX MEDLINE=98034386; PubMed=9369453;
RA Hsu S.Y., Kaipia A., Zhu L., Hsueh A.J.W.;
RT "Interference of BAD (Bcl-xL/Bcl-2-associated death promoter)-induced
RT apoptosis in mammalian cells by 14-3-3 isoforms and P11.";
RL Mol. Endocrinol. 11:1858-1867(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98194755; PubMed=9535132;
RA D'Agata V., Magro G., Travali S., Musco S., Cavallaro S.;
RT "Cloning and expression of the programmed cell death regulator BAD in
RT the rat brain.";
RL Neurosci. Lett. 243:137-140(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC TISSUE=Brain;
RX MEDLINE=21109372; PubMed=11161472;
RA Hammer S., Arumae U., Yu L.-Y., Sun Y.-F., Saarma M., Lindholm D.;
RT "Functional characterization of two splice variants of rat BAD and

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RT their interaction with Bcl-w in sympathetic neurons.";
RL Mol. Cell. Neurosci. 17:97-106(2001).
CC -!- FUNCTION: Promotes cell death. Successfully competes for the
CC binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level
CC of heterodimerization of these proteins with BAX. Can reverse the
CC death repressor activity of Bcl-x(L), but not that of Bcl-2 (By
CC similarity). Appears to act as a link between growth factor
CC receptor signaling and the apoptotic pathways.
CC -!- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-
CC x(L), Bcl-2 and Bcl-w. Also binds protein S100A10. The Ser-
CC 113/Ser-137 phosphorylated form binds 14-3-3 proteins.
CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon
CC phosphorylation, locates to the cytoplasm (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Alpha;
CC IsoId=O35147-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=O35147-2; Sequence=YSP_000534;
CC -!- TISSUE SPECIFICITY: Expressed in all tissues tested, including
CC brain, liver, spleen and heart. In the brain, restricted to
CC epithelial cells of the choroid plexus. Isoform alpha is the more
CC abundant form.
CC -!- DOMAIN: Intact BH3 domain is required by BIK, BID, BAX, BAD AND
CC BAX for their pro-apoptotic activity and for their interaction
CC with anti-apoptotic members of the Bcl-2 family.
CC -!- PTM: Phosphorylated on Ser-113 in response to survival stimuli.
CC Subsequent phosphorylation on Ser-137 promotes heterodimerization
CC with 14-3-3 proteins. This interaction then facilitates the
CC phosphorylation at Ser-156, a site within the BH3 domain, leading
CC to the release of Bcl-x(L) and the promotion of cell survival.
CC Ser-137 is the major site of AKT/PKB phosphorylation, Ser-156 the
CC major site of protein kinase A (CAPK) phosphorylation (By
CC similarity).
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF003523; AAC53374.1; -.
CC EMBL: AF031227; AAC15100.1; -.
CC EMBL: AF279910; AAF91427.1; -.
CC EMBL: AF279911; AAF91428.1; -.
CC HSP: Q92934; IG5J.
CC InterPro: IPR000712; Bcl2_BH.
CC PROSITE: PS01259; BH3; FALSE_NEG.
KW Apoptosis; Phosphorylation; Alternative splicing.
FT DOMAIN 148 162 BH3.
FT MOD_RES 113 113 PHOSPHORYLATION (BY PKA AND PKB)
FT (BY SIMILARITY).
FT MOD_RES 137 137 PHOSPHORYLATION (BY PKA AND PKB)
FT (BY SIMILARITY).
FT MOD_RES 156 156 PHOSPHORYLATION (BY PKA AND PKB)
FT (BY SIMILARITY).
FT VARSPPLIC 166 205 LPRKSGATQMRQSASWTRIIQSWDRNLKGGSTPSQ
FT -> EELTYSVEFLPVRAIMEGWFLWSFQSFHTLPTTPP
FT EVAMFPLRYWTALRLIC (in isoform Beta).
FT /FTId=VSP_000534.
FT S->A: NO EFFECT ON HETERODIMERIZATION
FT WITH 14-3-3 PROTEINS.
FT MUTAGEN 113 113 S->A: NO HETERODIMERIZATION WITH 14-3-3
FT PROTEINS. NO EFFECT ON HETERODIMERIZATION
FT WITH BCL2 NOR WITH PROTEIN P11.
FT MUTAGEN 137 137 S->A: NO HETERODIMERIZATION WITH 14-3-3
FT PROTEINS. NO EFFECT ON HETERODIMERIZATION
FT WITH BCL2 NOR WITH PROTEIN P11.
FT CONFLICT 29 34 SDAGGR -> ERGRK (IN REF. 1).
FT SEQUENCE 205 AA; 22228 MW; 7AFA71DA95CF4A81 CRC64;
Query Match 76.8%; Score 109; DB 1; Length 205;

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Best Local Similarity 87.5%; Pred. No. 1.2e-08;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 NLWAAQYGRGLRRMSDEVDSPK 24  
||||| ||||||||| |||  
Db 141 NLWAAQYGRGLRRMSDEVDSPK 164

RESULT 4  
HT2A\_HUMAN  
ID HT2A\_HUMAN STANDARD; PRT; 653 AA.  
AC Q13049; O9NOP8;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Zinc-finger protein HT2A (72 kDa Tat-interacting protein) (Tripartite  
DE motif-containing protein 32).  
GN TRIM32 OR HT2A.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95297135; PubMed=7778269;  
RA Fridell R.A., Harding L.S., Bogerd H.P., Cullen B.R.;  
RT "Identification of a novel human zinc finger protein that  
RT specifically interacts with the activation domain of lentiviral Tat  
RT proteins";  
RL Virology 209:347-357(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Sehra H.;  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skin;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrincci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: MAY PLAY A SIGNIFICANT ROLE IN MEDIATING THE BIOLOGICAL  
CC ACTIVITY OF THE HIV-1 TAT PROTEIN IN VIVO. BINDS SPECIFICALLY TO  
CC THE ACTIVATION DOMAIN OF HIV-1 TAT AND CAN ALSO INTERACT WITH THE  
CC HIV-2 AND EIAV TAT PROTEINS IN VIVO.  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- TISSUE SPECIFICITY: SPLEEN, THYMUS, PROSTATE, TESTIS, OVARY,  
CC INTESTINE AND COLON.  
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.  
CC -!- SIMILARITY: Contains 1 B box-type zinc finger.  
CC -----  
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CC -----

DR EMBL; U18543; AAA86474.1; -.  
DR EMBL; AL133284; CAB92723.1; -.  
DR EMBL; BC003154; AAH03154.1; -.  
DR HSSP; P29590; IBOR.  
DR Genew; HGNC:16380; TRIM32.  
DR MIM; 602290; -.  
DR GO; GO:0005634; C:nucleus; TAS.  
DR GO; GO:0003713; F:transcription co-activator activity; TAS.

DR InterPro; IPR001258; NHL.  
DR InterPro; IPR000315; Znf\_Box.  
DR InterPro; IPR001841; Znf\_ring.  
DR Pfam; PF01436; NHL; 5.  
DR Pfam; PF00643; zf-B\_box; 1.  
DR Pfam; PF00097; zf-C3HC4; 1.  
DR SMART; SM00336; BBOX; 1.  
DR SMART; SM00184; RING; 1.  
DR PROSITE; PS00119; ZF\_BOX; 1.  
DR PROSITE; PS00518; ZF\_RING; 1.  
DR PROSITE; PS50089; ZF\_RING\_2; 1.

KW zinc-finger; Nuclear protein.  
FT DOMAIN 2 6 POLY-ALA.  
FT ZN\_FING 20 65 RING-TYPE.  
FT ZN\_FING 103 133 B\_BOX-TYPE.

FT CONFLICT 27 27 F -> I (IN REF. 1).  
SQ SEQUENCE 653 AA; 71988 MW; D83B1595CA8378FD CRC64;

Query Match 35.9%; Score 51; DB 1; Length 653;  
Best Local Similarity 57.9%; Pred. No. 11;  
Matches 11; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 6 QEYGRGLRRMSDEVDSPK 24  
||||| |||: || | |  
Db 186 QEYGRGLRRMSDEVDSPK 204

RESULT 5  
MTBR\_BPRH1  
ID MTBR\_BPRH1 STANDARD; PRT; 503 AA.  
AC P09915;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Modification methylase Rho1SI (EC 2.1.1.73) (Cytosine-specific  
DE methyltransferase Rho1SI) (Bsu Pils) (M.Rho1SI).  
OS Bacteriophage rho-1ls.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;  
OC Lambda-like viruses.  
OX NCBI\_TaxID=10735;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87246516; PubMed=3109889;  
RA Behrens B., Noyer-Weidner M., Pawlek B., Lauster R., Balganesch T.S.,  
RA Trautner T.A.;  
RT "Organization of multispecific DNA methyltransferases encoded by  
RT temperate Bacillus subtilis phages.";  
RL EMBO J. 6:1137-1142(1987).  
RN [2]  
RP REVISION TO 476.  
RA Trautner T.A.;  
RL Submitted (SEP-1987) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: THIS ENZYME METHYLATES CYTOSINE WITHIN THE SEQUENCES  
CC GGC AND GAGTC.  
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + DNA cytosine = S-  
CC adenosyl-L-homocysteine + DNA 5-methylcytosine.  
CC -!- SIMILARITY: BELONGS TO THE C5-METHYLTRANSFERASE FAMILY.  
CC -----  
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DR EMBL; X05242; CAA28869.1; -.  
 DR PIR; A28137; CTBPRH.  
 DR HSP; P05102; 6MT.  
 DR REBASE; 2835; M.RhollisI.  
 DR InterPro; IPR001525; C5\_DNA\_meth.  
 DR Pfam; PF00145; DNA\_methylase; 1.  
 DR PRINTS; PR00105; C5METTRFRASE.  
 DR TIGRFAMS; TIGR00675; dcm; 1.  
 DR PROSITE; PS00094; C5\_MTASE\_1; 1.  
 DR PROSITE; PS00095; C5\_MTASE\_2; 1.  
 KW Transferase; Methyltransferase; Restriction system.  
 FT ACT\_SITE 78 BY SIMILARITY.  
 SQ SEQUENCE 503 AA; 57129 MW; AAFB0FE01B8129E CRC64;

Query Match 35.6%; Score 50.5; DB 1; Length 503;  
 Best Local Similarity 50.0%; Pred. No. 9.5;  
 Matches 10; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

QY 3 WAAQB-YGRELRRMSDEFVD 21  
 I::I: ||| :|:|  
 Db 207 WSAQIVGRRLRLREYVD 226

## RESULT 6

PPCK\_THETN  
 ID PPCK\_THETN STANDARD; PRT; 521 AA.  
 AC Q8R943;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Phosphoenolpyruvate carboxykinase [ATP] (EC 4.1.1.49) (PEP  
 DE carboxykinase) (Phosphoenolpyruvate carboxylase) (PEPCK).  
 GN PCKA OR PPE1783.  
 OS Thermoanaerobacter tengcongensis.  
 OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;  
 OC Thermoanaerobacteriaceae; Thermoanaerobacter.  
 OX NCBI\_TaxID=119072;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=MB4 / JCM 11007;  
 RX MEDLINE=21992816; PubMed=11997336;  
 RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,  
 RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,  
 RA Tan H., Chen R., Wang J., Yu J., Yang H.;  
 RL "A complete sequence of T. tengcongensis genome.";  
 RL Genome Res. 12:689-700(2002).  
 CC -|- CATALYTIC ACTIVITY: ATP + oxaloacetate = ADP + phosphoenolpyruvate  
 CC + CO(2).  
 CC -|- PATHWAY: Rate-limiting gluconeogenic enzyme.  
 CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -|- SIMILARITY: Belongs to the phosphoenolpyruvate carboxykinase [ATP]  
 CC family.

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DR EMBL; AE013131; AM24977.1; -.  
 DR HAMAP; MF\_00453; -; 1.  
 DR InterPro; IPR001272; PEPCK\_ATP.  
 DR Pfam; PF01293; PEPCK\_ATP; 1.  
 DR ProDom; PD004723; PEPCK\_ATP; 1.  
 DR TIGRFAMS; TIGR00224; pckA; 1.  
 DR PROSITE; PS00532; PEPCK\_ATP; 1.  
 KW Gluconeogenesis; Lyase; Decarboxylase; ATP-binding; Complete proteome.

FT NP\_BIND 227 234 ATP (BY SIMILARITY).  
 SQ SEQUENCE 521 AA; 58771 MW; 1783A3320B106341 CRC64;

Query Match 35.6%; Score 50.5; DB 1; Length 521;  
 Best Local Similarity 30.8%; Pred. No. 9.9;  
 Matches 8; Conservative 9; Mismatches 8; Indels 1; Gaps 1;

QY 1 NLWA-AQEGYGRRLRRMSDEFVDSFKK 25  
 I::I: ||| :|:|  
 Db 481 NTWKDEYDTAKLQAFRIENFQK 506

## RESULT 7

AROG\_YEAST  
 ID AROG\_YEAST STANDARD; PRT; 370 AA.  
 AC P32449;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited  
 DE (EC 4.1.2.15) (Phospho-2-keto-3-deoxyheptonate aldolase) (DAHP  
 DE synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase).  
 GN ARO4 OR YBR249C OR YBR1701.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OX NCBI\_TaxID=4932;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=92225349; PubMed=1348717;  
 RA Kuenzler M., Paravicini G., Egli C., Irniger S., Braus G.H.;  
 RT "Cloning, primary structure and regulation of the ARO4 gene, encoding  
 RT the tyrosine-inhibited 3-deoxy-D-arabino-heptulosonate-7-phosphate  
 RT synthase from Saccharomyces cerevisiae.";  
 RL Gene 113:67-74(1992).  
 RN [2]  
 RP REVISIONS TO 205-207.  
 RA Kuenzler M.;  
 RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.  
 RN [3]

RP SEQUENCE FROM N.A.  
 RC STRAIN=S288c;  
 RX MEDLINE=94078675; PubMed=8256522;  
 RA Daignon F., Biteau N., Aigle M., Crouzet M.;  
 RT "The complete sequence of a 6794 bp segment located on the right arm  
 RT of chromosome II of Saccharomyces cerevisiae. Finding of a putative  
 RT dUTase in a yeast.";  
 RL Yeast 9:1131-1137(1993).  
 RN [4]

RP SEQUENCE FROM N.A.  
 RC STRAIN=S288c;  
 RA Aljinovic G., Pohl F.M., Pohl T.M.;  
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.  
 CC -|- FUNCTION: STEREOSPECIFIC CONDENSATION OF PHOSPHOENOLPYRUVATE (PEP)  
 CC AND D-ERYTHROSE-4-PHOSPHATE (E4P) GIVING RISE TO 3-DEOXY-D-  
 CC ARABINO-HEPTULOSONATE-7-PHOSPHATE (DAHP).  
 CC -|- CATALYTIC ACTIVITY: 2-dehydro-3-deoxy-D-arabino-heptonate 7-  
 CC phosphate + phosphate = phosphoenolpyruvate + D-erythrose 4-  
 CC phosphate + H(2)O.  
 CC -|- ENZYME REGULATION: INHIBITED BY TYROSINE.  
 CC -|- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;  
 CC first step.  
 CC -|- INDUCTION: By amino acid starvation.  
 CC -|- SIMILARITY: BELONGS TO CLASS-I DAHP SYNTHETASE FAMILY.

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DR EMBL; X61107; CAA43419.1; -.
DR EMBL; L20296; AAA65607.1; -.
DR EMBL; Z36118; CAA85212.1; -.
DR PIR; S38185; S38185.
DR HSSP; P00886; 1QR7.
DR SGD; S0000453; ARO4.
DR GO; GO:0003849; F:2-dehydro-3-deoxyphosphoheptonate aldolase . . . ; IDA.
DR InterPro; IPR006219; AroFGH.
DR InterPro; IPR006218; DAHP1/KDSA.
DR Pfam; PF00793; DAHP_synth_1; 1.
DR ProDom; PD005060; AroFGH; 1.
DR TIGRFAMS; TIGR00034; aroFGH; 1.
KW Aromatic amino acid biosynthesis; Lyase; Multigene family.
SQ SEQUENCE 370 AA; 39749 MW; 594ED48F24175979 CRC64;

Query Match 35.2%; Score 50; DB 1; Length 370;
Best Local Similarity 55.6%; Pred. No. 8.1;
Matches 10; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 NLWAAQYGRLELRMSDE 18
Db 80 DLRAAQYALRLKLSDE 97

RESULT 8
EXD1_DROME
ID EXD1_DROME STANDARD; PRT; 320 AA.
AC Q9VEB3; Q95084;
DT 16-OCT-2003 (Rel. 40, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Brix domain containing protein 1 homolog.
GN CG7993.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]

SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
RA Foslø C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glöck A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattie B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

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RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=22426066; PubMed=12537569;
RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
RA George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
RA Rubin G.M., Celniker S.E.;
RT "A Drosophila full-length cDNA resource.";
RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar (By similarity).
CC -!- SIMILARITY: Contains 1 Brix domain.
CC -!- CAUTION: Ref.1 sequence differs from that shown due to erroneous
CC gene model prediction.
CC -----
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CC -----
DR EMBL; AE003721; AAF55314.1; ALT_SEQ.
DR EMBL; AY058248; BAI13477.1; -.
DR FlyBase; FBgn0038585; CG7993.
DR InterPro; IPR007109; Brix.
DR Pfam; PF04427; Brix; 1.
KW Hypothetical protein; Nuclear protein.
FT DOMAIN 30 243 BRIX.
FT CONFLICT 188 188 I -> T (IN REF. 1).
SQ SEQUENCE 320 AA; 36509 MW; EE98936DD68B3703 CRC64;

Query Match 34.9%; Score 49.5; DB 1; Length 320;
Best Local Similarity 43.5%; Pred. No. 8.1;
Matches 10; Conservative 6; Mismatches 4; Indels 3; Gaps 1;

QY 3 WAAQYGRLELRMSDEFVDSFKK 25
Db 149 WAQTE---ELRLRLNLFDTFQR 168

RESULT 9
HXK_DEBOC
ID HXK_DEBOC STANDARD; PRT; 478 AA.
AC P50506;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Hexokinase (EC 2.7.1.1).
GN HXK.
OS Debaryomyces occidentalis (Yeast) (Schwanniomyces occidentalis).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
OX NCBI_TaxID=27300;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 2322 / CBS 819;
RX MEDLINE=95339407; PubMed=7614556;
RA Rose M.;
RT "Molecular and biochemical characterization of the hexokinase from
RT the starch-utilizing yeast Schwanniomyces occidentalis.";
RL Curr. Genet. 27:330-338(1995).
CC -!- CATALYTIC ACTIVITY: ATP + D-hexose = ADP + D-hexose 6-phosphate.
CC -!- PATHWAY: FIRST STEP OF SEVERAL METABOLIC PATHWAYS.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SIMILARITY: BELONGS TO THE HEXOKINASE FAMILY.

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CC -----
DR EMBL; S78714; AAB34892.1; -.
DR PIR; S57203; S57203.
DR HSP; Q26609; LBDG.
DR InterPro; IPR001312; Hexokinase.
DR Pfam; PF03727; hexokinase2; 1.
DR Pfam; PF00349; hexokinase; 1.
DR PRINTS; PR00475; HEXOKINASE.
DR PRODOM; PD001109; Hexokinase; 1.
DR PROSITE; PS00378; HEXOKINASES; 1.
KW Transferase; Kinase; Glycolysis; Allosteric enzyme; ATP-binding.
FT BINDING 111 111 ATP (BY SIMILARITY).
FT DOMAIN 151 177 GLUCOSE-BINDING (POTENTIAL).
SQ SEQUENCE 478 AA; 53066 MW; 080D5F9134478ABA CRC64;

Query Match 34.5%; Score 49; DB 1; Length 478;
Best Local Similarity 42.1%; Pred. No. 15;
Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 9 GRELRMSDEFVDFPKGL 27
D 38 GETLRKITDFISELEKGL 56

RESULT 10
AROG_CANAL STANDARD; PRT; 370 AA.
AC P79023;
DT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited
DE (EC 4.1.2.15) (Phospho-2-keto-3-deoxyheptonate aldolase) (DHP
DE synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase).
GN ARO4.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 11651 / B792;
RA Sousa S., Pereira S.A., Livi G.P.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP PARTIAL SEQUENCE FROM N.A.
RX MEDLINE=96207468; PubMed=8625423;
RA Pereira S.A., Livi G.P.;
RT "Aromatic amino-acid biosynthesis in Candida albicans: identification
RT of the ARO4 gene encoding a second DHP synthase.";
RL Curr. Genet. 29:441-445(1996).
CC -!- FUNCTION: STEREOSPECIFIC CONDENSATION OF PHOSPHOENOLPYRUVATE (PEP)
CC AND D-ERYTHROSE-4-PHOSPHATE (E4P) GIVING RISE TO 3-DEOXY-D-
CC ARABINO-HEPTULOSONATE-7-PHOSPHATE (DHP).
CC -!- CATALYTIC ACTIVITY: 2-dehydro-3-deoxy-D-arabino-heptonate 7-
CC phosphate + phosphate = phosphoenolpyruvate + D-erythrose 4-
CC phosphate + H(2O).
CC -!- ENZYME REGULATION: INHIBITED BY TYROSINE (BY SIMILARITY).
CC -!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC first step.
CC -!- SIMILARITY: BELONGS TO CLASS-I DHP SYNTHETASE FAMILY.
CC -----
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CC -----
DR EMBL; U53216; AAB48240.1; -.
DR HSP; P00886; IQR7.
DR InterPro; IPR006219; AROFGH.
DR InterPro; IPR006218; DAHP1/KDSA.
DR Pfam; PF00793; DAHP_synth_1; 1.
DR PRODOM; PD005060; AroFGH; 1.
DR TIGRfams; TIGR00034; aroFGH; 1.
KW Aromatic amino acid biosynthesis; Lyase; Multigene family.
SQ SEQUENCE 370 AA; 40291 MW; 11E5E324C8D7B6DB CRC64;

Query Match 33.8%; Score 48; DB 1; Length 370;
Best Local Similarity 47.1%; Pred. No. 16;
Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 5 AQEYGRELRMSDEFVD 21
D 74 ALEYGKRLKLADELKD 90

RESULT 11
VP5_BTIV2A STANDARD; PRT; 526 AA.
AC P30209;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Outer capsid protein VP5.
GN S6.
OS Bluetongue virus (serotype 2 / isolate USA).
OC Viruses; dsRNA viruses; Reoviridae; Orbivirus.
OX NCBI_TaxID=10907;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90209358; PubMed=2157314;
RA Hirasawa T., Roy P.;
RT "The complete nucleotide sequence of VP5 of a strain of bluetongue
RT virus of serotype 2 isolated in the USA reveals its close
RT relationship with a virus of serotype 1 isolated in Australia.";
RL Virus Res. 15:107-112(1990).
CC -!- FUNCTION: THE VP5 PROTEIN IS ONE OF THE TWO PROTEINS (WITH VP2)
CC WHICH CONSTITUTE THE VIRUS PARTICLE OUTER CAPSID.
CC -!- SIMILARITY: BELONGS TO THE REOVIRUSES VP5 FAMILY.
CC -----
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CC -----
DR EMBL; X62283; CAA44172.1; -.
DR PIR; A43486; P5XRBU.
DR InterPro; IPR00145; Orbi_VP5.
DR Pfam; PF00901; Orbi_VP5; 1.
KW Coat protein.
SQ SEQUENCE 526 AA; 58953 MW; DE50D6013B983A04 CRC64;

Query Match 33.8%; Score 48; DB 1; Length 526;
Best Local Similarity 41.7%; Pred. No. 23;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 4 AQEYGRELRMSDEFVDFKGL 27
D 309 AIQENHKELMHKIDELTPFKKAM 332

RESULT 12
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SYN\_THEME  
ID SYM\_THEME STANDARD; PRT; 629 AA.  
AC O33925;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase)  
DE (Meths).  
GN METG OR METS OR TM1085.  
OS Thermotoga maritima.  
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.  
OX NCBI\_TaxID=2336;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MSB8 / DSM 3109;  
RX MEDLINE=98021416; PubMed=9380682;  
RA Guipaud O., Marquet E., Noll K.M., de la Tour C.B., Forterre P.;  
RT "Both DNA gyrase and reverse gyrase are present in the  
RT hyperthermophilic bacterium Thermotoga maritima."  
RL Proc. Natl. Acad. Sci. U.S.A. 94:10606-10611(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MSB8 / DSM 3109;  
RX MEDLINE=9287316; PubMed=10360571;  
RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,  
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,  
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,  
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,  
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,  
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;  
RT "Evidence for lateral gene transfer between Archaea and Bacteria from  
RT genome sequence of Thermotoga maritima."  
RL Nature 399:323-329(1999).  
CC -!- FUNCTION: Is required not only for elongation of protein synthesis  
CC but also for the initiation of all mRNA translation through  
CC initiator tRNA(fMet) aminoacylation (By similarity).  
CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + tRNA(Met) = AMP +  
CC diphosphate + L-methionyl-tRNA(Met).  
CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).  
CC -!- SUBUNIT: Homodimer (By similarity).  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.  
CC MetG subfamily 2A.  
CC -!- SIMILARITY: Contains 1 tRNA-binding domain.  
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CC -----  
DR EMBL; U76417; AAB87143.1; -;  
DR EMBL; AE001768; AAD36162.1; -;  
DR PIR; E72297; E72297.  
DR HSSP; P23395; LA88.  
DR TIGR; TM1085; -;  
DR HAMAP; MF\_01228; fused; 1.  
DR InterPro; IPR004495; MetG\_Cterm.  
DR InterPro; IPR002300; tRNA-synt\_1a.  
DR InterPro; IPR001412; tRNA-synt\_1.  
DR InterPro; IPR002304; tRNA-synt\_met.  
DR InterPro; IPR002547; tRNA\_bind.  
DR Pfam; PF00133; tRNA-synt\_1; 1.  
DR Pfam; PF01588; tRNA\_bind; 1.  
DR PIRSF; PIRSF001528; METS dimerising; 1.  
DR PRINTS; PR01041; TRNASYNTHMET.  
DR TIGRFAMS; TIGR00398; metG; 1.  
DR TIGRFAMS; TIGR00399; metG\_Cterm; 1.  
DR PROSITE; PS00178; AA\_TRNA\_LIGASE\_I; FALSE\_NEG.  
DR PROSITE; PS00886; TRSD; 1.  
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;

KW RNA-binding; tRNA-binding; Metal-binding; Zinc; Complete proteome.  
FT SITE 10 20 "HIGH" REGION.  
FT SITE 297 301 "KMSKS" REGION.  
FT DOMAIN 529 629 TRNA-BINDING.  
FT METAL 125 125 ZINC (BY SIMILARITY).  
FT METAL 128 128 ZINC (BY SIMILARITY).  
FT METAL 146 146 ZINC (BY SIMILARITY).  
FT METAL 149 149 ZINC (BY SIMILARITY).  
FT BINDING 300 300 ATP (BY SIMILARITY).  
SQ SEQUENCE 629 AA; 73004 MW; B0E0759F7C78ACEC CRC64;  
  
Query Match 33.8%; Score 48; DB 1; Length 629;  
Best Local Similarity 37.5%; Pred. No. 28;  
Matches 9; Conservative 6; Mismatches 9; Indels 0; Gaps 0;  
  
QY 2 LWAQYGYRELRMSDFVDSFKK 25  
| ||| : : : || : ||:  
Db 55 LQAQAGKDPQEFCELAEKFKR 78  
  
RESULT 13  
PPCK\_RHISN  
ID PPCK\_RHISN STANDARD; PRT; 537 AA.  
AC P43086;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Phosphoenolpyruvate carboxylase [ATP] (EC 4.1.1.49) (PEP  
DE carboxylase) (Phosphoenolpyruvate carboxylase) (PEPCK).  
GN PCKA.  
OS Rhizobium sp. (strain NGR234).  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.  
OX NCBI\_TaxID=394;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92079905; PubMed=1720862;  
RA Oesterbaas M., Finan T.M., Stanley J.;  
RT "Site-directed mutagenesis and DNA sequence of pckA of Rhizobium  
RT NGR234, encoding phosphoenolpyruvate carboxylase: gluconeogenesis  
RT and host-dependent symbiotic phenotype.";  
RL Mol. Genet. 230:257-269(1991).  
CC -!- CATALYTIC ACTIVITY: ATP + oxaloacetate = ADP + phosphoenolpyruvate  
CC + CO(2).  
CC -!- PATHWAY: Rate-limiting gluconeogenic enzyme.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -!- SIMILARITY: Belongs to the phosphoenolpyruvate carboxylase [ATP]  
CC family.  
CC -----  
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CC -----  
DR EMBL; X63291; CAA44925.1; -;  
DR HSSP; P22259; 1AQ2.  
DR HAMAP; MF\_00453; -; 1.  
DR InterPro; IPR001272; PEPCK\_ATP.  
DR Pfam; PF01293; PEPCK\_ATP; 1.  
DR ProDom; PD004723; PEPCK\_ATP; 1.  
DR TIGRFAMS; TIGR00224; pckA; 1.  
DR PROSITE; PS00532; PEPCK\_ATP; 1.  
KW Gluconeogenesis; Lyase; Decarboxylase; ATP-binding.  
FT NP\_BIND 236 243 ATP (BY SIMILARITY).  
SQ SEQUENCE 537 AA; 58370 MW; B2CED7FA54326B1E CRC64;  
  
Query Match 33.5%; Score 47.5; DB 1; Length 537;  
Best Local Similarity 41.7%; Pred. No. 28;  
Matches 10; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

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QY 3 WAA-QEYGRRLRMSDEFVDSFKK 25
   ||||| : ||| : ||| : |||
Db 493 WSAGQAYDAQARRLVDMFIANFAK 516

RESULT 14
VG13_BPMD2
ID VG13_BPMD2 STANDARD; PRT; 595 AA.
AC O64206;
DT 13-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gene 13 protein (GP13).
GN 13.
OS Mycobacteriophage D29.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=28369;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98300335; PubMed=9636706;
RA Ford M.E., Sarkis G.J., Belanger A.E., Hendrix R.W., Hatfull G.F.;
RT "Genome structure of mycobacteriophage D29: implications for phage
   evolution.";
RL J. Mol. Biol. 279:143-164(1998).
CC -!- SIMILARITY: BELONGS TO THE PHAGE TERMINASE FAMILY.
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CC EMBL; AF022214; AAC18453.1; -.
DR PIR; B72801; B72801.
DR InterPro; IPR005021; Phage_termin.
DR Pfam; PF03354; Phage_terminase; 1.
SQ SEQUENCE 595 AA; 66397 MW; AFD123ED5371E263 CRC64;

Query Match 33.5%; Score 47.5; DB 1; Length 595;
Best Local Similarity 45.5%; Pred. No. 31;
Matches 10; Conservative 5; Mismatches 4; Indels 3; Gaps 1;

QY 1 NLWAAQYGRRLRMSDEFVDS 22
   :||| : ||| : ||| :
Db 435 DIWDPQYGGVEVPR---EFVDA 453

RESULT 15
RPSD_BORBU
ID RPSD_BORBU STANDARD; PRT; 631 AA.
AC P52323;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE RNA polymerase sigma factor rpoD (Sigma-70).
GN RPOD OR B80712.
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE OF 89-631 FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RA Pan M.;
RL Thesis (1994), National Taiwan University, Taiwan.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RX MEDLINE=98065943; PubMed=9403685;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
   Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
   Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
```

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RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
   van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
   Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
   Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
   Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochaete, Borrelia
   burgdorferi.";
RL Nature 390:580-586(1997).
RN [3]
RP SEQUENCE OF 165-614 FROM N.A.
RC STRAIN=297;
RA Pan M., Yeh J., Tsai C.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES
   ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND
   THEN IS RELEASED. THIS IS THE PRIMARY SIGMA-FACTOR OF THIS
   BACTERIA.
CC -!- SIMILARITY: Belongs to the sigma-70 factor family.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
   between the Swiss Institute of Bioinformatics and the EMBL outstation -
   the European Bioinformatics Institute. There are no restrictions on its
   use by non-profit institutions as long as its content is in no way
   modified and this statement is not removed. Usage by and for commercial
   entities requires a license agreement (See http://www.isb-sib.ch/announce/
   or send an email to license@isb-sib.ch).
-----
CC EMBL; U17591; AAC44104.1; -.
DR EMBL; AB001171; AAC67061.1; -.
DR EMBL; U68006; AAC45100.1; -.
DR PIR; G70188; G70188.
DR HSSP; P00579; ISIG.
DR TIGR; BB0712; -.
DR InterPro; IPR000943; Sigma_70.
DR Pfam; PF03979; sigma70_r1_1; 1.
DR Pfam; PF00140; sigma70_r1_2; 1.
DR Pfam; PF04542; sigma70_r2; 1.
DR Pfam; PF04539; sigma70_r3; 1.
DR Pfam; PF04545; sigma70_r4; 1.
DR PROSITE; PS00715; SIGMA70_1; 1.
DR PROSITE; PS00716; SIGMA70_2; 1.
KW Transcription regulation; Sigma factor; DNA-directed RNA polymerase;
KW DNA-binding; Complete proteome.
FT DOMAIN 419 432 POLYMERASE CORE BINDING (POTENTIAL).
   H-T-H MOTIF (BY SIMILARITY).
FT DNA_BIND 589 608
SQ SEQUENCE 631 AA; 73642 MW; BD565AB7D8F44796 CRC64;

Query Match 33.1%; Score 47; DB 1; Length 631;
Best Local Similarity 50.0%; Pred. No. 39;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 8 YGRELRRMSDEFVDSFKK 25
   | ||| ||| : ||| :
Db 279 YQEELRIFSDDYIDSANK 296

Search completed: September 23, 2003, 09:47:46
Job time : 26 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model  
Run on: September 23, 2003, 09:43:16 ; Search time 96 Seconds  
(without alignments)  
72.577 Million cell updates/sec

Title: US-09-544-664B-2  
Perfect score: 142  
Sequence: 1 NLWAAQEGRELRMSDEFVDFKKGK 27

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues  
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : SPTREMBL\_23:\*
- 1: sp\_archaea.\*
  - 2: sp\_bacteria.\*
  - 3: sp\_fungi.\*
  - 4: sp\_human.\*
  - 5: sp\_invertebrate.\*
  - 6: sp\_mammal.\*
  - 7: sp\_mhc.\*
  - 8: sp\_organelle.\*
  - 9: sp\_phage.\*
  - 10: sp\_plant.\*
  - 11: sp\_rodent.\*
  - 12: sp\_virus.\*
  - 13: sp\_vertebrate.\*
  - 14: sp\_unclassified.\*
  - 15: sp\_virus.\*
  - 16: sp\_bacteriap.\*
  - 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	84	59.2	146	13 Q9I9N2	Q9i9n2 brachydanio
2	54	38.0	606	10 Q8H4M3	Q8h4m3 oryza sativ
3	53	37.3	85	16 Q8R8Y1	Q8r8y1 thermoanaer
4	52	36.6	889	10 Q8LMF2	Q8lmf2 oryza sativ
5	51	35.9	335	10 Q649Z2	Q649z2 arabidopsis
6	51	35.9	722	17 Q8TVX8	Q8tvx8 methanopyru
7	51	35.9	1248	16 Q9HZQ3	Q9hzz3 pseudomonas
8	50	35.2	173	4 Q8N9S5	Q8n9s5 homo sapien
9	50	35.2	230	16 Q8XXS6	Q8xxs6 raistonia s
10	50	35.2	330	16 Q8F5R1	Q8f5r1 leptospira
11	50	35.2	363	16 Q8EH69	Q8eh69 shewanella
12	50	35.2	371	5 Q9U1L1	Q9ull1 drosophila
13	50	35.2	389	5 Q9W5B6	Q9w5b6 drosophila
14	49.5	34.9	330	5 Q95U84	Q95u84 drosophila
15	49	34.5	214	16 Q8KDC3	Q8kdc3 chlorobium
16	49	34.5	247	2 Q9AJL5	Q9ajl5 streptomyce

17	49	34.5	378	17 Q8PYK0	Q8pyk0 methanosarc
18	49	34.5	564	16 Q9RUK9	Q9ruk9 deinococcus
19	49	34.5	1039	17 Q8TME7	Q8tme7 methanosarc
20	49	34.5	1350	5 O17342	O17342 caenorhabdi
21	49	34.5	1690	17 Q9HKL0	Q9hk10 thermoplasm
22	49	34.5	1713	17 Q97B15	Q97b15 thermoplasm
23	48.5	34.2	130	16 Q8R937	Q8r937 thermoanaer
24	48.5	34.2	937	16 Q97H37	Q97h37 clostridium
25	48.5	34.2	1303	12 Q9QBU0	Q9qbu0 potato mop-
26	48	33.8	196	16 Q8VJS3	Q8vjs3 mycobacteri
27	48	33.8	223	16 Q10843	Q10843 mycobacteri
28	48	33.8	288	10 Q94ID5	Q94id5 oryza sativ
29	48	33.8	295	16 Q9HY62	Q9hy62 pseudomonas
30	48	33.8	339	10 Q9FQ05	Q9fq05 atrichum an
31	48	33.8	357	16 Q8PPY8	Q8ppv8 xanthomonas
32	48	33.8	370	10 Q94ID4	Q94id4 oryza sativ
33	48	33.8	373	10 Q9FU53	Q9fu53 oryza sativ
34	48	33.8	373	10 Q94IE4	Q94ie4 oryza sativ
35	48	33.8	526	12 Q8BAD7	Q8bad7 bluetongue
36	48	33.8	526	12 Q8BAD6	Q8bad6 bluetongue
37	48	33.8	709	10 Q8GUI8	Q8gui8 arabidopsis
38	47.5	33.5	233	17 Q90007	Q90007 archaeoglob
39	47.5	33.5	234	16 Q8ZAP2	Q8zap2 versinia pe
40	47.5	33.5	238	16 Q9GUU3	Q9guu3 staphylococ
41	47.5	33.5	279	10 Q8W4Z1	Q8w4z1 brassica ol
42	47.5	33.5	309	10 Q9SXJ6	Q9sxj6 arabidopsis
43	47.5	33.5	309	10 Q94JY6	Q94jy6 arabidopsis
44	47.5	33.5	310	10 Q82421	Q82421 arabidopsis
45	47.5	33.5	311	10 Q9ST19	Q9st19 brassica ca

ALIGNMENTS

RESULT 1

Q9I9N2 PRELIMINARY; PRT; 146 AA.  
AC Q9I9N2;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE Bad.  
GN BAD.  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20373792; PubMed=10917738;  
RA Inohara N., Nunez G.;  
RT "Genes with homology to mammalian apoptosis regulators identified in zebrafish."  
RL Cell Death Differ. 7:509-510(2000).  
DR EMBL; AF231017; AAF66962.2; -.  
DR HSSP; Q92934; 1G5J.  
DR ZFIN; ZDB-GENE-000616-1; bad.  
SQ SEQUENCE 146 AA; 16546 MW; 28A5650BB5107ECB CRC64;

Query Match 59.2%; Score 84; DB 13; Length 146;  
Best Local Similarity 62.5%; Pred. No. 0.00023;  
Matches 15; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 LWAAQEGRELRMSDEFVDFKKGK 25  
||||:||||:||||:|  
Db 89 LWAAKKGQQLRMSDEFDKGMR 112

RESULT 2

Q8H4M3 PRELIMINARY; PRT; 606 AA.  
ID Q8H4M3  
AC Q8H4M3;









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OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium.
OX NCBI_TaxID=1097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TLS / ATCC 49652 / DSM 12025;
RX MEDLINE=22103685; PubMed=12093901;
RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
RA Dodson R.J., Deboy R., Gwinn M.L., Nelson W.C., Haft D.H.,
RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,
RA Holt I., Umayam I.A., Mason T., Brenner M., Shea T.P., Parksey D.,
RA Niernan W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,
RA Vamathevan J., Khouri H., White O., Gruber T.M., Ketchum K.A.,
RA Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;
RT "The complete genome sequence of Chlorobium tepidum TLS, a
RT photosynthetic, anaerobic, green-sulfur bacterium.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
DR EMBL; AE012874; AAM72364.1; -.
DR TIGR; CT1131; -.
DR InterPro; IPR002785; DUF83.
DR TIGRFAMS; TIGR00372; TIGR00372; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 214 AA; 24004 MW; 56D389219D60B6AD CRC64;

Query Match      34.5%; Score 49; DB 16; Length 214;
Best Local Similarity 37.0%; Pred. No. 43;
Matches 10; Conservative 8; Mismatches 7; Indels 2; Gaps 1;

QY      1 NLWAAQYEGRELRLMSDEFVDSFKKGL 27
      ||: | : ||: : | | : ||:
DB     35 NLYTAE--GREMHERADSAVTSYREGV 59

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Search completed: September 23, 2003, 09:45:06  
Job time : 101 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 15, 2003, 17:16:01 ; Search time 38.1857 Seconds  
(without alignments)  
112.231 Million cell updates/sec

Title: US-09-544-664-3

Perfect score: 145

Sequence: 1 NLWAAQRYGRELRRMSDFEGSKGLP (27)

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_19Jun03.\*

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- 2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*
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- 19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*
- 20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*
- 21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*
- 22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*
- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	145	100.0	27	21 AAB37003	Bcl2 polypeptide B
2	145	100.0	162	22 AAB70370	Shorter murine BAD
3	145	100.0	204	17 AAR95168	bcl-x(L)/bcl-2 ass
4	145	100.0	204	19 AAW61315	Murine BCL-XL/BCL-
5	145	100.0	204	19 AAW61316	Mutant BCL-XL/BCL-
6	145	100.0	204	19 AAW61317	Mutant BCL-XL/BCL-
7	145	100.0	204	19 AAW61318	Mutant BCL-XL/BCL-
8	145	100.0	204	19 AAW58832	Murine BAD protein
9	145	100.0	204	22 AAB70369	Longer murine BAD

10	145	100.0	204	24 ABR39082	Murine BAD protein
11	145	100.0	567	22 AAB00220	Bad-DTR apoptosis
12	138	95.2	26	21 AAB37001	Bcl2 polypeptide B
13	138	95.2	26	21 AAB37002	Bcl2 polypeptide B
14	138	95.2	27	21 AAB37056	Bcl2 polypeptide B
15	138	95.2	28	21 AAB37055	Bcl2 polypeptide B
16	120.5	83.1	166	18 AAW32476	BBC6 protein for r
17	120.5	83.1	168	19 AAW55779	Human Bcl-XL/Bcl-2
18	120.5	83.1	168	21 AAB13512	Human cell prolif
19	120.5	83.1	168	22 AAB70368	Human BAD mutant a
20	120.5	83.1	168	22 AAB48287	Human Bad protein.
21	120.5	83.1	168	22 AAG667888	Amino acid sequenc
22	120.5	83.1	168	24 ABR39081	Human BAD protein
23	120.5	83.1	201	23 AAB41630	Human ovarian anti
24	114	78.6	24	23 AAB78627	Human Bad peptide
25	114	78.6	25	23 AAB56161	PTPC-interacting T
26	114	78.6	25	23 AAG78484	Mutant Bcl2 compet
27	114	78.6	25	23 AAG78493	Mutant Bcl2 compet
28	114	78.6	25	23 AAB78610	Human Bad peptide
29	114	78.6	25	23 AAB78620	Human Bad peptide
30	113	77.9	23	17 AAR95166	bcl-x(L)/bcl-2 ass
31	111	76.6	25	23 AAG78490	Mutant Bcl2 compet
32	111	76.6	25	23 AAB78617	Human Bad peptide
33	110	75.9	25	23 AAG78488	Mutant Bcl2 compet
34	110	75.9	25	23 AAG78489	Mutant Bcl2 compet
35	110	75.9	25	23 AAB78615	Human Bad peptide
36	110	75.9	25	23 AAB78616	Human Bad peptide
37	109	75.2	23	23 AAB78628	Human Bad peptide
38	109	75.2	25	23 AAG78486	Mutant Bcl2 compet
39	109	75.2	25	23 AAG78492	Mutant Bcl2 compet
40	109	75.2	25	23 AAB78497	Human Bad peptide
41	109	75.2	25	23 AAB78612	Human Bad peptide
42	109	75.2	25	23 AAB78619	Human Bad peptide
43	109	75.2	25	23 AAB78624	Human Bad peptide
44	108	74.5	25	23 AAG78485	Mutant Bcl2 compet
45	108	74.5	25	23 AAB78611	Human Bad peptide

ALIGNMENTS

RESULT 1  
AAB37003  
ID AAB37003 standard; peptide; 27 AA.  
AC AAB37003;  
DT 28-FEB-2001 (first entry)  
XX Bcl2 polypeptide BH3 domain peptide #3.

Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;  
cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;  
apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;  
colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;  
melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;  
stroke; myocardial infarction.

Homo sapiens.  
WO200059526-A1.  
12-OCT-2000.  
06-APR-2000; 2000WO-US09352.  
07-APR-1999; 99US-0128202.  
(UYJE-) UNIV JEFFERSON THOMAS.  
Huang Z, Wang J, Zhang Z, Shan S, Lu Z;  
WPI; 2000-679325/66.

XX New peptide conjugates for modulating apoptosis or for inhibiting B  
 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for  
 PT treating neurodegenerative disorders, stroke, or cancer  
 XX  
 PS Claim 18; Page 17; 74pp; English.  
 XX  
 CC The invention relates to a peptide conjugate having the formula:  
 CC (R-X)n-peptide where n = 1-10; X = C=O, when the R-X group is attached  
 CC to the N-terminus of the peptide, or a side chain of the peptide where  
 CC the functional group of the side chain is NH<sub>2</sub> or OH; or X = O or NH,  
 CC when the R-X group is attached to the C-terminus of the peptide, or a  
 CC side chain of the peptide, where the side chain functional group is COOH  
 CC or CONH<sub>2</sub>; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one  
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally  
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,  
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain  
 CC alkyl group, or benzyl. The peptides AAB7001-B37058 represent examples  
 CC of the peptide portion of the conjugate. The peptides represent analogues  
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of  
 CC the BH3 domain of the cell death agonist Bad. The peptide conjugate is  
 CC useful for modulating apoptosis in the cells of a subject, or for  
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of  
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2  
 CC function. In particular, the peptide conjugate is useful for treating a  
 CC subject afflicted with a cancer characterized by cancer cells that  
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,  
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or  
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide  
 CC conjugate is also useful for treating disorders characterized by  
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired  
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.  
 XX  
 SQ Sequence 27 AA;  
 Query Match 100.0%; Score 145; DB 21; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-15;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 NLWAAQRYGRELRRMSDEFGSGFKGLP 27  
 |||||  
 DB 1 NLWAAQRYGRELRRMSDEFGSGFKGLP 27  
 |||||  
 RESULT 2  
 AAB70370  
 ID AAB70370 standard; protein; 162 AA.  
 XX  
 AC AAB70370;  
 XX  
 DT 02-MAY-2001 (first entry)  
 XX  
 DE Shorter murine BAD mutant amino acid sequence SEQ ID NO:3.  
 XX  
 KW Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;  
 KW immunostimulant; neuroprotective; neurotropic; antiischaemic; vulnary;  
 KW cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing;  
 KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;  
 KW immunodeficiency disease; neurodegenerative disease; viral infection;  
 KW ischaemic cell death; reperfusion cell death; arthritis; infertility;  
 KW lymphoproliferative condition; inflammation; autoimmune disease.  
 XX  
 OS Mus musculus.  
 OS Synthetic.  
 XX  
 XX WO200110888-A1.  
 PN  
 XX  
 PD 15-FEB-2001.  
 XX  
 XX 30-MAY-2000; 2000WO-US11864.  
 PF  
 XX 28-MAY-1999; 99US-0136783.  
 PR  
 XX

PA (APOF-) APOPTOSIS TECHNOLOGY INC.  
 XX  
 PI Zhou X;  
 XX  
 DR WPI; 2001-138734/14.  
 XX  
 PS New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,  
 PT useful for screening for candidate compounds which induce or inhibit  
 PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or  
 PT Ser113 -  
 XX  
 PS Claim 7; Page 148-149; 157pp; English.  
 XX  
 CC The present invention describes an isolated or synthetic polypeptide  
 CC (I) comprising a less than full length amino acid sequence of a mutant  
 CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its  
 CC fragment, which contains amino acid substitutions at Ser118 of a human  
 CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine  
 CC BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,  
 CC neurotropic, antiischaemic, vulnary, cytostatic, antiviral,  
 CC antiarthritic, antiinflammatory and immunosuppressive activities, and  
 CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and  
 CC polynucleotides can be used for screening candidate compounds and drugs  
 CC for activity that promote cell survival or apoptosis. Other uses include  
 CC inducing or inhibiting apoptosis in a cell. Candidate compounds  
 CC identified and (mutant) BAD polypeptides are useful in treating  
 CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell  
 CC death, reperfusion cell death, wound healing, cancer, viral infections,  
 CC lymphoproliferative conditions, arthritis, infertility, inflammation and  
 CC autoimmune diseases. The present sequence represents a specifically  
 CC claimed shorter murine BAD mutant amino acid sequence from the present  
 CC invention.  
 XX  
 SQ Sequence 162 AA;  
 Query Match 100.0%; Score 145; DB 22; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-14;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 NLWAAQRYGRELRRMSDEFGSGFKGLP 27  
 |||||  
 DB 98 NLWAAQRYGRELRRMSDEFGSGFKGLP 124  
 |||||  
 RESULT 3  
 AAR95168  
 ID AAR95168 standard; Protein; 204 AA.  
 XX  
 AC AAR95168;  
 XX  
 DT 06-JAN-1997 (first entry)  
 XX  
 DE bcl-x(L)/bcl-2 associated death promoter protein.  
 XX  
 KW Epitope; murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke;  
 KW polypeptide; bcl-x; cell death; regulate; BH1; BH2; apoptotic cell death;  
 KW cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS;  
 KW neurodegenerative disease; senescence; ischaemia; neoplasia.  
 XX  
 OS Mus musculus.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 147..149  
 FT /note= "BH1 conserved amino acids"  
 FT Region 191..192  
 FT /note= "BH2 conserved amino acids"  
 FT Domain 38..61  
 FT /note= "PEST sequence"  
 FT Domain 111..130  
 FT /note= "PEST sequence"  
 XX  
 PN WO9613614-A1.  
 XX

PD 09-MAY-1996.  
XX  
PF 31-OCT-1995; 95WO-US14246.  
XX  
XX 31-OCT-1994; 94US-0333565.  
PR  
XX (UNIW ) UNIV WASHINGTON.  
PA  
XX  
XX  
PI Korsmeyer SJ;  
XX  
XX WPI; 1996-251465/25.  
DR N-PSDB; AAT29479.  
DR  
XX Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter -  
PT useful to treat neoplasia and apoptosis and to identify agents  
PT inhibiting its binding to bcl-2 or bcl-x(L) to form heteromultimers  
XX  
XX  
PS Claim 3; Fig 1; 130pp; English.  
XX  
CC This sequence represents the murine bcl-x(L)/bcl-2 associated death  
CC promoter (Bad) gene. Bad is a 22.1 kD protein which interacts with  
CC bcl-2 and bcl-x proteins and regulates cell death. It has homology  
CC to the bcl-2-related family clustered in the BH1 and BH2 domain. Bad  
CC has been found to hybridise to bcl-x(L) and bcl-2 in yeast two-hybrid  
CC assays and in vivo in mammalian cells. Overexpressed Bad counters the  
CC death inhibitory activity of bcl-x(L), but is much less effective at  
CC countering the death inhibitory activity of bcl-2. Bad expression can  
CC accelerate apoptotic cell death induced by cytokine deprivation in an  
CC IL-3 dependent cell line expressing bcl-x(L), and its also counters the  
CC death repressor activity of bcl-x(L). Bad competes with Bax for binding  
CC to bcl-x(L). Bad may be used to identify agents which inhibit its  
CC binding to bcl-2 or bcl-x(L) to form heterodimers. Such agents may be  
CC used to treat neurodegenerative diseases, immunodeficiency diseases,  
CC e.g. AIDS, senescence or ischaemia.  
XX  
SQ Sequence 204 AA;  
Query Match 100.0%; Score 145; DB 17; Length 204;  
Best Local Similarity 100.0%; Pred. No. 2.4e-14;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NLWAAQRYGRELRRMSDEFGSFKGLP 27  
Db ||||||||||||||||||||||||||||  
140 NLWAAQRYGRELRRMSDEFGSFKGLP 166  
RESULT 4  
AAW61315  
ID AAW61315 standard; Protein; 204 AA.  
XX  
XX AAW61315;  
AC  
XX  
XX 07-OCT-1998 (first entry)  
DT  
XX  
DE Murine BCL-XL/BCL-2 associated cell death regulator.  
XX  
XX Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;  
KW serine substituted mutant; apoptosis; cancer; viral infection.  
XX  
XX Mus sp.  
OS  
XX  
XX WO9817682-A1.  
PN  
XX  
XX 30-APR-1998.  
PD  
XX  
XX 17-OCT-1997; 97WO-US19175.  
PF  
XX  
XX 18-OCT-1996; 96US-0733505.  
PR  
XX (UNIW ) UNIV WASHINGTON.  
PA  
XX Korsmeyer SJ;  
PI  
XX

DR WPI; 1998-261422/23.  
DR N-PSDB; AAV27833.  
XX  
PT New mutant BAD polypeptide with phosphorylatable serine replaced -  
PT useful for, e.g. treating reduced apoptosis such as in cancer or  
PT viral infection  
XX  
XX  
PS Claim 1; Fig 10; 95pp; English.  
XX  
CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell  
CC death regulator) proteins, having an amino acid other than Ser at  
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The  
CC present sequence is the murine BAD protein. Also described are: (1)  
CC fragments of mutant BAD protein able to decrease cell viability; (2)  
CC fusion proteins of mutant BAD with a heterologous polypeptide that  
CC increases intracellular delivery. Mutant BAD proteins are used to treat  
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,  
CC viral infection, lymphoproliferation, arthritis, infertility,  
CC inflammation and autoimmune disease. Polynucleotide sequences encoding  
CC mutant BAD proteins can be used similarly by gene therapy or to produce  
CC transgenic animals for use as disease models or in drug screening. BAD  
CC proteins phosphorylated at specified Ser are used to screen for enhancers  
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful  
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,  
CC aging or ischaemic cell death. The apoptotic status of cells is  
CC determined by measuring relative amounts of phosphorylated and non-  
CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have  
CC greater death-promoting activity than wild-type BAD which can become  
CC phosphorylated on the specified Ser, forming a product that does not  
CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family  
CC proteins in the cytosol, thus promoting cell survival. The mutants with  
CC Ser substituted cannot bind 14-3-3.  
XX  
SQ Sequence 204 AA;  
Query Match 100.0%; Score 145; DB 19; Length 204;  
Best Local Similarity 100.0%; Pred. No. 2.4e-14;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NLWAAQRYGRELRRMSDEFGSFKGLP 27  
Db ||||||||||||||||||||||||||||  
140 NLWAAQRYGRELRRMSDEFGSFKGLP 166  
RESULT 5  
AAW61316  
ID AAW61316 standard; Protein; 204 AA.  
XX  
XX AAW61316;  
AC  
XX  
XX 07-OCT-1998 (first entry)  
DT  
XX  
DE Mutant BCL-XL/BCL-2 associated cell death regulator #1.  
XX  
XX Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;  
KW serine substituted mutant; apoptosis; cancer; viral infection.  
XX  
XX Mus sp.  
OS  
XX  
XX Synthetic.  
PN  
XX  
XX WO9817682-A1.  
PN  
XX  
XX 30-APR-1998.  
PD  
XX  
XX 17-OCT-1997; 97WO-US19175.  
PF  
XX  
XX 18-OCT-1996; 96US-0733505.  
PR  
XX (UNIW ) UNIV WASHINGTON.  
PA  
XX Korsmeyer SJ;  
PI  
XX  
XX WPI; 1998-261422/23.  
DR

DR N-PSDB; AAV27834.

XX New mutant BAD polypeptide with phosphorylatable serine replaced -

PT useful for, e.g. treating reduced apoptosis such as in cancer or

PT viral infection

XX

PS Claim 7; Page 59; 95pp; English.

XX

CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell

CC death regulator) proteins, having an amino acid other than Ser at

CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The

CC present sequence represents a mutant BAD protein. Also described are: (1)

CC fragments of mutant BAD protein able to decrease cell viability; (2)

CC fusion proteins of mutant BAD with a heterologous polypeptide that

CC increases intracellular delivery. Mutant BAD proteins are used to treat

CC or prevent diseases associated with reduced apoptosis, e.g. cancer,

CC viral infection, lymphoproliferation, arthritis, infertility,

CC inflammation and autoimmune disease. Polynucleotide sequences encoding

CC mutant BAD proteins can be used similarly by gene therapy or to produce

CC transgenic animals for use as disease models or in drug screening. BAD

CC proteins phosphorylated at specified Ser are used to screen for enhancers

CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful

CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,

CC aging or ischaemic cell death. The apoptotic status of cells is

CC determined by measuring relative amounts of phosphorylated and non-

CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have

CC greater death-promoting activity than wild-type BAD which can become

CC phosphorylated on the specified Ser, forming a product that does not

CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family

CC proteins in the cytosol, thus promoting cell survival. The mutants with

CC Ser substituted cannot bind 14-3-3.

XX

SQ Sequence 204 AA;

Query Match 100.0%; Score 145; DB 19; Length 204;

Best Local Similarity 100.0%; Pred. No. 2.4e-14;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFEGSFKGLP 27

Db 140 NLWAAQRYGRELRRMSDEFEGSFKGLP 166

RESULT 6

AAW61317

ID AAW61317 standard; Protein; 204 AA.

XX

AC AAW61317;

XX

DT 07-OCT-1998 (first entry)

XX

DE Mutant BCL-XL/BCL-2 associated cell death regulator #2.

XX

KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;

KW serine substituted mutant; apoptosis; cancer; viral infection.

XX

OS Mus sp.

OS Synthetic.

XX

PN W09817682-A1.

XX

PD 30-APR-1998.

XX

PF 17-OCT-1997; 97WO-US19175.

XX

PR 18-OCT-1996; 96US-0733505.

XX

PA (UNIW ) UNIV WASHINGTON.

XX

PI Korsmeyer SJ;

XX

DR WPI; 1998-261422/23.

DR N-PSDB; AAV27835.

XX New mutant BAD polypeptide with phosphorylatable serine replaced -

PT useful for, e.g. treating reduced apoptosis such as in cancer or

PT viral infection

XX

PS Claim 7; Page 60; 95pp; English.

XX

CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell

CC death regulator) proteins, having an amino acid other than Ser at

CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The

CC present sequence represents a mutant BAD protein. Also described are: (1)

CC fragments of mutant BAD protein able to decrease cell viability; (2)

CC fusion proteins of mutant BAD with a heterologous polypeptide that

CC increases intracellular delivery. Mutant BAD proteins are used to treat

CC or prevent diseases associated with reduced apoptosis, e.g. cancer,

CC viral infection, lymphoproliferation, arthritis, infertility,

CC inflammation and autoimmune disease. Polynucleotide sequences encoding

CC mutant BAD proteins can be used similarly by gene therapy or to produce

CC transgenic animals for use as disease models or in drug screening. BAD

CC proteins phosphorylated at specified Ser are used to screen for enhancers

CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful

CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,

CC aging or ischaemic cell death. The apoptotic status of cells is

CC determined by measuring relative amounts of phosphorylated and non-

CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have

CC greater death-promoting activity than wild-type BAD which can become

CC phosphorylated on the specified Ser, forming a product that does not

CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family

CC proteins in the cytosol, thus promoting cell survival. The mutants with

CC Ser substituted cannot bind 14-3-3.

XX

SQ Sequence 204 AA;

Query Match 100.0%; Score 145; DB 19; Length 204;

Best Local Similarity 100.0%; Pred. No. 2.4e-14;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFEGSFKGLP 27

Db 140 NLWAAQRYGRELRRMSDEFEGSFKGLP 166

RESULT 7

AAW61318

ID AAW61318 standard; Protein; 204 AA.

XX

AC AAW61318;

XX

DT 07-OCT-1998 (first entry)

XX

DE Mutant BCL-XL/BCL-2 associated cell death regulator #3.

XX

KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;

KW serine substituted mutant; apoptosis; cancer; viral infection.

XX

OS Mus sp.

OS Synthetic.

XX

PN W09817682-A1.

XX

PD 30-APR-1998.

XX

PF 17-OCT-1997; 97WO-US19175.

XX

PR 18-OCT-1996; 96US-0733505.

XX

PA (UNIW ) UNIV WASHINGTON.

XX

PI Korsmeyer SJ;

XX

DR WPI; 1998-261422/23.

DR N-PSDB; AAV27836.

PT New mutant BAD polypeptide with phosphorylatable serine replaced -  
 PT useful for, e.g. treating reduced apoptosis such as in cancer or  
 PT viral infection  
 XX  
 PS Claim 7; Page 60-61; 95pp; English.  
 XX  
 CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell  
 CC death regulator) proteins, having an amino acid other than Ser at  
 CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The  
 CC present sequence represents a mutant BAD protein. Also described are: (1)  
 CC fragments of mutant BAD protein able to decrease cell viability; (2)  
 CC fusion proteins of mutant BAD with a heterologous polypeptide that  
 CC increases intracellular delivery. Mutant BAD proteins are used to treat  
 CC or prevent diseases associated with reduced apoptosis, e.g. cancer,  
 CC viral infection, lymphoproliferation, arthritis, infertility,  
 CC inflammation and autoimmune disease. Polynucleotide sequences encoding  
 CC mutant BAD proteins can be used similarly by gene therapy or to produce  
 CC transgenic animals for use as disease models or in drug screening. BAD  
 CC proteins phosphorylated at specified Ser are used to screen for enhancers  
 CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful  
 CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,  
 CC aging or ischaemic cell death. The apoptotic status of cells is  
 CC determined by measuring relative amounts of phosphorylated and non-  
 CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have  
 CC greater death-promoting activity than wild-type BAD which can become  
 CC phosphorylated on the specified Ser, forming a product that does not  
 CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family  
 CC proteins in the cytosol, thus promoting cell survival. The mutants with  
 CC Ser substituted cannot bind 14-3-3.  
 XX  
 SQ Sequence 204 AA;

Query Match 100.0%; Score 145; DB 19; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-14;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFEGSFKGLP 27  
 |||||  
 Db 140 NLWAAQRYGRELRRMSDEFEGSFKGLP 166

RESULT 8  
 AAW58832  
 ID AAW58832 standard; protein; 204 AA.  
 XX  
 AC AAW58832;  
 XX  
 DT 23-JUL-1998 (first entry)  
 XX  
 DE Murine BAD protein.  
 XX  
 KW BAD protein; Bcl-XL/Bcl-2 associated cell death regulator; 14-3-3;  
 KW serine phosphorylation; post-translational modification; apoptosis;  
 KW signal transduction regulator; phosphoserine phosphatase; senescence;  
 KW immunodeficiency disease; neurodegenerative disease; infertility;  
 KW cancer, viral infection; lymphoproliferative condition; arthritis;  
 KW inflammation; autoimmune diseases.  
 XX  
 OS Mus sp.

XX  
 XX WO9809643-A1.  
 PN  
 XX  
 PD 12-MAR-1998.  
 XX  
 XX 09-SEP-1997; 97WO-US15871.  
 PF  
 XX 09-SEP-1996; 96US-0707868.  
 PR  
 XX (UNIV ) UNIV WASHINGTON.  
 PA  
 XX Korsmeyer SJ;  
 XX  
 PI  
 XX WPI; 1998-207049/18.  
 DR

XX Serine-phosphorylated Bcl-X-L/Bcl-2 Associated cell Death regulator  
 PT polypeptide - useful for modulation of apoptosis associated with,  
 PT e.g. cancer and immunodeficiency diseases  
 XX  
 PS Claim 3; Fig 8; 61pp; English.  
 XX  
 CC This sequence represents a novel serine-phosphorylated protein, BAD  
 CC (Bcl-XL/Bcl-2 associated cell death regulator). The serine residue is  
 CC phosphorylated in a post-translational modification and allows binding  
 CC to the 14-3-3 protein which is a signal transduction regulator.  
 CC Modulators of phosphorylated BAD, which act through inhibition/activation  
 CC of a phosphoserine phosphatase, are useful for preventing/treating  
 CC increased/decreased apoptosis in a cell. The increased apoptosis may  
 CC result from immunodeficiency diseases, senescence, neurodegenerative  
 CC disease, ischaemic cell death, reperfusion cell death, infertility and  
 CC wound-healing. Decreased apoptosis may result from cancer, viral  
 CC infection, lymphoproliferative conditions, arthritis, infertility,  
 CC inflammation and autoimmune diseases. Measuring the amount of  
 CC phosphorylated compared to unphosphorylated BAD polypeptide and/or total  
 CC BAD in a cell is useful for determining the apoptotic state of a cell.  
 XX  
 SQ Sequence 204 AA;

Query Match 100.0%; Score 145; DB 19; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-14;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFEGSFKGLP 27  
 |||||  
 Db 140 NLWAAQRYGRELRRMSDEFEGSFKGLP 166

RESULT 9  
 AAB70369  
 ID AAB70369 standard; protein; 204 AA.

XX  
 AC AAB70369;  
 XX  
 DT 02-MAY-2001 (first entry)  
 XX

DE Longer murine BAD mutant amino acid sequence SEQ ID NO:2.  
 XX  
 KW Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;  
 KW immunostimulant; neuroprotective; nootropic; antiischaemic; vulnery;  
 KW cytostatic; antiviral; antiarthritis; antiinflammatory; wound healing;  
 KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;  
 KW immunodeficiency disease; neurodegenerative disease; viral infection;  
 KW ischaemic cell death; reperfusion cell death; arthritis; infertility;  
 KW lymphoproliferative condition; inflammation; autoimmune disease.

XX  
 OS Mus musculus.  
 OS Synthetic.  
 XX  
 PN WO200110888-A1.  
 XX  
 PD 15-FEB-2001.  
 XX  
 XX 30-MAY-2000; 2000WO-US11864.  
 PF  
 XX 28-MAY-1999; 99US-0136783.  
 PR  
 XX (APOPTOSIS TECHNOLOGY INC.  
 PA  
 XX Zhou X;  
 PI  
 XX WPI; 2001-138734/14.  
 DR

XX New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,  
 PT useful for screening for candidate compounds which induce or inhibit  
 PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or  
 PT Ser113 -  
 XX

PS Claim 4; Page 148; 157pp; English.

XX The present invention describes an isolated or synthetic polypeptide  
 CC (I) comprising a less than full length amino acid sequence of a mutant  
 CC Bcl-Xl/Bcl-2 associated cell death regulator polypeptide (BAD) or its  
 CC fragment, which contains amino acid substitutions at Ser118 of a human  
 CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine  
 CC BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,  
 CC nootropic, antiischaemic, vulnerary, cytostatic, antiviral,  
 CC antiarthritic, antiinflammatory and immunosuppressive activities, and  
 CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and  
 CC polynucleotides can be used for screening candidate compounds and drugs  
 CC for activity that promote cell survival or apoptosis. Other uses include  
 CC inducing or inhibiting apoptosis in a cell. Candidate compounds  
 CC identified and (mutant) BAD polypeptides are useful in treating  
 CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell  
 CC death, reperfusion cell death, wound healing, cancer, viral infections,  
 CC lymphoproliferative conditions, arthritis, infertility, inflammation and  
 CC autoimmune diseases. The present sequence represents a specifically  
 CC claimed longer murine BAD mutant amino acid sequence from the present  
 CC invention.

XX Sequence 204 AA;

Query Match 100.0%; Score 145; DB 22; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-14;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFGSKGLP 27

Db 140 NLWAAQRYGRELRRMSDEFGSKGLP 166

RESULT 10

ABR39082  
 ID ABR39082 standard; Protein; 204 AA.

XX ABR39082;

XX 10-MAY-2003 (first entry)

DE Murine BAD protein SEQ ID NO:4.

XX Murine; BAD; herpes simplex virus; HSV; US3; herpes virus; apoptosis;  
 KW virucide; infection.

XX Mus musculus.

XX WO2003012049-A2.

PN 13-FEB-2003.

XX 31-JUL-2002; 2002WO-US24177.

PF 31-JUL-2001; 2001US-308929P.

XX (UYCH-) UNIV CHICAGO.

XX Munger J, Roizman B;

XX WPI; 2003-248168/24.

DR N-PSDB; ABZ81201.

XX Inducing apoptosis in a cell infected with herpes simplex virus, HSV,  
 PT by administering to the cell, a composition comprising an agent that  
 PT inhibits phosphorylation of pro-apoptotic polypeptide BAD by HSV US3 -

XX Claim 15; Page 168; 192pp; English.

XX The present invention describes a method (M1) for inducing apoptosis in  
 CC a cell infected with herpes simplex virus (HSV), which comprises  
 CC administering to the cell, a composition having an agent that inhibits  
 CC phosphorylation of pro-apoptotic polypeptide BAD by HSV US3. Also

CC described is a method (M2) for treating a patient infected with HSV, by  
 CC administering to the patient, a composition comprising a peptide  
 CC comprising a sequence of 4-100 continuous amino acids of a 168 residue  
 CC amino acid sequence (see ABR39081), where the peptide comprises Ser112,  
 CC Ser135, or Ser155, or their combinations. BAD has virucide activity.  
 CC M1 is useful for inducing apoptosis in a cell infected with HSV, where  
 CC the cell is in a human. M2 is useful for treating a patient infected  
 CC with HSV. The present sequence represents murine BAD, which is used in  
 CC the exemplification of the present invention.

XX Sequence 204 AA;

Query Match 100.0%; Score 145; DB 24; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-14;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFGSKGLP 27

Db 140 NLWAAQRYGRELRRMSDEFGSKGLP 166

RESULT 11

AAU00220  
 ID AAU00220 standard; Protein; 567 AA.

XX AAU00220;

XX 31-MAY-2001 (first entry)

DE Bad-DTRR apoptosis-modifying fusion protein.

XX Mouse; Bad-DTRR; apoptosis; cancer; spinal muscular atrophy;

KW diphtheria toxin receptor binding domain; DTR; neoplasm; tumour;

KW hyper-proliferation; Alzheimer's disease; neurodegenerative disorder;

KW transient ischaemic neuronal injury; stroke; spinal cord injury;

KW Huntington's disease.

XX Chimeric - Mus sp.

OS Chimeric - Corynebacterium diphtheriae.

OS Chimeric - Synthetic.

XX Key Location/Qualifiers

FT Region 3..12

FT /note= "10x histidine tag"

XX WO200112661-A2.

PN 22-FEB-2001.

XX 15-AUG-2000; 2000WO-US22293.

XX 16-AUG-1999; 99US-0149220.

XX (HARD ) HARVARD COLLEGE.

PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Youle RJ, Liu X, Collier RJ;

XX WPI; 2001-218343/22.

DR N-PSDB; AAS00248.

XX Novel fusion protein for modifying apoptosis in target cell and  
 PT reducing apoptosis after transient ischaemic neuronal injury, has two  
 PT domains which targets protein to a cell and modifies apoptotic response  
 PT of cell -

XX Claim 4; Page 59-61; 65pp; English.

XX The sequence represents the amino acid sequence of Bad-DTRR apoptosis-  
 CC modifying fusion protein comprising Bad gene sequence fused via a short  
 CC linker to diphtheria toxin translocation domain (DTRR). The  
 CC functional apoptosis-modifying fusion protein is capable of binding a  
 CC target cell and integrating into or crossing a cellular membrane of the

CC target cell. The apoptosis-modifying fusion protein comprises at least  
CC two domains: the DTR domain, which targets the fusion protein to the  
CC target cell and the Bcl-XL domain, which modifies an apoptotic response  
CC of the target cell. The fusion protein is useful for modifying  
CC (inhibiting or enhancing) apoptosis in a target cell, such as neuron,  
CC lymphocyte, cancer, neoplasm, macrophage, epithelial, stem, tumour or  
CC hyper-proliferative cell or an adipocyte. It is also useful for reducing  
CC apoptosis in a subject after transient ischaemic neuronal injury,  
CC especially spinal cord injury. The fusion protein may be used to treat  
CC various diseases and injury conditions through inhibition or enhancement  
CC of apoptotic cellular response, including neurodegenerative disorders  
CC such as Alzheimer's disease, Huntington's disease, spinal muscular  
CC atrophy, stroke episodes and unregulated cell growth as in tumours and  
CC various cancers. The apoptosis-modifying fusion protein can be delivered  
CC effectively throughout the body and targeted to selective tissue and  
CC cells.

XX  
SQ Sequence 567 AA;  
Query Match 100.0%; Score 145; DB 22; Length 567;  
Best Local Similarity 100.0%; Pred. No. 7.4e-14;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDFEGSFKGLP 27  
Db 161 NLWAAQRYGRELRRMSDFEGSFKGLP 187  
|||||

RESULT 12  
AAB37001  
ID AAB37001 standard; peptide; 26 AA.  
XX  
AC AAB37001;  
XX  
DT 28-FEB-2001 (first entry)  
XX  
DE Bcl2 polypeptide BH3 domain peptide #1.  
XX  
KW Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;  
KW cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;  
KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;  
KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;  
KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;  
KW stroke; myocardial infarction.  
XX  
OS Homo sapiens.  
XX  
PN WO200059526-A1.  
XX  
PD 12-OCT-2000.  
XX  
PF 06-APR-2000; 2000WO-US09352.  
XX  
PR 07-APR-1999; 99US-0128202.  
XX  
PA (UYJE-) UNIV JEFFERSON THOMAS.  
XX  
PI Huang Z, Wang J, Zhang Z, Shan S, Lu Z;  
XX  
DR WPI; 2000-679325/66.  
XX  
PT New peptide conjugates for modulating apoptosis or for inhibiting B  
PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for  
PT treating neurodegenerative disorders, stroke, or cancer -  
XX  
PS Claim 18; Page 17; 74pp; English.  
XX  
CC The invention relates to a peptide conjugate having the formula:  
CC (R-X)n-peptide where n = 1-10; X = C=O, when the R-X group is attached  
CC to the N-terminus of the peptide, or a side chain of the peptide where  
CC the functional group of the side chain is NH2 or OH; or X = O or NH,  
CC when the R-X group is attached to the C-terminus of the peptide, or a  
CC side chain of the peptide, where the side chain functional group is COOH

CC or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl containing one  
CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally  
CC monosubstituted with a 1-5C straight or branched chain alkyl group,  
CC phenyl optionally monosubstituted with a 1-5C straight or branched chain  
CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples  
CC of the peptide portion of the conjugate. The peptides represent analogues  
CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of  
CC the BH3 domain of the cell death agonist Bad. The peptide conjugate is  
CC useful for modulating apoptosis in the cells of a subject, or for  
CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of  
CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2  
CC function. In particular, the peptide conjugate is useful for treating a  
CC subject afflicted with a cancer characterized by cancer cells that  
CC express Bcl-2. The cancer includes prostate, colorectal, gastric,  
CC non-small lung, renal or thyroid cancers, neuroblastoma, or  
CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide  
CC conjugate is also useful for treating disorders characterized by  
CC increased apoptosis, e.g. neurodegenerative disorders, acquired  
CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.

XX  
SQ Sequence 26 AA;  
Query Match 95.2%; Score 138; DB 21; Length 26;  
Best Local Similarity 100.0%; Pred. No. 3e-14;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 NLWAAQRYGRELRRMSDFEGSFKGL 26  
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RESULT 13  
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ID AAB37002 standard; peptide; 26 AA.  
XX  
AC AAB37002;  
XX  
DT 28-FEB-2001 (first entry)  
XX  
DE Bcl2 polypeptide BH3 domain peptide #2.  
XX  
KW Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;  
KW cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;  
KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;  
KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;  
KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;  
KW stroke; myocardial infarction.  
XX  
OS Homo sapiens.  
XX  
PN WO200059526-A1.  
XX  
PD 12-OCT-2000.  
XX  
PF 06-APR-2000; 2000WO-US09352.  
XX  
PR 07-APR-1999; 99US-0128202.  
XX  
PA (UYJE-) UNIV JEFFERSON THOMAS.  
XX  
PI Huang Z, Wang J, Zhang Z, Shan S, Lu Z;  
XX  
DR WPI; 2000-679325/66.  
XX  
PT New peptide conjugates for modulating apoptosis or for inhibiting B  
PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for  
PT treating neurodegenerative disorders, stroke, or cancer -  
XX  
PS Claim 18; Page 17; 74pp; English.  
XX  
CC The invention relates to a peptide conjugate having the formula:  
CC (R-X)n-peptide where n = 1-10; X = C=O, when the R-X group is attached  
CC to the N-terminus of the peptide, or a side chain of the peptide where  
CC the functional group of the side chain is NH2 or OH; or X = O or NH,  
CC when the R-X group is attached to the C-terminus of the peptide, or a  
CC side chain of the peptide, where the side chain functional group is COOH

CC the functional group of the side chain is NH2 or OH; or X = O or NH,  
 CC when the R-X group is attached to the C-terminus of the peptide, or a  
 CC side chain of the peptide, where the side chain functional group is COOH  
 CC or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one  
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally  
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,  
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain  
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples  
 CC of the peptide portion of the conjugate. The peptides represent analogues  
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of  
 CC the BH3 domain of the cell death agonist Bad. The peptide conjugate is  
 CC useful for modulating apoptosis in the cells of a subject, or for  
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of  
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2  
 CC function. In particular, the peptide conjugate is useful for treating a  
 CC subject afflicted with a cancer characterized by cancer cells that  
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,  
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or  
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide  
 CC conjugate is also useful for treating disorders characterized by  
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired  
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.  
 XX  
 SQ Sequence 26 AA;

Query Match 95.2%; Score 138; DB 21; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 3e-14;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFGSKGL 26  
 |||||  
 DB 1 NLWAAQRYGRELRRMSDEFGSKGL 26

RESULT 14  
 AAB37056  
 ID AAB37056 standard; peptide; 27 AA.

XX AAB37056;

DT 28-FEB-2001 (first entry)

XX Bcl2 polypeptide BH3 domain peptide #56.

XX Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;  
 KW cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;  
 KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;  
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;  
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;  
 KW stroke; myocardial infarction.

XX Homo sapiens.

XX WO200059526-A1.

XX 12-OCT-2000.

XX 06-APR-2000; 2000WO-US09352.

XX 07-APR-1999; 99US-0128202.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Huang Z, Wang J, Zhang Z, Shan S, Lu Z;

XX WPI; 2000-679325/66.

XX New peptide conjugates for modulating apoptosis or for inhibiting B  
 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for  
 PT treating neurodegenerative disorders, stroke, or cancer

XX Claim 18; Page 19; 74pp; English.

CC The invention relates to a peptide conjugate having the formula:  
 CC (R-X)n-peptide where n = 1-10; X = C=O, when the R-X group is attached  
 CC to the N-terminus of the peptide, or a side chain of the peptide where  
 CC the functional group of the side chain is NH2 or OH; or X = O or NH,  
 CC when the R-X group is attached to the C-terminus of the peptide, or a  
 CC side chain of the peptide, where the side chain functional group is COOH  
 CC or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one  
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally  
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,  
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain  
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples  
 CC of the peptide portion of the conjugate. The peptides represent analogues  
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of  
 CC the BH3 domain of the cell death agonist Bad. The peptide conjugate is  
 CC useful for modulating apoptosis in the cells of a subject, or for  
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of  
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2  
 CC function. In particular, the peptide conjugate is useful for treating a  
 CC subject afflicted with a cancer characterized by cancer cells that  
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,  
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or  
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide  
 CC conjugate is also useful for treating disorders characterized by  
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired  
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.  
 XX  
 SQ Sequence 27 AA;

Query Match 95.2%; Score 138; DB 21; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-14;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 2 NLWAAQRYGRELRRMSDEFGSKGL 27

RESULT 15

AAB37055

ID AAB37055 standard; peptide; 28 AA.

XX AAB37055;

DT 28-FEB-2001 (first entry)

XX Bcl2 polypeptide BH3 domain peptide #55.

XX Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;  
 KW cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;  
 KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;  
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;  
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;  
 KW stroke; myocardial infarction.

XX Homo sapiens.

XX WO200059526-A1.

XX 12-OCT-2000.

XX 06-APR-2000; 2000WO-US09352.

XX 07-APR-1999; 99US-0128202.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Huang Z, Wang J, Zhang Z, Shan S, Lu Z;

XX WPI; 2000-679325/66.

XX New peptide conjugates for modulating apoptosis or for inhibiting B  
 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for  
 PT treating neurodegenerative disorders, stroke, or cancer

XX Claim 18; Page 19; 74pp; English.

PS The invention relates to a peptide conjugate having the formula:

XX (R-X)<sub>n</sub>-peptide where n = 1-10; X = C=O, when the R-X group is attached

CC to the N-terminus of the peptide, or a side chain of the peptide where

CC the functional group of the side chain is NH<sub>2</sub> or OH; or X = O or NH,

CC when the R-X group is attached to the C-terminus of the peptide, or a

CC side chain of the peptide, where the side chain functional group is COOH

CC or CONH<sub>2</sub>; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one

CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally

CC monosubstituted with a 1-5C straight or branched chain alkyl group,

CC phenyl optionally monosubstituted with a 1-5C straight or branched chain

CC alkyl group, or benzyl. The peptides AB37001-B37058 represent examples

CC of the peptide portion of the conjugate. The peptides represent analogues

CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of

CC the BH3 domain of the cell death agonist Bad. The peptide conjugate is

CC useful for modulating apoptosis in the cells of a subject, or for

CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of

CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2

CC function. In particular, the peptide conjugate is useful for treating a

CC subject afflicted with a cancer characterized by cancer cells that

CC express Bcl-2. The cancer includes prostate, colorectal, gastric,

CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or

CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide

CC conjugate is also useful for treating disorders characterized by

CC increased apoptosis, e.g. neurodegenerative disorders, acquired

CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.

XX

SQ Sequence 28 AA;

Query Match 95.2%; Score 138; DB 21; Length 28;

Best Local Similarity 100.0%; Pred. No. 3.2e-14;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDFEGSPKGL 26

Db |||||

2 NLWAAQRYGRELRRMSDFEGSPKGL 27

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Job time : 38.1857 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

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81.144 Million cell updates/sec

Title: US-09-544-664-3

Perfect score: 145  
Sequence: 1 NLWAAQRYGRELKMSDFEGSKGLP 27

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2.6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2.6/ptodata/1/iaa/6B\_COMB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	145	100.0	204	1	US-08-333-565-2
2	145	100.0	204	2	US-08-661-479-2
3	145	100.0	204	2	US-08-733-505A-1
4	145	100.0	204	2	US-08-733-505A-12
5	145	100.0	204	2	US-08-733-505A-13
6	145	100.0	204	2	US-08-733-505A-14
7	142	97.9	204	2	US-08-717-123-3
8	142	97.9	204	4	US-09-375-257-3
9	120.5	83.1	166	1	US-08-665-617-2
10	120.5	83.1	168	2	US-08-717-123-2
11	120.5	83.1	168	3	US-08-985-335-1
12	120.5	83.1	168	3	US-08-985-335-7
13	120.5	83.1	168	3	US-09-410-372-1
14	120.5	83.1	168	3	US-09-410-372-7
15	120.5	83.1	168	4	US-09-375-257-2
16	113	77.9	23	1	US-08-333-565-10
17	113	77.9	23	2	US-08-661-479-10
18	102	70.3	59	2	US-08-733-505A-55
19	102	70.3	59	2	US-08-733-505A-56
20	102	70.3	59	2	US-08-733-505A-57
21	102	70.3	59	2	US-08-733-505A-58
22	86	59.3	16	1	US-08-333-565-26
23	86	59.3	16	2	US-08-661-479-26
24	61	42.1	11	2	US-08-733-505A-34
25	61	42.1	11	2	US-08-706-741B-69
26	61	42.1	11	2	US-08-924-695A-69
27	53	36.6	946	3	US-09-074-579-3

Sequence 3, Appli  
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Sequence 40, Appl  
Sequence 18296, A  
Sequence 27, Appl  
Sequence 4656, Ap  
Sequence 31348, A  
Sequence 30979, A  
Sequence 19594, A  
Sequence 32466, A  
Sequence 23807, A  
Sequence 5164, Ap  
Sequence 2, Appli  
Sequence 4, Appli  
Sequence 2, Appli  
Sequence 2, Appli

28 53 36.6 946 3 US-09-388-774-3  
29 53 36.6 946 4 US-09-546-153-1  
30 51 35.2 66 2 US-08-867-087B-40  
31 50.5 34.8 467 4 US-09-252-991A-18296  
32 49 33.8 263 4 US-09-651-656-27  
33 49 33.8 263 4 US-09-650-855-27  
34 48.5 33.4 904 4 US-09-328-352-4656  
35 46.5 32.1 415 4 US-09-252-991A-31348  
36 46 31.7 322 4 US-09-252-991A-30979  
37 46 31.7 610 4 US-09-252-991A-19594  
38 45.5 31.4 351 4 US-09-252-991A-32466  
39 45.5 31.4 906 4 US-09-252-991A-31458  
40 45 31.0 229 4 US-09-252-991A-23807  
41 45 31.0 303 4 US-09-328-352-5164  
42 45 31.0 356 4 US-09-235-103-4  
43 45 31.0 513 1 US-08-464-340A-2  
44 45 31.0 513 5 PCT-US94-08449A-2  
45 45 31.0

#### ALIGNMENTS

RESULT 1  
US-08-333-565-2  
; Sequence 2, Application US/08333565  
; Patent No. 5622852  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, Stanley J.  
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourile and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/333,565  
; FILING DATE: 31-OCT-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 15726A-000700  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 204 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..204  
; OTHER INFORMATION: /note= "Deduced amino acid sequence  
; OTHER INFORMATION: of mouse BAD."  
US-08-333-565-2

Query Match 100.0%; Score 145; DB 1; Length 204;  
Best Local Similarity 100.0%; Pred. No. 1.4e-14;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 140 NLWAAQRYGRELRRMSDEFGSKGLP 166

## RESULT 2

US-08-661-479-2  
; Sequence 2, Application US/08661479  
; Patent No. 5834209  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, Stanley J.  
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH  
; TITLE OF INVENTION: REGULATOR  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/661,479  
; FILING DATE: 11-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/333,565  
; FILING DATE: 31-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 15726A-000700  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 204 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..204  
; OTHER INFORMATION: /note= "Deduced amino acid sequence  
; OTHER INFORMATION: of mouse BAD."  
US-08-661-479-2

Query Match 100.0%; Score 145; DB 2; Length 204;  
Best Local Similarity 100.0%; Pred. No. 1.4e-14;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFGSKGLP 27  
|||||  
Db 140 NLWAAQRYGRELRRMSDEFGSKGLP 166

## RESULT 3

US-08-733-505A-1  
; Sequence 1, Application US/08733505A  
; Patent No. 5856445  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, STANLEY J.  
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF  
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BLVD., SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: USA  
; ZIP: 63105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/733,505A  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 965458  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 727-5188  
; TELEFAX: (314) 727-6092  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 204 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-733-505A-1  
Query Match 100.0%; Score 145; DB 2; Length 204;  
Best Local Similarity 100.0%; Pred. No. 1.4e-14;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NLWAAQRYGRELRRMSDEFGSKGLP 27  
|||||  
Db 140 NLWAAQRYGRELRRMSDEFGSKGLP 166  
RESULT 4  
US-08-733-505A-12  
; Sequence 12, Application US/08733505A  
; Patent No. 5856445  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, STANLEY J.  
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF  
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BLVD., SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: USA  
; ZIP: 63105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/733,505A  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 965458  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 727-5188  
; TELEFAX: (314) 727-6092  
; INFORMATION FOR SEQ ID NO: 12:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-733-505A-12

Query Match          100.0%; Score 145; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 1.4e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFGSKGLP 27
    |||||
Db 140 NLWAAQRYGRELRRMSDEFGSKGLP 166

RESULT 5
US-08-733-505A-13
; Sequence 13, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,505A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-733-505A-13

Query Match          100.0%; Score 145; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 1.4e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFGSKGLP 27
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Db 140 NLWAAQRYGRELRRMSDEFGSKGLP 166

RESULT 6
US-08-733-505A-14
; Sequence 14, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
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; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,505A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-733-505A-14

Query Match          100.0%; Score 145; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 1.4e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFGSKGLP 27
    |||||
Db 140 NLWAAQRYGRELRRMSDEFGSKGLP 166

RESULT 7
US-08-717-123-3
; Sequence 3, Application US/08717123
; Patent No. 5965703
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
; TITLE OF INVENTION: Acids and Methods of Use
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/717,123
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
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; REFERENCE/DOCKET NUMBER: P-ID 1929  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 204 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-717-123-3

Query Match 97.9%; Score 142; DB 2; Length 204;  
Best Local Similarity 96.3%; Pred. No. 4.1e-14;  
Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFGSKGLP 27  
|||||  
Db 140 NLWAAQRYGRELRRMTDEFGSKGLP 166

## RESULT 8

US-09-375-257-3

; Sequence 3, Application US/09375257  
; Patent No. 6504022

; GENERAL INFORMATION:

; APPLICANT: Horne, William A.

; APPLICANT: Oltersdorf, Tilman

; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC

; TITLE OF INVENTION: ACIDS AND METHODS OF USE

; FILE REFERENCE: 480140.428D1

; CURRENT APPLICATION NUMBER: US/09/375,257

; CURRENT FILING DATE: 1999-08-16

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 204

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-375-257-3

Query Match 97.9%; Score 142; DB 4; Length 204;

Best Local Similarity 96.3%; Pred. No. 4.1e-14;

Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFGSKGLP 27  
|||||  
Db 140 NLWAAQRYGRELRRMTDEFGSKGLP 166

## RESULT 9

US-08-665-617-2

; Sequence 2, Application US/08665617

; Patent No. 5663316

; GENERAL INFORMATION:

; APPLICANT: Xudong, Yin

; TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Saliwanchik & Saliwanchik

; STREET: 2421 N.W. 41st Street, Suite A-1

; CITY: Gainesville

; STATE: Florida

; COUNTRY: USA

; ZIP: 32606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/665,617

; FILING DATE:

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: CL-8  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (352) 375-8100  
; TELEFAX: (352) 372-5800  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 166 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-665-617-2

Query Match 83.1%; Score 120.5; DB 1; Length 166;  
Best Local Similarity 89.3%; Pred. No. 6.2e-11;  
Matches 25; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 NLWAAQRYGRELRRMSDEFGSF-KGLP 27  
|||||  
Db 101 NLWAAQRYGRELRRMSDEFVDSFKKGLP 128

## RESULT 10

US-08-717-123-2

; Sequence 2, Application US/08717123

; Patent No. 5965703

; GENERAL INFORMATION:

; APPLICANT: Horne, William A.

; APPLICANT: Oltersdorf, Tilman

; TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic

; TITLE OF INVENTION: Acids and Methods of Use

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Campbell and Flores

; STREET: 4370 La Jolla Village Drive, Suite 700

; CITY: San Diego

; STATE: California

; COUNTRY: United States

; ZIP: 92122

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/717,123

; FILING DATE: 20-SEP-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Campbell, Cathryn A.

; REGISTRATION NUMBER: 31,815

; REFERENCE/DOCKET NUMBER: P-ID 1929

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 535-9001

; TELEFAX: (619) 535-8949

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 168 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-717-123-2

Query Match 83.1%; Score 120.5; DB 2; Length 168;  
Best Local Similarity 89.3%; Pred. No. 6.3e-11;  
Matches 25; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 NLWAAQRYGRELRRMSDEFGSF-KGLP 27  
|||||  
Db 103 NLWAAQRYGRELRRMSDEFVDSFKKGLP 130

```
RESULT 11
US-08-985-335-1
; Sequence 1, Application US/08985335
; Patent No. 6080847
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,335
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0421 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Synorab01
; CLONE: 358673
; US-08-985-335-1

Query Match      83.1%; Score 120.5; DB 3; Length 168;
Best Local Similarity 89.3%; Pred. No. 6.3e-11;
Matches 25; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy      1 NLWAAQRYGRELRRMSDFEGSF-KGLP 27
Db      103 NLWAAQRYGRELRRMSDFVDSFKKGLP 130

RESULT 12
US-08-985-335-7
; Sequence 7, Application US/08985335
; Patent No. 6080847
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; NUMBER OF SEQUENCES: 9
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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,335
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0421 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1683637
; US-08-985-335-7

Query Match      83.1%; Score 120.5; DB 3; Length 168;
Best Local Similarity 89.3%; Pred. No. 6.3e-11;
Matches 25; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy      1 NLWAAQRYGRELRRMSDFEGSF-KGLP 27
Db      103 NLWAAQRYGRELRRMSDFVDSFKKGLP 130

RESULT 13
US-09-410-372-1
; Sequence 1, Application US/09410372
; Patent No. 6281334
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/410,372
; FILING DATE:
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;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/985,335  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Billings, Lucy J.  
;; REGISTRATION NUMBER: 36,749  
;; REFERENCE/DOCKET NUMBER: PF-0421 US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 650-855-0555  
;; TELEFAX: 650-845-4166  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 168 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; IMMEDIATE SOURCE:  
;; LIBRARY: SYNORAB01  
;; CLONE: 358673  
US-09-410-372-1

Query Match 83.1%; Score 120.5; DB 3; Length 168;  
Best Local Similarity 89.3%; Pred. No. 6.3e-11;  
Matches 25; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 NLWAAQRYGRELRRMSDEFGSF-KGLP 27  
|||||  
Db 103 NLWAAQRYGRELRRMSDEFVDSFKKGLP 130

RESULT 14  
US-09-410-372-7  
;; Sequence 7, Application US/09410372  
;; Patent No. 6281334  
;; GENERAL INFORMATION:  
;; APPLICANT: Hillman, Jennifer L.  
;; APPLICANT: Yue, Henry  
;; APPLICANT: Lai, Preeti  
;; APPLICANT: Shah, Purvi  
;; APPLICANT: Corley, Neil C.  
;; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL  
;; TITLE OF INVENTION: PROLIFERATION  
;; NUMBER OF SEQUENCES: 9  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
;; STREET: 3174 Porter Dr.  
;; CITY: Palo Alto  
;; STATE: CA  
;; COUNTRY: USA  
;; ZIP: 94304  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: DOS  
;; SOFTWARE: FastSeq for Windows Version 2.0  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/410,372  
;; FILING DATE:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/985,335  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Billings, Lucy J.  
;; REGISTRATION NUMBER: 36,749  
;; REFERENCE/DOCKET NUMBER: PF-0421 US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 650-855-0555  
;; TELEFAX: 650-845-4166  
;; INFORMATION FOR SEQ ID NO: 7:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 168 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single

;; TOPOLOGY: linear  
;; IMMEDIATE SOURCE:  
;; LIBRARY: GenBank  
;; CLONE: 1683637  
US-09-410-372-7

Query Match 83.1%; Score 120.5; DB 3; Length 168;  
Best Local Similarity 89.3%; Pred. No. 6.3e-11;  
Matches 25; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 NLWAAQRYGRELRRMSDEFGSF-KGLP 27  
|||||  
Db 103 NLWAAQRYGRELRRMSDEFVDSFKKGLP 130

RESULT 15  
US-09-375-257-2  
;; Sequence 2, Application US/09375257  
;; Patent No. 6504022  
;; GENERAL INFORMATION:  
;; APPLICANT: Horne, William A.  
;; APPLICANT: Altersdorf, Tilman  
;; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC  
;; TITLE OF INVENTION: ACIDS AND METHODS OF USE  
;; FILE REFERENCE: 480140.428D1  
;; CURRENT APPLICATION NUMBER: US/09/375,257  
;; CURRENT FILING DATE: 1999-08-16  
;; NUMBER OF SEQ ID NOS: 15  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 2  
;; LENGTH: 168  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-375-257-2

Query Match 83.1%; Score 120.5; DB 4; Length 168;  
Best Local Similarity 89.3%; Pred. No. 6.3e-11;  
Matches 25; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 NLWAAQRYGRELRRMSDEFGSF-KGLP 27  
|||||  
Db 103 NLWAAQRYGRELRRMSDEFVDSFKKGLP 130

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Job time : 14.0786 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

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(without alignments)  
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Title: US-09-544-664-3

Perfect score: 145

Sequence: 1 NLWAAQRYGRELRLRMSDEFEFGSKGLP 27

Scoring table: BLOSUM62

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Searched: 541936 seqs, 145912426 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	120.5	83.1	168	9	US-09-894-657-1
5	120.5	83.1	168	9	US-09-894-657-7
6	120.5	83.1	168	14	US-10-066-179-2
7	114	78.6	25	15	US-10-059-261-258
8	71	49.0	15	15	US-10-174-105A-147
9	53	36.6	946	9	US-09-828-423-3
10	50	34.5	215	15	US-10-156-761-9145
11	47	32.4	35	15	US-10-092-750-1
12	47	32.4	138	15	US-10-092-750-241
13	46	31.7	682	12	US-10-238-075-1077
14	45.5	31.4	852	9	US-09-752-639-153
15	45.5	31.4	852	10	US-09-984-198-153

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Sequence 2, Appli  
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Sequence 160, Appli  
Sequence 12, Appli  
Sequence 435, App  
Sequence 435, App  
Sequence 649, App  
Sequence 8, Appli  
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Sequence 560, App  
Sequence 11541, A  
Sequence 5704, Ap  
Sequence 8, Appli  
Sequence 12463, A  
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Sequence 20, Appli  
Sequence 13485, A  
Sequence 18, Appli  
Sequence 238, App  
Sequence 162, App  
Sequence 2, Appli  
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Sequence 3, Appli  
Sequence 62, Appli

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18 45 31.0 513 15 US-10-325-891-2  
19 44.5 30.7 144 12 US-09-903-190-160  
20 44.5 30.7 146 15 US-10-121-757B-12  
21 44.5 30.7 160 10 US-09-738-973-435  
22 44.5 30.7 160 10 US-09-854-133-435  
23 44.5 30.7 160 15 US-10-144-649A-435  
24 44.5 30.7 309 15 US-10-102-806-649  
25 44.5 30.7 334 10 US-09-794-715A-8  
26 44.5 30.7 334 12 US-10-286-581-8  
27 44.5 30.7 334 15 US-10-046-924-8  
28 44 30.3 81 9 US-09-925-297-560  
29 44 30.3 272 15 US-10-156-761-11541  
30 44 30.3 426 9 US-09-815-242-5704  
31 44 30.3 699 14 US-10-008-355-8  
32 44 30.3 705 9 US-09-815-242-12463  
33 44 30.3 712 14 US-10-008-355-2  
34 44 30.3 877 12 US-10-369-294-20  
35 43.5 30.0 543 15 US-10-156-761-13485  
36 43 29.7 213 9 US-09-843-846-18  
37 43 29.7 232 10 US-09-881-752A-238  
38 43 29.7 270 11 US-09-934-455-162  
39 43 29.7 380 9 US-09-149-045-2  
40 43 29.7 380 15 US-10-166-359-2  
41 43 29.7 380 15 US-10-166-113-2  
42 43 29.7 380 15 US-10-166-357-2  
43 43 29.7 380 15 US-10-166-372-2  
44 43 29.7 380 15 US-10-184-722-3  
45 43 29.7 380 15 US-10-251-385-62

#### ALIGNMENTS

RESULT 1  
US-09-922-378-3  
; Sequence 3, Application US/09922378  
; Patent No. US20020037869A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, William A.  
; APPLICANT: Oltersdorf, Tilman  
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC  
; TITLE OF INVENTION: ACIDS AND METHODS OF USE  
; FILE REFERENCE: 480140.428D3  
; CURRENT APPLICATION NUMBER: US/09/922,378  
; CURRENT FILING DATE: 2001-08-03  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 204  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-922-378-3

Query Match 97.9%; Score 142; DB 9; Length 204;  
Best Local Similarity 96.3%; Pred. No. 2.5e-13;  
Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLWAAQRYGRELRLRMSDEFEFGSKGLP 27  
|||||  
Db 140 NLWAAQRYGRELRLRMTDEFEFGSKGLP 166

RESULT 2  
US-10-066-179-3  
; Sequence 3, Application US/10066179  
; Publication No. US20020115631A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, William A.  
; APPLICANT: Oltersdorf, Tilman  
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC  
; TITLE OF INVENTION: ACIDS AND METHODS OF USE

```
; FILE REFERENCE: 480140.428C1
; CURRENT APPLICATION NUMBER: US/10/066,179
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-066-179-3
```

```
Query Match          97.9%; Score 142; DB 14; Length 204;
Best Local Similarity 96.3%; Pred. No. 2.5e-13;
Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 NLWAAQRYGRELRRMSDFEGSFKGLP 27
Db      140 NLWAAQRYGRELRRMTDFEGSFKGLP 166
      |||||
```

## RESULT 3

```
US-09-922-378-2
; Sequence 2, Application US/09922378
; Patent No. US20020037869A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
; TITLE OF INVENTION: ACIDS AND METHODS OF USE
; FILE REFERENCE: 480140.428D3
; CURRENT APPLICATION NUMBER: US/09/922,378
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 15
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-922-378-2
```

```
Query Match          83.1%; Score 120.5; DB 9; Length 168;
Best Local Similarity 89.3%; Pred. No. 3.2e-10;
Matches 25; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
```

```
QY      1 NLWAAQRYGRELRRMSDFEGSF-KGLP 27
Db      103 NLWAAQRYGRELRRMSDFVDSFKKGLP 130
      |||||
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## RESULT 4

```
US-09-894-657-1
; Sequence 1, Application US/09894657
; Patent No. US20020098569A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Hillman, Jennifer L.
; Yue, Henry
; Lal, Preeti
; Shah, Purvi
; Corley, Neil C.
```

```
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; PROLIFERATION
```

```
; NUMBER OF SEQUENCES: 9
```

```
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
```

```
; CITY: Palo Alto
```

```
; STATE: CA
```

```
; COUNTRY: USA
```

```
; ZIP: 94304
```

```
; COMPUTER READABLE FORM:
```

```
; MEDIUM TYPE: Diskette
```

```
; COMPUTER: IBM Compatible
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```
; OPERATING SYSTEM: DOS
```

```
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/894,657
; FILING DATE: 28-Jun-2001
```

```
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER: 09/410,372
```

```
; FILING DATE: <Unknown>
```

```
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Billings, Lucy J.
```

```
; REGISTRATION NUMBER: 36,749
```

```
; REFERENCE/DOCKET NUMBER: PF-0421 US
```

```
; TELECOMMUNICATION INFORMATION:
```

```
; TELEPHONE: 650-855-0555
```

```
; TELEFAX: 650-845-4166
```

```
; INFORMATION FOR SEQ ID NO: 1:
```

```
; SEQUENCE CHARACTERISTICS:
```

```
; LENGTH: 168 amino acids
```

```
; TYPE: amino acid
```

```
; STRANDEDNESS: single
```

```
; TOPOLOGY: linear
```

```
; IMMEDIATE SOURCE:
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```
; LIBRARY: SYNORAB01
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```
; CLONE: 358673
```

```
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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```
US-09-894-657-1
```

```
Query Match          83.1%; Score 120.5; DB 9; Length 168;
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```
Best Local Similarity 89.3%; Pred. No. 3.2e-10;
```

```
Matches 25; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
```

```
QY      1 NLWAAQRYGRELRRMSDFEGSF-KGLP 27
```

```
Db      103 NLWAAQRYGRELRRMSDFVDSFKKGLP 130
```

```
      |||||
```

## RESULT 5

```
US-09-894-657-7
```

```
; Sequence 7, Application US/09894657
```

```
; Patent No. US20020098569A1
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Hillman, Jennifer L.
```

```
; Yue, Henry
```

```
; Lal, Preeti
```

```
; Shah, Purvi
```

```
; Corley, Neil C.
```

```
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
```

```
; PROLIFERATION
```

```
; NUMBER OF SEQUENCES: 9
```

```
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
```

```
; STREET: 3174 Porter Dr.
```

```
; CITY: Palo Alto
```

```
; STATE: CA
```

```
; COUNTRY: USA
```

```
; ZIP: 94304
```

```
; COMPUTER READABLE FORM:
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```
; MEDIUM TYPE: Diskette
```

```
; COMPUTER: IBM Compatible
```

```
; OPERATING SYSTEM: DOS
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```
; SOFTWARE: FastSeq for Windows Version 2.0
```

```
; CURRENT APPLICATION DATA:
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```
; APPLICATION NUMBER: US/09/894,657
```

```
; FILING DATE: 28-Jun-2001
```

```
; PRIOR APPLICATION DATA:
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```
; APPLICATION NUMBER: 09/410,372
```

```
; FILING DATE: <Unknown>
```

```
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Billings, Lucy J.
```

```
; REGISTRATION NUMBER: 36,749
```

```
; REFERENCE/DOCKET NUMBER: PF-0421 US
```

```
; TELECOMMUNICATION INFORMATION:
```

```
; TELEPHONE: 650-855-0555
```

```
; TELEFAX: 650-845-4166
```

```

; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 168 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; IMMEDIATE SOURCE:
;   LIBRARY: GenBank
;   CLONE: 1683637
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-894-657-7

Query Match      83.1%; Score 120.5; DB 9; Length 168;
Best Local Similarity 89.3%; Pred. No. 3.2e-10;
Matches 25; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY      1 NLWAAQRYGRELRRMSDEFGSF-KGLP 27
DB      103 NLWAAQRYGRELRRMSDEFGSF-KGLP 130

RESULT 6
US-10-066-179-2
; Sequence 2, Application US/10066179
; Publication No. US20020115631A1
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
;   ACIDS AND METHODS OF USE
; FILE REFERENCE: 480140.428C1
; CURRENT APPLICATION NUMBER: US/10/066,179
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-066-179-2

Query Match      83.1%; Score 120.5; DB 14; Length 168;
Best Local Similarity 89.3%; Pred. No. 3.2e-10;
Matches 25; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY      1 NLWAAQRYGRELRRMSDEFGSF-KGLP 27
DB      103 NLWAAQRYGRELRRMSDEFGSF-KGLP 130

RESULT 7
US-10-059-261-258
; Sequence 258, Application US/10059261
; Publication No. US20030077826A1
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: JACOTOT, ETIENNE DANIEL FRANCOIS
; APPLICANT: BRIAND, JEAN-PAUL
; TITLE OF INVENTION: CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET
;   SPECIFIC CELLS AND A MODULE REGULATING THE APOPTOGENIC
;   FUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX
; TITLE OF INVENTION: (PTPC)
; FILE REFERENCE: 03495.0216
; CURRENT APPLICATION NUMBER: US/10/059,261
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/365,594
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 258
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Unknown Organism

; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 168 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; IMMEDIATE SOURCE:
;   LIBRARY: GenBank
;   CLONE: 1683637
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-894-657-7

Query Match      83.1%; Score 120.5; DB 9; Length 168;
Best Local Similarity 89.3%; Pred. No. 3.2e-10;
Matches 25; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY      1 NLWAAQRYGRELRRMSDEFGSF-KGLP 27
DB      103 NLWAAQRYGRELRRMSDEFGSF-KGLP 130

RESULT 6
US-10-066-179-2
; Sequence 2, Application US/10066179
; Publication No. US20020115631A1
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
;   ACIDS AND METHODS OF USE
; FILE REFERENCE: 480140.428C1
; CURRENT APPLICATION NUMBER: US/10/066,179
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-066-179-2

Query Match      83.1%; Score 120.5; DB 14; Length 168;
Best Local Similarity 89.3%; Pred. No. 3.2e-10;
Matches 25; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY      1 NLWAAQRYGRELRRMSDEFGSF-KGLP 27
DB      103 NLWAAQRYGRELRRMSDEFGSF-KGLP 130

RESULT 7
US-10-059-261-258
; Sequence 258, Application US/10059261
; Publication No. US20030077826A1
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: JACOTOT, ETIENNE DANIEL FRANCOIS
; APPLICANT: BRIAND, JEAN-PAUL
; TITLE OF INVENTION: CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET
;   SPECIFIC CELLS AND A MODULE REGULATING THE APOPTOGENIC
;   FUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX
; TITLE OF INVENTION: (PTPC)
; FILE REFERENCE: 03495.0216
; CURRENT APPLICATION NUMBER: US/10/059,261
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/365,594
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 258
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Unknown Organism

; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: TOX peptide
US-10-059-261-258

Query Match      78.6%; Score 114; DB 15; Length 25;
Best Local Similarity 91.7%; Pred. No. 4.1e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 NLWAAQRYGRELRRMSDEFGSF-K 24
DB      1 NLWAAQRYGRELRRMSDEFGSF-K 24

RESULT 8
US-10-174-105A-147
; Sequence 147, Application US/10174105A
; Publication No. US20030068652A1
; GENERAL INFORMATION:
; APPLICANT: Cell Signaling Technology, Inc.
; APPLICANT: ZHANG, Hui
; APPLICANT: COMB, Michael J.
; APPLICANT: TAN, Yi
; TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPECI
;   FIC REFERENCE: CST-138 CIP3
; CURRENT APPLICATION NUMBER: US/10/174,105A
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 09/148,712
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 09/535,364
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 147
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; NAME/KEY: MOD_RES
; LOCATION: (8)..(8)
; OTHER INFORMATION: PHOSPHORYLATION; serine at position 8 is phosphorylated
US-10-174-105A-147

Query Match      49.0%; Score 71; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 GRELRMSDEFGS 22
DB      1 GRELRMSDEFGS 14

RESULT 9
US-09-828-423-3
; Sequence 3, Application US/09828423
; Patent No. US20020099178A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Patterson, Chandra
; TITLE OF INVENTION: GROWTH-ASSOCIATED TRYPSIN-TYPE
;   INHIBITOR HEAVY CHAIN PRECURSOR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:

```

QY 6 QRYGRELRRMSDEFEG 21  
: : | : | | | : |

RESULT 13  
US-10-238-075-1077  
; Sequence 1077, Application US/10238075  
; Publication No. US20030148324A1  
; GENERAL INFORMATION:  
; APPLICANT: I.N.S.E.R.M.  
; TITLE OF INVENTION: Polynucleotides w  
; TITLE OF INVENTION: E.coli, and bicol

FILE REFERENCE: BLANDINE  
; CURRENT APPLICATION NUMBER: US/10/238,075  
; CURRENT FILING DATE: 2002-09-10  
; PRIOR APPLICATION NUMBER: 0003145  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 1576  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 1077  
; LENGTH: 682  
; TYPE: PRT  
; ORGANISM: Escherichia coli  
US-10-238-075-1077

Query Match 31.7%; Score 46; DB 12; Length 682;  
Best Local Similarity 40.0%; Pred. No. 1.6e+02;  
Matches 10; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 2 LWAAQRYGRLRRMSDFEGSFKGL 26  
:||||| : : : : ||  
Db 610 IWAQRGAKVPRVRNGFTSMDIGL 634

RESULT 14  
US-09-752-639-153  
; Sequence 153, Application US/09752639  
; Patent No. US20020091243A1  
; GENERAL INFORMATION:  
; APPLICANT: Gatanaga, T.  
; APPLICANT: Granger, G.A.  
; TITLE OF INVENTION: Factors Altering Tumor Necrosis  
; TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods  
; TITLE OF INVENTION: of Use Thereof  
; NUMBER OF SEQUENCES: 154  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/752,639  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US99/10793  
; FILING DATE:  
; APPLICATION NUMBER: 09/081,385  
; FILING DATE:  
; APPLICATION NUMBER: 08/964,747  
; FILING DATE: 05-NOV-1997  
; APPLICATION NUMBER: 60/030,761  
; FILING DATE: 06-NOV-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wu, Frank  
; REGISTRATION NUMBER: 41,386  
; REFERENCE/DOCKET NUMBER: 22000-20577.21  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-813-5600  
; TELEFAX: 650-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 153:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 852 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-752-639-153

Query Match 31.4%; Score 45.5; DB 9; Length 852;  
Best Local Similarity 35.3%; Pred. No. 2.4e+02;  
Matches 12; Conservative 5; Mismatches 10; Indels 7; Gaps 2;

QY 1 NLWAA-----QRY-GRELRRMSDFEGSFKGLP 27  
:|: |||:| :|:| :|  
Db 552 DIWSTYLTAKFIARYGGRKLERARDLFEQALDQCP 585

RESULT 15  
US-09-984-198-153  
; Sequence 153, Application US/09984198  
; Patent No. US20020106679A1  
; GENERAL INFORMATION:  
; APPLICANT: Gatanaga, T.  
; APPLICANT: Granger, G.A.  
; TITLE OF INVENTION: Factors Altering Tumor Necrosis  
; TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods  
; TITLE OF INVENTION: of Use Thereof  
; NUMBER OF SEQUENCES: 154  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/984,198  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US99/10793  
; FILING DATE:  
; APPLICATION NUMBER: 09/081,385  
; FILING DATE:  
; APPLICATION NUMBER: 08/964,747  
; FILING DATE: 05-NOV-1997  
; APPLICATION NUMBER: 60/030,761  
; FILING DATE: 06-NOV-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wu, Frank  
; REGISTRATION NUMBER: 41,386  
; REFERENCE/DOCKET NUMBER: 22000-20577.21  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-813-5600  
; TELEFAX: 650-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 153:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 852 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-984-198-153

Query Match 31.4%; Score 45.5; DB 10; Length 852;  
Best Local Similarity 35.3%; Pred. No. 2.4e+02;  
Matches 12; Conservative 5; Mismatches 10; Indels 7; Gaps 2;

QY 1 NLWAA-----QRY-GRELRRMSDFEGSFKGLP 27  
:|: |||:| :|:| :|  
Db 552 DIWSTYLTAKFIARYGGRKLERARDLFEQALDQCP 585

Search completed: September 15, 2003, 17:47:52  
Job time : 21.4071 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 15, 2003, 17:18:16 ; Search time 12.15 Seconds  
(without alignments)  
213.708 Million cell updates/sec

Title: US-09-544-664-3  
Perfect score: 145  
Sequence: 1 NLWAAQRYGRELRLRMSDFEGSKGLP 27

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

PIR\_76:\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	145	100.0	204	2 A55671	bad protein - mous
2	61	42.1	946	2 JC5575	inter-alpha-trypsi
3	60	41.4	946	2 S54354	inter-alpha-inhibi
4	53	36.6	223	2 D70760	hypothetical prote
5	53	36.6	946	1 IYHU2	inter-alpha-trypsi
6	52	35.9	370	2 S38185	2-dehydro-3-deoxy
7	51	35.2	232	2 A42095	focal homeotic pr
8	50	34.5	374	2 C84338	spermidine/putresc
9	50	34.5	516	2 A96753	probable threonine
10	49	33.8	263	2 A64807	endonuclease VIII
11	49	33.8	263	2 A85572	hypothetical prote
12	49	33.8	263	2 C90721	hypothetical prote
13	49	33.8	263	2 AD0590	endonuclease VIII
14	49	33.8	453	2 E83517	conserved hypothet
15	48.5	33.4	134	2 S40376	Ig kappa chain - h
16	48.5	33.4	314	2 T02975	annexin p35 - maiz
17	48	33.1	206	2 C36365	transforming prote
18	48	33.1	220	2 F72289	oxidoreductase, so
19	48	33.1	526	2 T08545	threonine synthase
20	47.5	32.8	779	2 B81287	hypothetical prote
21	47	32.4	597	2 G82308	oxaloacetate decar
22	47	32.4	967	2 F82668	oxoglutarate dehyd
23	47	32.4	5138	2 B96695	hypothetical prote
24	46.5	32.1	314	2 T02961	annexin p33 - maiz
25	46.5	32.1	435	2 A44308	hypothetical prote
26	46.5	32.1	1140	2 T09486	probable polyamine
27	46	31.7	599	2 T35440	alkaline proteinase
28	46	31.7	497	2 C98318	hypothetical prote
29	46	31.7	1164	2 T24806	hypothetical prote

30 46 31.7 1378 2 AB1393 DNA-directed RNA p  
31 45.5 31.4 194 2 C75420 hypothetical prote  
32 45.5 31.4 261 2 G89510 conserved hypothet  
33 45.5 31.4 263 2 B81148 probable transfera  
34 45.5 31.4 287 2 S43852 neuropeptide Pol-R  
35 45.5 31.4 328 2 E83337 probable transmembr  
36 45.5 31.4 334 2 A39172 Antho-Ramide neur  
37 45.5 31.4 562 2 C71473 hypothetical prote  
38 45.5 31.4 905 2 G83314 NADH dehydrogenase  
39 45 31.0 165 2 S59899 chlorocruorin chai  
40 45 31.0 295 2 F83201 conserved hypothet  
41 45 31.0 346 2 H95406 conserved hypothet  
42 45 31.0 513 2 JC5920 potassium channel  
43 45 31.0 591 2 B44465 sodium ion pump ox  
44 45 31.0 591 2 AB0509 oxaloacetate decar  
45 45 31.0 591 2 AE0909 oxaloacetate decar

#### ALIGNMENTS

##### RESULT 1

A55671  
bad protein - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 03-Mar-1995 #sequence\_revision 03-Mar-1995 #text\_change 05-Nov-1999  
C:Accession: A55671  
R:Yang, E.; Zha, J.; Jockel, J.; Boise, L.H.; Thompson, C.B.; Korsmeyer, S.J.  
Cell 80, 285-291, 1995  
A>Title: Bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promot  
A:Reference number: A55671; MUID:95136361; PMID:7834748  
A:Accession: A55671  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-204 <YAN>  
A:Cross-references: GB:L37296; NID:9639778; PIDN:AAA64465.1; PID:9639779  
C:Keywords: heterodimer

Query Match 100.0%; Score 145; DB 2; Length 204;  
Best Local Similarity 100.0%; Pred. No. 1e-13;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRLRMSDFEGSKGLP 27  
|||||  
DB 140 NLWAAQRYGRELRLRMSDFEGSKGLP 166

##### RESULT 2

JC5575  
inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster  
C:Species: Mesocricetus auratus (golden hamster)  
C>Date: 23-Sep-1997 #sequence\_revision 23-Sep-1997 #text\_change 20-Jun-2000  
C:Accession: JC5575; PC4485  
R:Nakatani, T.; Suzuki, Y.; Yamamoto, T.; Sinozawa, H.  
J. Biochem. 122, 71-82, 1997  
A>Title: Molecular cloning and sequencing of cDNAs encoding three heavy-chain precurs  
sin inhibitor heavy chain family.  
A:Reference number: JC5574; MUID:97420688; PMID:9276673  
A:Accession: JC5575  
A:Molecule type: mRNA  
A:Residues: 1-946 <NAK>  
A:Cross-references: DBJ:D89286; NID:g1694689; PIDN:BAAL3939.1; PID:g1694690  
A:Experimental source: liver  
A:Accession: PC4485  
A:Molecule type: protein  
A:Residues: 55-64;140-146;151-156;424-447;500-528;577-605 <NA2>  
C:Comment: In the plasma three inter-alpha-trypsin inhibitor heavy chains 1, 2 and 3  
that the complexes play important role for pancreatic cancer.  
C:Superfamily: inter-alpha-trypsin inhibitor complex component II  
F:261-264,717-916/Disulfide bonds: #status predicted

Query Match 42.1%; Score 61; DB 2; Length 946;  
Best Local Similarity 37.0%; Pred. No. 1;

Matches 10; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFEGFKGLP 27  
I::: | : ||| !::!  
Db 212 NWVIVLQGMRFLLHVPDTFEGHFQGV 238

RESULT 3  
S54354  
inter-alpha-inhibitor H2 chain - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 20-Aug-1999  
C:Accession: S54354  
R:Chan, P.; Risler, J.L.; Raguenez, G.; Salier, J.P.  
Biochem. J. 306, 505-512, 1995  
A:Title: The three heavy-chain precursors for the inter-alpha-inhibitor family in mouse  
A:Reference number: S54353; MUID:95194326; PMID:7534067  
A:Accession: S54354  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-946 <CHA>  
A:Cross-references: EMBL:X70392; NID:G695633; PIDN:CAA49842.1; PID:G695634  
C:Superfamily: inter-alpha-trypsin inhibitor complex component II

Query Match 41.4%; Score 60; DB 2; Length 946;  
Best Local Similarity 37.0%; Pred. No. 1.4;  
Matches 10; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFEGFKGLP 27  
I::: | : ||| !::!  
Db 212 NWVIVLQGMRFLLHVPDTFEGHFQGV 238

RESULT 4  
D70760  
hypothetical protein Rv2014 - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999  
C:Accession: D70760  
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Nature 393, 537-544, 1998  
A:Authors: Scares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MUID:98295987; PMID:9634230  
A:Accession: D70760  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-223 <COL>  
A:Cross-references: GB:Z74025; GB:AL123456; NID:G3261586; PIDN:CAA98415.1; PID:el299911;  
A:Experimental source: strain H37RV  
C:Genetics:  
A:Gene: Rv2014

Query Match 36.6%; Score 53; DB 2; Length 223;  
Best Local Similarity 58.8%; Pred. No. 3.4;  
Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSD 17  
||||| | | : | |  
Db 165 NLWAAADRYNRAIARGHD 181

RESULT 5  
IYHU2  
inter-alpha-trypsin inhibitor heavy chain 2 precursor - human  
N:Alternate names: inter-alpha-trypsin inhibitor complex component II  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1990 #sequence\_revision 30-Sep-1990 #text\_change 04-Feb-2000  
C:Accession: S00346; S09064; B39967; S00632; B34245; S28929; C53642  
R:Gebhard, W.; Schreitmüller, T.; Hochstrasser, K.; Wachter, E.  
FEBS Lett. 229, 63-67, 1988

A:Title: Complementary DNA and derived amino acid sequence of the precursor of one of  
A:Reference number: S00346; MUID:88152237; PMID:2450046  
A:Accession: S00346  
A:Molecule type: mRNA  
A:Residues: 1-946 <GEB>  
A:Cross-references: EMBL:X07173  
A:Experimental source: liver  
A:Note: part of this sequence, including the amino end of the mature protein, was con  
ssing occurs at the carboxyl as well as the amino end to produce the mature protein  
A:Note: due to a double frameshift, the nucleic acid sequence of codons 363-372 is in  
A:Note: in one clone, a T is lacking from codon 716; this clone could code for a prot  
B:Schreitmüller, T.; Hochstrasser, K.; Reisinger, P.W.M.; Wachter, E.; Gebhard, W.  
Biol. Chem. Hoppe-Seyler 368, 963-970, 1987  
A:Title: cDNA cloning of human inter-alpha-trypsin inhibitor discloses three differen  
A:Reference number: S09064; MUID:88024442; PMID:3663330  
A:Accession: S09064  
A:Molecule type: mRNA  
A:Residues: 265, 'RR', 268-284, 'D', 286-946 <SCH>  
A:Note: this sequence has been revised in reference S00346  
R:Salier, J.P.; Diarra-Mehrpour, M.; Sesboue, R.; Bourguignon, J.; Benarous, R.; Ohku  
Proc. Natl. Acad. Sci. U.S.A. 84, 8272-8276, 1987  
A:Title: Isolation and characterization of cDNAs encoding the heavy chain of human in  
A:Reference number: A39967; MUID:88068576; PMID:2446322  
A:Accession: B39967  
A:Molecule type: mRNA  
A:Residues: 384-673, 'A', 675-704, 'S', 706-728, 'D', 730, 'A', 732-865 <SAL>  
A:Cross-references: GB:M18193; GB:J03013; NID:G338222; PIDN:AAA60558.1; PID:G553647  
A:Experimental source: liver  
R:Salier, J.P.; Diarra-Mehrpour, M.; Sesboue, R.; Bourguignon, J.; Martin, J.P.  
Biol. Chem. Hoppe-Seyler 369(Suppl.), 15-18, 1988  
A:Title: Human inter-alpha-trypsin inhibitor. Isolation and characterization of heavy  
A:Reference number: S00632; MUID:89076497; PMID:2462430  
A:Accession: S00632  
A:Molecule type: mRNA  
A:Residues: 384-673, 'A', 675-704, 'S', 706-728, 'D', 730, 'A', 732-766 <SA2>  
A:Cross-references: GB:M33033; NID:G186589; PIDN:AAA59195.1; PID:G186590  
R:Englund, J.J.; Thøgersen, I.B.; Pizzo, S.V.; Salvesen, G.  
J. Biol. Chem. 264, 15975-15981, 1989  
A:Title: Analysis of inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre  
A:Reference number: A92736; MUID:89380192; PMID:2476436  
A:Accession: B34245  
A:Molecule type: protein  
A:Residues: 55-74 <ENG>  
R:Walski, N.; Balduvck, M.; Maes, P.; Capon, C.; Mizon, C.; Han, K.K.; Tartar, A.; Fou  
Biol. Chem. Hoppe-Seyler 373, 1009-1018, 1992  
A:Title: The heavy chains of human plasma inter-alpha-trypsin inhibitor: their isolat  
A:Reference number: S28928; MUID:93039735; PMID:1384548  
A:Accession: S28929  
A:Molecule type: protein  
A:Residues: 55-64 <MAL>  
R:Wisniewski, H.G.; Burgess, W.H.; Oppenheim, J.D.; Vilcek, J.  
Biochemistry 33, 7423-7429, 1994  
A:Title: TSG-6, an arthritis-associated hyaluronan binding protein, forms a stable co  
A:Reference number: A53642; MUID:94271799; PMID:7516184  
A:Accession: C53642  
A:Molecule type: protein  
A:Residues: 55-64 <WIS>  
C:Comment: Inter-alpha-trypsin inhibitor is a complex of three proteins, each derivin  
C:Comment: This protein is a heterodimer of heavy and light chains.  
C:Genetics:  
A:Gene: GDB:ITIH2  
A:Cross-references: GDB:120108; OMIM:146640  
A:Map position: 10p15-10p15  
C:Superfamily: inter-alpha-trypsin inhibitor complex component II  
C:Keywords: carboxylglutamic acid; glycoprotein; heterodimer; serine proteinase inhibi  
F:1-18/Domain: signal sequence #status predicted <SIG>  
F:19-54/Domain: propeptide #status predicted <PRO>  
F:55-698/Product: inter-alpha-trypsin inhibitor heavy chain 2 #status predicted <MAT>  
F:96,445/Binding site: carboxylate (Asn) (covalent) #status experimental  
F:118,671/Binding site: carboxylate (Asn) (covalent) #status predicted  
F:282,283/Modified site: gamma-carboxylglutamic acid (Glu) #status predicted  
F:421,422,423/Binding site: calcium (Asp, Gly, Asp) #status predicted

D6 80 DLEAAQRYVALRLKLSDELKG 100

!! ||| | :||:|||| :

RESULT 7

A42095  
floral homeotic protein APETALA3 (AP3) - Arabidopsis thaliana  
N;Alternate names: homeotic protein APETALA3; MADS-box regulatory protein AP3  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jul-2000  
C;Accession: A42095; S52633; T47593  
R;Jack, T.; Brockman, L.L.; Meyerowitz, E.M.  
Cell 68, 683-697, 1992  
A;Title: The homeotic gene APETALA3 of Arabidopsis thaliana encodes a MADS box and is  
A;Reference number: A42095; MUID:92154682; PMID:1346756  
A;Accession: A42095  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-232 <JRC>  
A:CROSS-references: GB:M86357; NTD:g166607; PIDN:AAA32740.1; PID:g166608  
A;Experimental source: petals, stamens  
A>Note: sequence extracted from NCBI backbone (NCBIN:82520, NCBI:P:82521)  
R;Okamoto, H.; Yano, A.; Shiraiishi, H.; Okada, K.; Shimura, Y.  
Plant Mol. Biol. 26, 465-472, 1994  
A;Title: Genetic complementation of a floral homeotic mutation, apetalal3, with an Ara  
A;Reference number: S52633; MUID:95036018; PMID:7948893  
A;Accession: S52633  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-63 <OKA>  
A:CROSS-references: GB:D21125  
R;Bloecker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat M.Me  
submitted to the Protein Sequence Database, March 2000  
A;Reference number: Z24469  
A;Accession: T47593  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-232 <BLD>  
A:CROSS-references: EMBL:AL132971  
A;Experimental source: cultivar Columbia; BAC clone TL2E18  
C;Genetics:  
A;Map position: 3  
A;Intons: 63/2; 85/3; 106/2; 139/3; 153/3; 168/3  
A;Note: TL2E18.30  
C;Superfamily: transcription factor squa; serum response factor DNA-binding domain h  
C;Keywords: DNA binding; nucleus; transcription regulation  
F:2-57/Domain: serum response factor DNA-binding domain homology <SRP>

Query Match 35.2%; Score 51; DB 2; Length 232;  
Best Local Similarity 44.4%; Pred.No. 7;  
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;

QY 6 QRYG-----RELFRMSDEFEGSFK 24  
||| :|||: |||:

D6 107 QRUGCELDLDIQELRRLEDMENTFFK 133

RESULT 8

C84338  
spermidine/putrescine ABC transporter [imported] - Halobacterium sp. NRC-1  
C;Species: Halobacterium sp. NRC-1  
C>Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C;Accession: C84338  
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Laskey,  
Leithauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jaleel,  
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.  
A;Title: Genome sequence of Halobacterium species NRC-1.  
A;Reference number: A84160; MUID:20504483; PMID:11016950  
A;Accession: C84338  
A>Status: preliminary  
A:Molecule type: DNA

A;Residues: 1-374 <STO>  
 A;Cross-references: GB:AE004437; NID:gl0581314; PIDN:AAG20071.1; GSPDB:GN00138  
 C;Genetics:  
 A;Gene: potA2

Query Match 34.5%; Score 50; DB 2; Length 374;  
 Best Local Similarity 76.9%; Pred. No. 16;  
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 11 ELRRMSDEFEFGS 23  
 |||||:| | |||

Db 197 ELRRSDAVEGSF 209  
 |||||:| | |||

RESULT 9

A96753

probable threonine synthase [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001

C;Accession: A96753

R;Rheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
 anseu, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: A96753

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-516 <STO>

A;Cross-references: GB:AE005173; NID:q5903070; PIDN:AAD55628.1; GSPDB:GN00141

C;Genetics:

A;Gene: F3W23.1

A;Map position: 1

Query Match 34.5%; Score 50; DB 2; Length 516;

Best Local Similarity 35.3%; Pred. No. 23;

Matches 12; Conservative 7; Mismatches 7; Indels 8; Gaps 1;

QY 1 NLWAAQRYGRELRRMSD-----EFEGSFKGL 26  
 ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

Db 163 NLFWAERFGQYLOMNDLWVKHGIGSHTGSKDL 196  
 ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

RESULT 10

A64807

endonuclease VIII (EC 3.2.2.-) - Escherichia coli (strain K-12)

C;Species: Escherichia coli

C;Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 01-Mar-2002

C;Accession: A64807

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co  
 .A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Accession: A64807

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-263 <BLAT>

A;Cross-references: GB:AE000174; GB:U00096; NID:gl786920; PIDN:AAC73808.1; PID:gl786932;

A;Experimental source: strain K-12, substrain MG1655

C;Genetics:

A;Gene: nei

A;Map position: 16 min

C;Function:

A;Description: DNA N-glycosylase with an apurinic lyase activity; recognizes and removes

C;Superfamily: formamidopyrimidine-DNA glycosidase

C;Keywords: DNA repair; glycosidase; hydrolase; lyase

Query Match 33.8%; Score 49; DB 2; Length 263;  
 Best Local Similarity 47.4%; Pred. No. 16;  
 Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 9 GRELRMSDEFEFGSKGLP 27  
 |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

Db 4 GPEIRRAADNLEAAIKGKP 22  
 |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

RESULT 11

A85572

hypothetical protein nei [imported] - Escherichia coli (strain O157:H7, substrain EDL

C;Species: Escherichia coli

C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 17-May-2002

C;Accession: A85572

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May  
 iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda

Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: A85572

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-263 <STO>

A;Cross-references: GB:AE005174; NID:gl2513625; PIDN:AAG55037.1; GSPDB:GN00145; UWGP:

A;Experimental source: strain O157:H7, substrain EDL933

C;Genetics:

A;Gene: nei

C;Superfamily: formamidopyrimidine-DNA glycosidase

Query Match 33.8%; Score 49; DB 2; Length 263;

Best Local Similarity 47.4%; Pred. No. 16;

Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 9 GRELRMSDEFEFGSKGLP 27  
 |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

Db 4 GPEIRRAADNLEAAIKGKP 22  
 |:|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~

RESULT 12

C90721

hypothetical protein ECs0739 [imported] - Escherichia coli (strain O157:H7, substrain

C;Species: Escherichia coli

C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 17-May-2002

C;Accession: C90721

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C  
 gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g

A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: C90721

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-263 <HAY>

A;Cross-references: GB:BA000007; PIDN:BA834162.1; PID:gl3360197; GSPDB:GN00154

A;Experimental source: strain O157:H7, substrain RMD 0509952

C;Genetics:

A;Gene: ECs0739

C;Superfamily: formamidopyrimidine-DNA glycosidase

Query Match 33.8%; Score 49; DB 2; Length 263;

Best Local Similarity 47.4%; Pred. No. 16;

Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 9 GRELRMSDEFEFGSKGLP 27  
 |:|:|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~

Db 4 GPEIRRAADNLEAAIKGKP 22  
 |:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~

RESULT 13

AD0590

endonuclease VIII, DNA N-glycosylase with an AP lyase activity STY0771 [imported] - S

C:Species: Salmonella enterica subsp. enterica serovar Typhi  
 A:Note: this species has also been called Salmonella typhi  
 C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
 C:Accession: AD0590  
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.  
 Nature 413, 848-852, 2001  
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
 A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov  
 A:Reference number: AB0502; MUID:21534947; PMID:11677608  
 A:Accession: AD0590  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-263 <PAR>  
 A:Cross-references: GB:AL513382; PIDN:CAD05190.1; PID:gl6501960; GSPDB:GN00176  
 C:Genetics:  
 A:Gene: STY0771  
 C:Superfamily: formamidopyrimidine-DNA glycosidase

Query Match 33.8%; Score 49; DB 2; Length 263;  
 Best Local Similarity 47.4%; Pred. No. 16;  
 Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 9 GRELRMSDEFEGSKGLP 27  
 | | | | | | | | | |  
 Db 4 GPEIRRAADNLEAIAIKGP 22

## RESULT 14

E83517  
 conserved hypothetical protein PA1031 [imported] - Pseudomonas aeruginosa (strain PA01)  
 C:Species: Pseudomonas aeruginosa  
 C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
 C:Accession: E83517  
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br  
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
 .; Lory, S.; Olson, M.V.  
 Nature 406, 959-964, 2000  
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
 A:Reference number: A82950; MUID:20437337; PMID:10984043  
 A:Accession: E83517  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-453 <STO>  
 A:Cross-references: GB:AE004535; GB:AE004091; NID:g9946936; PIDN:AAG04420.1; GSPDB:GN001  
 A:Experimental source: strain PA01  
 C:Genetics:  
 A:Gene: PA1031

Query Match 33.8%; Score 49; DB 2; Length 453;  
 Best Local Similarity 55.6%; Pred. No. 28;  
 Matches 10; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

QY 3 WAAQRYGR--ELRRMSDE 18  
 | | | | | | | | | |  
 Db 65 WASERQGRFEELRLRLASE 82

## RESULT 15

S40376  
 Ig kappa chain - human  
 C:Species: Homo sapiens (man)  
 C:Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
 C:Accession: S40376  
 R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
 Eur. J. Immunol. 23, 3248-3271, 1993  
 A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
 A:Reference number: S40312; MUID:94080891; PMID:8258341  
 A:Accession: S40376  
 A:Status: preliminary; translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-134 <KLE>

A:Cross-references: EMBL:X72486; NID:g441440; PIDN:CAA51154.1; PID:g441441  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:34-113/Domain: immunoglobulin homology <IMM>

Query Match 33.4%; Score 48.5; DB 2; Length 134;  
 Best Local Similarity 38.2%; Pred. No. 9.3;  
 Matches 13; Conservative 1; Mismatches 9; Indels 11; Gaps 1;

QY 3 WAAQRYGRELRM-----SDEFEGSFKG 25  
 | | | | | | | | | |  
 Db 58 WFEQRPGSPRLIYNVSKRDSGVSDPFGSGSG 91

Search completed: September 15, 2003, 17:27:01  
 Job time : 13.15 secs

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: September 15, 2003, 17:16:55 ; Search time 6.36429 Seconds  
(without alignments)  
199.507 Million cell updates/sec

Title: US-09-544-664-3  
Perfect score: 145  
Sequence: 1 NLWAAQRYGRELRRMSDEFFGSEKGLP 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	145	100.0	204	1 BAD_MOUSE	Q61337 mus musculus
2	145	100.0	205	1 BAD_RAT	Q35147 rattus norv
3	120.5	83.1	168	1 BAD_HUMAN	Q92934 homo sapien
4	61	42.1	946	1 ITH2_MESAU	P97279 mesocricetu
5	60	41.4	946	1 ITH2_MOUSE	Q61703 mus musculus
6	53	36.6	946	1 ITH2_HUMAN	P19823 homo sapien
7	52	35.9	370	1 AROG_YEAST	P32449 saccharomyc
8	51	35.2	232	1 AP3_ARATH	P35632 arabidopsis
9	50	34.5	851	1 CE05_MOUSE	Q8x2h3 mus musculus
10	49.5	34.1	506	1 MATK_LEDPA	O62992 ledum palus
11	49.5	34.1	506	1 MATK_RHOFR	O62984 rhododendro
12	49.5	34.1	506	1 MATK_RHOTS	O62991 rhododendro
13	49	33.8	262	1 END8_ECO57	Q8x9c6 escherichia
14	49	33.8	262	1 END8_ECOLI	P50465 escherichia
15	49	33.8	262	1 END8_SALTI	Q8z8d2 salmonella
16	49	33.8	262	1 END8_SALTY	Q8zuq6 salmonella
17	49	33.8	453	1 RMTC_PSEAE	Q914u3 pseudomonas
18	48	33.1	205	1 RAS3_RHIRA	P22280 rhizomucor
19	48	33.1	220	1 6PGL_THEMA	Q9x0r8 thermotoga
20	48	33.1	519	1 THRC_SOLTU	Q9mt28 solanum tub
21	48	33.1	526	1 THRC_ARATH	Q9s7b5 arabidopsis
22	47	32.4	198	1 BIM_HUMAN	O43521 homo sapien
23	46.5	32.1	429	1 FMR2_ANTEL	Q16994 anthopleura
24	46.5	32.1	435	1 FMR1_ANTEL	P10419 anthopleura
25	46.5	32.1	855	1 XAB2_MOUSE	Q9dcd2 mus musculus
26	46.5	32.1	855	1 XAB2_RAT	Q99pk0 rattus norv
27	46	31.7	738	1 SEC6_DROME	Q9v8k2 drosophila
28	46	31.7	1378	1 RPOB_CAMJE	Q61124 campylobact
29	45.5	31.4	287	1 PREA_POLPE	P21259 polychelis
30	45.5	31.4	334	1 FMR3_CALPA	Q01133 calliactis
31	45.5	31.4	507	1 MATK_LOIPR	O47169 loiseleuria
32	45.5	31.4	855	1 XAB2_HUMAN	Q9hcs7 homo sapien
33	45	31.0	328	1 SNF4_KLULA	Q9p869 kluyveromyc

## RESULT 1

BAD\_MOUSE

ID BAD\_MOUSE STANDARD; PRT; 204 AA.

AC Q61337;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component  
DE 6) (Bcl-XL/Bcl-2 associated death promoter).  
GN BAD OR BCL6.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain, and Thymus;

RX MEDLINE=95136361; PubMed=7834748;

RA Yang E., Zha J., Jockel J., Boise L.H., Thompson C.B., Korsmeyer S.J.;  
RT "Bad, a heterodimeric partner for Bcl-XL and Bcl-2, displaces Bax and  
RT Promotes cell death.";  
RL Cell 80:285-291(1995).

RN [2]

RP PHOSPHORYLATION, AND MUTAGENESIS OF SER-112 AND SER-136.

RX MEDLINE=98022383; PubMed=9381178;

RA Del Peso L., Gonzalez-Garcia M., Page C., Herrera R., Nunez G.;

RT "Interleukin-3-induced phosphorylation of BAD through the protein

RT Kinase Akt.";

RL Science 278:687-689(1997).

RN [3]

RP MUTAGENESIS OF SERINE RESIDUES.

RX MEDLINE=20403302; PubMed=10949026;

RA Data S.R., Katsov A., Hu L., Petros A., Fesik S.W., Yaffe M.B.,

Greenberg M.E.;

RT "14-3-3 proteins and survival kinases cooperate to inactivate BAD by

RT BH3 domain phosphorylation.";

RL Mol. Cell 6:41-51(2000).

CC -!- FUNCTION: Promotes cell death. Successfully competes for the  
CC binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level  
CC of heterodimerization of these proteins with BAX. Can reverse the  
CC death repressor activity of Bcl-x(L), but not that of Bcl-2.  
CC Appears to act as a link between growth factor receptor signaling  
CC and the apoptotic pathways.

CC -!- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-  
CC x(L), Bcl-2 and Bcl-w. Also binds protein S100A10 (By similarity).  
CC The Ser-112/Ser-136 phosphorylated form binds 14-3-3 proteins.

CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon

CC phosphorylation, locates to the cytoplasm.

CC -!- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND

CC BAX for their pro-apoptotic activity and for their interaction

CC with anti-apoptotic members of the Bcl-2 family.

CC -!- PTM: Phosphorylated on Ser-112 in response to survival stimuli.  
CC Subsequent phosphorylation on Ser-136 promotes heterodimerization  
CC with 14-3-3 proteins. This interaction then facilitates the  
CC phosphorylation at Ser-155, a site within the BH3 domain, leading  
CC to the release of Bcl-x(L) and the promotion of cell survival.

## ALIGNMENTS

34	45	31.0	513	1	KCGL_HUMAN	Q9uix4 homo sapien
35	45	31.0	590	1	DCOA_SALTY	Q03030 salmonella
36	45	31.0	595	1	DCOA_KLEPN	P13187 klebsiella
37	45	31.0	653	1	HT2A_HUMAN	Q13049 homo sapien
38	45	31.0	865	1	ENV_SIVAT	P05886 simian immu
39	45	31.0	1535	1	IMLI_CABEL	Q18823 caenorhabdi
40	44.5	30.7	143	1	NB6M_HUMAN	Q9p0j0 h nadh-ubiq
41	44.5	30.7	907	1	NUOG_ECOLI	P33602 escherichia
42	44.5	30.7	907	1	NUOG_SALTY	P33900 salmonella
43	44	30.3	196	1	BIM_MOUSE	O54918 mus musculus
44	44	30.3	196	1	BIM_RAT	O88498 rattus norv
45	44	30.3	768	1	ENV_SIVAT	P27757 simian immu

CC Ser-136 is the major site of AKT/PKB phosphorylation, Ser-155 the  
 CC major site of protein kinase A (CAPK) phosphorylation.  
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.  
 CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; L37296; AAA64465.1; -;  
 CC PIR; A55671; A55671.  
 CC HSP; Q92934; IG5J.  
 CC MGD; MGI:1096330; Bad.  
 CC InterPro; IPR000712; Bcl2\_BH.  
 CC PROSITE; PS01259; BH3; FALSE\_NEG.  
 CC Apoptosis; Phosphorylation.  
 CC DOMAIN 147 161 BH3.  
 CC MOD\_RES 112 112 PHOSPHORYLATION (BY PKA AND PKB).  
 CC MOD\_RES 136 136 PHOSPHORYLATION (BY PKA AND PKB).  
 CC MOD\_RES 155 155 PHOSPHORYLATION (BY PKA AND PKB).  
 CC MUTAGEN 112 112 S->A: NO PHOSPHORYLATION.  
 CC MUTAGEN 136 136 S->A: NO PHOSPHORYLATION.  
 CC MUTAGEN 155 155 S->A: NO PHOSPHORYLATION; INTERACTS WITH  
 CC BCL-X(L).  
 CC SEQUENCE 204 AA; 22080 MW; 6C2BA91020503F7 CRC64;  
 CC  
 CC Query Match 100.0%; Score 145; DB 1; Length 204;  
 CC Best Local Similarity 100.0%; Pred. No. 1.4e-14;  
 CC Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC Qy 1 NLWAAQRYGRELRRMSDFEGSFKGLP 27  
 CC |||||  
 CC Db 140 NLWAAQRYGRELRRMSDFEGSFKGLP 166  
 CC  
 CC RESULT 2  
 CC BAD\_RAT  
 CC ID BAD\_RAT STANDARD; PRT; 205 AA.  
 CC AC Q35147; Q70256; Q9JHX1;  
 CC DT 16-OCT-2001 (Rel. 40, Created)  
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 CC DE Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component  
 CC 6) (Bcl-xL/Bcl-2 associated death promoter).  
 CC GN BAD.  
 CC OS Rattus norvegicus (Rat).  
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 CC OX NCBI\_TaxID=10116;  
 CC RN [1]  
 CC RP SEQUENCE FROM N.A., AND MUTAGENESIS OF SER-113 AND SER-137.  
 CC RC TISSUE=Ovary;  
 CC RX MEDLINE=98034386; PubMed=9369453;  
 CC RA Hsu S.Y., Kaipia A., Zhu L., Hsueh A.J.W.;  
 CC RT "Interference of BAD (Bcl-xL/Bcl-2-associated death promoter)-induced  
 CC apoptosis in mammalian cells by 14-3-3 isoforms and P11";  
 CC RL Mol. Endocrinol. 11:1858-1867(1997).  
 CC RN [2]  
 CC RP SEQUENCE FROM N.A.  
 CC RC TISSUE=Brain;  
 CC RX MEDLINE=98194755; PubMed=9535132;  
 CC RA D'Agata V., Magro G., Travali S., Musco S., Cavallaro S.;  
 CC RT "Cloning and expression of the programmed cell death regulator BAD in  
 CC the rat brain";  
 CC RL Neurosci. Lett. 243:137-140(1998).  
 CC RN [3]  
 CC RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).  
 CC RC TISSUE=Brain;  
 CC RX MEDLINE=21109372; PubMed=11161472;

RA Hamner S., Arumae U., Yu L.-Y., Sun Y.-F., Saarma M., Lindholm D.;  
 RT "Functional characterization of two splice variants of rat BAD and  
 RT their interaction with Bcl-w in sympathetic neurons.";  
 RL Mol. Cell. Neurosci. 17:97-106(2001).  
 CC -!- FUNCTION: Promotes cell death. Successfully competes for the  
 CC binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level  
 CC of heterodimerization of these proteins with BAX. Can reverse the  
 CC death repressor activity of Bcl-x(L), but not that of Bcl-2 (By  
 CC similarity). Appears to act as a link between growth factor  
 CC receptor signaling and the apoptotic pathways.  
 CC -!- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-  
 CC x(L), Bcl-2 and Bcl-w. Also binds protein S100A10. The Ser-  
 CC 113/Ser-137 phosphorylated form binds 14-3-3 proteins.  
 CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon  
 CC phosphorylation, locates to the cytoplasm (By similarity).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=2;  
 CC Name=Alpha;  
 CC IsoId=Q35147-1; Sequence=Displayed;  
 CC Name=Beta;  
 CC IsoId=Q35147-2; Sequence=VSP\_000534;  
 CC -!- TISSUE SPECIFICITY: Expressed in all tissues tested, including  
 CC brain, liver, spleen and heart. In the brain, restricted to  
 CC epithelial cells of the choroid plexus. Isoform alpha is the more  
 CC abundant form.  
 CC -!- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND  
 CC BAX for their pro-apoptotic activity and for their interaction  
 CC with anti-apoptotic members of the Bcl-2 family.  
 CC -!- PTM: Phosphorylated on Ser-113 in response to survival stimuli.  
 CC Subsequent phosphorylation on Ser-137 promotes heterodimerization  
 CC with 14-3-3 proteins. This interaction then facilitates the  
 CC phosphorylation at Ser-156, a site within the BH3 domain, leading  
 CC to the release of Bcl-x(L) and the promotion of cell survival.  
 CC Ser-137 is the major site of AKT/PKB phosphorylation, Ser-156 the  
 CC major site of protein kinase A (CAPK) phosphorylation (By  
 CC similarity).  
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.  
 CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; AF003523; AAC53374.1; -;  
 CC EMBL; AF031227; AAC15100.1; -;  
 CC EMBL; AF279910; AAF91427.1; -;  
 CC EMBL; AF279911; AAF91428.1; -;  
 CC HSP; Q92934; IG5J.  
 CC InterPro; IPR000712; Bcl2\_BH.  
 CC PROSITE; PS01259; BH3; FALSE\_NEG.  
 CC Apoptosis; Phosphorylation; Alternative splicing.  
 CC DOMAIN 148 162 BH3.  
 CC MOD\_RES 113 113 PHOSPHORYLATION (BY PKA AND PKB)  
 CC (BY SIMILARITY).  
 CC MOD\_RES 137 137 PHOSPHORYLATION (BY PKA AND PKB)  
 CC (BY SIMILARITY).  
 CC MOD\_RES 156 156 PHOSPHORYLATION (BY PKA AND PKB)  
 CC (BY SIMILARITY).  
 CC VARSPLIC 166 205 LPRPSAGTATQMRQASWTRIQSWDRNLKGGSTPSQ  
 CC -> EELTVSVFELPVRAIAMEGWPLLWFSQSPHTLPPTPP  
 CC EVAMEPLRWTAALRLC (in isoform Beta).  
 CC /FTIQ-VSP\_000534.  
 CC S->A: NO EFFECT ON HETERODIMERIZATION  
 CC WITH 14-3-3 PROTEINS.  
 CC S->A: NO HETERODIMERIZATION WITH 14-3-3  
 CC PROTEINS. NO EFFECT ON HETERODIMERIZATION  
 CC WITH BCL2 NOR WITH PROTEIN P11.  
 CC SDAGGR -> ERRGRK (IN REF. 1).  
 CC CONFLICT 29 34  
 CC SEQUENCE 205 AA; 22228 MW; 7AFA71DAE9CF4A81 CRC64;

Query Match 100.0%; Score 145; DB 1; Length 205;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-14;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDFEGSKGLP 27  
 |||||  
 Db 141 NLWAAQRYGRELRRMSDFEGSKGLP 167

RESULT 3  
 ID BAD\_HUMAN STANDARD; PRT; 168 AA.  
 AC Q92934; O14803;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component 6) (Bcl-  
 XL/Bcl-2 associated death promoter) (BCL2-like 8 protein).  
 GN BAD OR BBC6 OR BCL2L8.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Yin D.X., Li Z., Huang B., Chen S., Zhou H.;  
 RT "A human protein that interacts with Bcl-2 and have homology to mouse  
 BAD";  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A., AND PHOSPHORYLATION BY RAF-1.  
 RX MEDLINE=97083574; PubMed=8929532;  
 RA Wang H.-G., Rapp U.R., Reed J.C.;  
 RT "Bcl-2 targets the protein kinase Raf-1 to mitochondria";  
 RL Cell 87:629-638 (1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Takayama S., Reed J.C.;  
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A., AND DIMERIZATION.  
 RC TISSUE=Bone marrow;  
 RX MEDLINE=98049554; PubMed=9388232;  
 RA Ohtsile S., Diaz J.-L., Horne W., Chang J., Wang Y., Wilson G.,  
 RA Chang S., Weeks S., Fritz L.C., Oltersdorf T.;  
 RT "Dimerization properties of human BAD";  
 RL J. Biol. Chem. 272:30866-30872 (1997).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Buetow K.H., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [6]

RP STRUCTURE BY NMR OF 103-127.  
 RX MEDLINE=21073561; PubMed=11206074;  
 RA Petros A.M., Nettesheim D.G., Wang Y., Olejniczak E.T., Meadows R.P.,  
 RA Mack J., Swift K., Matayoshi E.D., Zhang H., Thompson C.B.,  
 RA Fesik S.W.; for Bcl-xL/Bad peptide complex formation from structure,  
 RT "Rationale for Bcl-xL/Bad peptide complex formation from structure,  
 RL Protein Sci. 9:2528-2534 (2000).  
 CC -!- FUNCTION: Promotes cell death. Successfully competes for the  
 CC binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level  
 CC of heterodimerization of these proteins with BAX. Can reverse the  
 CC death repressor activity of Bcl-x(L), but not that of Bcl-2 (By  
 CC similarity). Appears to act as a link between growth factor  
 CC receptor signaling and the apoptotic pathways.  
 CC -!- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-  
 CC x(L), Bcl-2 and Bcl-w. Also binds protein S100A10 (By similarity).  
 CC The Ser-75/Ser-99 phosphorylated form binds 14-3-3 proteins (By  
 CC similarity).  
 CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon  
 CC phosphorylation, locates to the cytoplasm.  
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.  
 CC -!- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND  
 CC BAX for their pro-apoptotic activity and for their interaction  
 CC with anti-apoptotic members of the Bcl-2 family.  
 CC -!- PTM: Phosphorylated on Ser-75 in response to survival stimuli.  
 CC Subsequent phosphorylation on Ser-99 promotes heterodimerization  
 CC with 14-3-3 proteins. This interaction then facilitates the  
 CC phosphorylation at Ser-118, a site within the BH3 domain, leading  
 CC to the release of Bcl-x(L) and the promotion of cell survival.  
 CC Ser-99 is the major site of AKT/PKB phosphorylation, Ser-118 the  
 CC major site of protein kinase A (CAK) phosphorylation (by  
 CC similarity).  
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.  
 CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -!- CAUTION: Ref.1 sequence differs from that shown due to frameshifts  
 CC in position 64 and 91.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; U66879; AAB36516.1; ALT\_FRAME.  
 CC EMBL; AF021792; AAB72092.1; -  
 CC EMBL; AF031523; AAB88124.1; -  
 CC EMBL; BC001901; AAH01901.1; -  
 CC PDB; 1GSJ; 07-FEB-01.  
 CC Genew; HGNC:936; BAD.  
 CC MIM; 603167; -  
 CC GO; GO:0005737; C:cytoplasm; NAS.  
 CC GO; GO:0005741; C:mitochondrial outer membrane; NAS.  
 CC GO; GO:0005515; F:protein binding activity; NAS.  
 CC GO; GO:0008632; P:apoptotic program; TAS.  
 CC GO; GO:0006917; P:induction of apoptosis; NAS.  
 CC InterPro; IPR000712; Bcl2\_BH.  
 CC PROSITE; PS01259; BH3; FALSE\_NEG.  
 CC Apoptosis; Phosphorylation; Polymorphism; 3D-structure.  
 FT DOMAIN 110 124 BH3  
 FT MOD\_RES 75 75 PHOSPHORYLATION (BY PKA AND PKB) (BY  
 FT SIMILARITY).  
 FT MOD\_RES 99 99 PHOSPHORYLATION (BY PKA AND PKB) (BY  
 FT SIMILARITY).  
 FT MOD\_RES 118 118 PHOSPHORYLATION (BY PKA AND PKB) (BY  
 FT SIMILARITY).  
 FT VARIANT 107 107 A -> S (in dbSNP:3729933).  
 FT HELIX 106 121  
 FT SEQUENCE 168 AA; 18392 MW; 69FD8D27DDE3241 CRC64;  
 SQ

Query Match 83.1%; Score 120.5; DB 1; Length 168;

Best Local Similarity 89.3%; Pred. No. 5.5e-11;  
Matches 25; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 NLWAAQRYGRELRRMSDEFEGSF-KGLP 27  
Db 103 NLWAAQRYGRELRRMSDEFVDSFKKGLP 130

RESULT 4  
ITH2\_MESAU  
ID ITH2\_MESAU STANDARD; PRT; 946 AA.  
AC P97279;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy  
chain H2) (Inter-alpha-inhibitor heavy chain 2) (HC2).  
GN ITH2.  
OS Mesocricetus auratus (Golden hamster).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
OC Mesocricetus.  
OX NCBI\_TaxID=10036;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=97420688; PubMed=9276673;  
RA Nakatani T., Suzuki Y., Yamamoto T., Sinohara H.;  
RT "Molecular cloning and sequencing of cDNAs encoding three heavy-chain  
precursors of the inter-alpha-trypsin inhibitor in Syrian hamster:  
RT implications for the evolution of the inter-alpha-trypsin inhibitor  
heavy chain family.";  
RL J. Biochem. 122:71-82(1997).  
RN [2]  
RP SEQUENCE OF 55-64; 140-146; 151-156; 424-447; 500-528 AND 577-605,  
AND SUBUNITS.  
RC TISSUE=Plasma;  
RX MEDLINE=97018241; PubMed=8864857;  
RA Yamamoto T., Yamamoto K., Sinohara H.;  
RT "Inter-alpha-trypsin inhibitor and its related proteins in Syrian  
hamster urine and plasma.";  
RL J. Biochem. 120:145-152(1996).  
CC -!- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A  
BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,  
INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE  
LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE  
ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY  
SIMILARITY).  
CC -!- SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM  
ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,  
BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2  
AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND  
BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.  
CC -!- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN  
4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY  
SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE ITH FAMILY.  
CC -!- SIMILARITY: Contains 1 VWFA domain.  
-----  
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-----  
DR EMBL; D89286; BAA13939.1; -.  
DR PIR; JC5575; JC5575.  
DR InterPro; IPR006587; VIT.  
DR InterPro; IPR002035; VWFA.  
DR Pfam; PF00092; vwa; 1.  
DR SMART; SM00609; VIT; 1.

DR SMART; SM00327; VWA; 1.  
DR PROSITE; PS50234; VWFA; 1.  
KW Serine protease inhibitor; Repeat; Signal; Multigene family;  
KW Glycoprotein.  
FT SIGNAL 1 18 POTENTIAL.  
FT PROPEP 19 54 BY SIMILARITY.  
FT CHAIN 55 702 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN  
H2.  
FT PROPEP 703 946 BY SIMILARITY.  
FT DOMAIN 308 468 VWFA.  
FT CARBOHYD 118 118 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 578 578 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT BINDING 702 702 CHONDROITIN 4-SULFATE, CROSS-LINK SITE  
(BY SIMILARITY).  
FT CONFLICT 510 510 V -> Y (IN REF. 2).  
FT CONFLICT 595 595 E -> I (IN REF. 2).  
SQ SEQUENCE 946 AA; 106580 MW; CA8BF565458E7B2E CRC64;  
Query Match 42.1%; Score 61; DB 1; Length 946;  
Best Local Similarity 37.0%; Pred. No. 0.34;  
Matches 10; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFEGSF-KGLP 27  
Db 212 NWVIVELQGMRFHLVDPDTFEGHFGQVP 238

RESULT 5  
ITH2\_MOUSE  
ID ITH2\_MOUSE STANDARD; PRT; 946 AA.  
AC Q61703;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy  
chain H2) (Inter-alpha-inhibitor heavy chain 2).  
GN ITH2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6N; TISSUE=Liver;  
RX MEDLINE=95194326; PubMed=7534067;  
RA Chan P., Risler J.-L., Raguenez G., Salier J.-P.;  
RT "The three heavy-chain precursors for the inter-alpha-inhibitor  
family in mouse: new members of the multicopper oxidase protein group  
with differential transcription in liver and brain.";  
RL Biochem. J. 306:505-512(1995).  
CC -!- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A  
BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,  
INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE  
LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE  
ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY  
SIMILARITY).  
CC -!- SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM  
ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,  
BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2  
AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND  
BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.  
CC -!- TISSUE SPECIFICITY: EXPRESSED IN BOTH LIVER AND BRAIN.  
CC -!- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN  
4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY  
SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE ITH FAMILY.  
CC -!- SIMILARITY: Contains 1 VWFA domain.  
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 -----

DR EMBL; X70392; CAA49842.1; -.  
 DR PIR; S54354; S54354.  
 DR MGI; 96619; Itih2.  
 DR InterPro; IPR006587; VIT.  
 DR InterPro; IPR002035; VWFA\_A.  
 DR Pfam; PF00092; vwa; 1.  
 DR SMART; SM00609; VIT; 1.  
 DR SMART; SM00327; VWA; 1.  
 DR PROSITE; PS0234; VWFA; 1.  
 KW Serine protease inhibitor; Repeat; Signal; Multigene family;  
 KW Glycoprotein.  
 FT SIGNAL 1 18 POTENTIAL.  
 FT PROPEP 19 54 BY SIMILARITY.  
 FT CHAIN 55 702 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN  
 H2.  
 FT PROPEP 703 946 BY SIMILARITY.  
 FT DOMAIN 308 468 VWFA.  
 FT CARBOHYD 118 118 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT BINDING 702 702 CHONDROITIN 4-SULFATE, CROSS-LINK SITE  
 .(BY SIMILARITY).  
 SQ SEQUENCE 946 AA; 105927 MW; 40DB6716433ED9DC CRC64;

Query Match 41.4%; Score 60; DB 1; Length 946;  
 Best Local Similarity 37.0%; Pred. NO. 0.47;  
 Matches 10; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRMSEFEFGSKGLP 27  
 I: I : I : I I I I I I:  
 Db 212 NWIIIEPQGMRELFHVPDFEGHFGVP 238

RESULT 6  
 ITH2\_HUMAN  
 ID ITH2\_HUMAN STANDARD; PRT; 946 AA.  
 AC P19823; Q14659; Q15484;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy  
 DE chain H2) (Inter-alpha-inhibitor heavy chain 2) (Inter-alpha-trypsin  
 DE inhibitor complex component II) (Serum-derived hyaluronan-associated  
 DE protein) (SHAP).  
 GN ITH2 OR IGHEP2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE=88152237; PubMed=2450046;  
 RA Gebhard W., Schreitmuller T., Hochstrasser K., Wachter E.;  
 RT "Complementary DNA and derived amino acid sequence of the precursor  
 RT of one of the three protein components of the inter-alpha-trypsin  
 RT inhibitor complex.";  
 RL FEBS Lett. 229:63-67(1988).  
 RN [2]  
 RN SEQUENCE OF 384-865 FROM N.A.  
 RX MEDLINE=88068576; PubMed=2446322;  
 RA Salier J.-P., Diarra-Mehrpour M., Sesboue R., Bourguignon J.,  
 RA Benarous R., Ohkubo I., Kurachi S., Kurachi K., Martin J.P.;  
 RT "Isolation and characterization of cDNAs encoding the heavy chain of  
 RT human inter-alpha-trypsin inhibitor (I alpha TI); unambiguous  
 RT evidence for multipolypeptide chain structure of I alpha TI.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:8272-8276(1987).  
 RN [3]  
 RN SEQUENCE OF 384-766 FROM N.A.

RX MEDLINE=89076497; PubMed=2462430;  
 RA Salier J.-P., Diarra-Mehrpour M., Sesboue R., Bourguignon J.,  
 RA Martin J.P.;  
 RT "Human inter-alpha-trypsin inhibitor. Isolation and characterization  
 RT of heavy (H) chain cDNA clones coding for a 383 amino-acid sequence  
 RT of the H chain.";  
 RL Biol. Chem. Hoppe-Seyler 369:15-18(1988).  
 RN [4]  
 RN PARTIAL SEQUENCE FROM N.A.  
 RP TISSUE=Liver;  
 RX MEDLINE=88024442; PubMed=3663330;  
 RA Schreitmuller T., Hochstrasser K., Resinger P.W.M., Wachter E.,  
 RA Gebhard W.;  
 RT "cDNA cloning of human inter-alpha-trypsin inhibitor discloses three  
 RT different proteins.";  
 RL Biol. Chem. Hoppe-Seyler 368:963-970(1987).  
 RN [5]  
 RN SEQUENCE OF 55-74; 116-127; 224-246; 295-307 AND 365-385.  
 RX MEDLINE=89380192; PubMed=2476436;  
 RA Enghild J.J., Thøgersen I.B., Pizzo S.V., Salvesen G.;  
 RT "Analysis of inter-alpha-trypsin inhibitor and a novel trypsin  
 RT inhibitor, pre-alpha-trypsin inhibitor, from human plasma.  
 RL Polypeptide chain stoichiometry and assembly by glycan.";  
 RN [6]  
 RN J. Biol. Chem. 264:15973-15981(1989).  
 RP SEQUENCE OF 55-64.  
 RC TISSUE=Plasma;  
 RX MEDLINE=93039735; PubMed=1384548;  
 RA Malki N., Balduyck M., Maes P., Capon C., Mizon C., Han K.K.,  
 RA Tartar A., Fournet B., Mizon J.;  
 RT "The heavy chains of human plasma inter-alpha-trypsin inhibitor: their  
 RT isolation, their identification by electrophoresis and partial  
 RT sequencing. Differential reactivity with concanavalin A.";  
 RL Biol. Chem. Hoppe-Seyler 373:1009-1018(1992).  
 RN [7]  
 RN SEQUENCE OF 55-64 AND 681-702, CROSS-LINK STRUCTURE, AND  
 RP CARBOHYDRATE-LINKAGE SITES THR-691.  
 RX MEDLINE=93232026; PubMed=7682553;  
 RA Enghild J.J., Salvesen G., Thøgersen I.B., Valnickova Z.,  
 RA Pizzo S.V., Hefta S.A.;  
 RT "Presence of the protein-glycosaminoglycan-protein covalent cross-link  
 RT in the inter-alpha-inhibitor-related proteinase inhibitor heavy chain  
 RT 2/bikunin.";  
 RL J. Biol. Chem. 268:8711-8716(1993).  
 RN [8]  
 RN SEQUENCE OF 67-101, AND HYALURONAN BINDING.  
 RP TISSUE=Serum;  
 RX MEDLINE=94075371; PubMed=7504674;  
 RA Huang L., Yoneda M., Kimata K.;  
 RT "A serum-derived hyaluronan-associated protein (SHAP) is the heavy  
 RT chain of the inter alpha-trypsin inhibitor.";  
 RL J. Biol. Chem. 268:26725-26730(1993).  
 RN [9]  
 RN SEQUENCE OF 699-702, AND COVALENT LINKAGE WITH CHONDROITIN SULFATE.  
 RP TISSUE=Plasma;  
 RX MEDLINE=94229087; PubMed=7513643;  
 RA Morelle W., Capon C., Balduyck M., Sautiere P., Kouach M.,  
 RA Michalski C., Fournet B., Mizon J.;  
 RT "Chondroitin sulphate covalently cross-links the three polypeptide  
 RT chains of inter-alpha-trypsin inhibitor.";  
 RL Eur. J. Biochem. 221:881-888(1994).  
 RN [10]  
 RN CARBOHYDRATE-LINKAGE SITES, AND MASS SPECTROMETRY.  
 RP MEDLINE=98343966; PubMed=9677337;  
 RX Flahaut C., Capon C., Balduyck M., Ricart G., Sautiere P., Mizon J.;  
 RA "Glycosylation pattern of human inter-alpha-inhibitor heavy chains.";  
 RL Biochem. J. 333:749-756(1998).  
 RN [11]  
 RN CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.  
 RX MEDLINE=98087700; PubMed=9425062;  
 RA Olsen E.H.N., Rahbek-Nielsen H., Thøgersen I.B., Roepstorff P.,  
 RA Enghild J.J.;  
 RT "Posttranslational modifications of human inter-alpha-inhibitor:

RT identification of glycans and disulfide bridges in heavy chains 1 and 2";

RL Biochemistry 37:408-416(1998).

CC -!- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES.

CC -!- SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN, BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2 AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.

CC -!- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN 4-SULFATE BRIDGE TO THEIR C-TERMINAL ASPARTATE.

CC -!- MASS SPECTROMETRY: MW=76508; METHOD=WALDI; RANGE=55-702.

CC -!- SIMILARITY: BELONGS TO THE ITIH FAMILY.

CC -!- SIMILARITY: Contains 1 VWFA domain.

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CC -----

DR EMBL; X07173; CAA30160.1; ALT\_SEQ.

DR EMBL; M18193; AAA60558.1; -.

DR EMBL; M33033; AAA59195.1; -.

DR PIR; S00346; IYHD2.

DR GlycosuitedB; P19823; -.

DR Genew; HGNC:6167; ITIH2.

DR MIM; 146640; -.

DR GO; GO:0005211; Fplasma glycoprotein; TAS.

DR InterPro; IPR006587; VIT.

DR InterPro; IPR002035; VWF\_A.

DR Pfam; PF00092; vwa; 1.

DR SMART; SM00609; VIT; 1.

DR SMART; SM00327; VWA; 1.

DR PROSITE; PS50234; VWFA; 1.

DR Serine protease inhibitor; Repeat; Signal; Multigene family;

KW Gamma-carboxyglutamic acid; Glycoprotein.

KW SIGNAL 1 18

FT PROPEP 19 54

FT CHAIN 55 702

FT INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2.

FT PROPEP 703 946

FT DOMAIN 308 468

FT DISULFID 261 264

FT DISULFID 650 651

FT CARBOHYD 118 118

FT CARBOHYD 666 666

FT CARBOHYD 671 671

FT CARBOHYD 673 673

FT CARBOHYD 675 675

FT CARBOHYD 691 691

FT MOD\_RES 282 282

FT MOD\_RES 283 283

FT BINDING 702 702

FT CONFLICT 374 374

FT CONFLICT 674 674

FT CONFLICT 705 705

FT CONFLICT 729 729

FT CONFLICT 731 731

FT SEQUENCE 946 AA; 106436 MW; 1478CF3E8F3BA776 CRC64;

Query Match 36.6%; Score 53; DB 1; Length 946;

Best Local Similarity 33.3%; Pred. No. 5.4; Matches 9; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRLMSDEFEGSGKGLP 27

DB 212 DVWVIEPQGLRFLHVPDTFEGHFDGVP 238

RESULT 7

AROG.YEAST STANDARD; PRT; 370 AA.

AC P32449;

DT 01-OCT-1993 (Rel. 27, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited (EC 4.1.2.15) (Phospho-2-keto-3-deoxyheptonate aldolase) (DAHP synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase).

GN ARO4 OR YBR249C OR YBR1701.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

OX NCBI\_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=9225349; PubMed=1348717;

RA Kuenzler M.; Paravicini G.; Egli C.; Irrniger S.; Braus G.H.;

RT "Cloning, primary structure and regulation of the ARO4 gene, encoding the tyrosine-inhibited 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase from Saccharomyces cerevisiae.";

RL Gene 113:67-74(1992).

RN [2]

RP REVISIONS TO 205-207.

RA Kuenzler M.;

RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=S288c;

RX MEDLINE=94078675; PubMed=8256522;

RA Doignon F.; Biteau N.; Aigle M.; Crouzet M.;

RT "The complete sequence of a 6794 bp segment located on the right arm of chromosome II of Saccharomyces cerevisiae. Finding of a putative DUTPase in a yeast.";

RT of chromosome II of Saccharomyces cerevisiae.

RL Yeast 9:1131-1137(1993).

RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN=S288c;

RA Aljinovic G.; Pohl F.M.; Pohl T.M.;

RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: STEREOSPECIFIC CONDENSATION OF PHOSPHOENOLPYRUVATE (PEP) AND D-ERYTHROSE-4-PHOSPHATE (E4P) GIVING RISE TO 3-DEOXY-D-ARABINO-HEPTULOSONATE-7-PHOSPHATE (DAHP).

CC -!- CATALYTIC ACTIVITY: 2-dehydro-3-deoxy-D-arabino-heptonate 7-phosphate + phosphate = phosphoenolpyruvate + D-erythrose 4-phosphate + H(2)O.

CC -!- ENZYME REGULATION: INHIBITED BY TYROSINE.

CC -!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway; first step.

CC -!- INDUCTION: By amino acid starvation.

CC -!- SIMILARITY: BELONGS TO CLASS-I DAHP SYNTHETASE FAMILY.

CC -----

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CC -----

DR EMBL; X61107; CAA43419.1; -.

DR EMBL; L20296; AAA65607.1; -.

DR EMBL; Z36118; CAA85212.1; -.

DR PIR; S38185; S38185.

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DR HSSP; P00886; 1QR7.
DR SGD; S0000453; ARO4.
DR GO; GO:0003849; F:2-dehydro-3-deoxyphosphoheptonate aldolase . . . ; IDA.
DR InterPro; IPR006219; AroFGH.
DR InterPro; IPR006218; DAHP1/KDSA.
DR Pfam; PF00793; DAHP_synth_1; 1.
DR ProDom; PD005060; AroFGH; 1.
DR TIGRFAMS; TIGR00034; aroFGH; 1.
KW Aromatic amino acid biosynthesis; Lyase; Multigene family.
SQ SEQUENCE 370 AA; 39749 MW; 594ED48F24175979 CRC64;

Query Match 35.9%; Score 52; DB 1; Length 370;
Best Local Similarity 47.6%; Pred. No. 2.7;
Matches 10; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEPEG 21
DB 80 DLRAAQEYALRKLSDELKG 100

RESULT 8
AP3_ARATH STANDARD; PRT; 232 AA.
ID AP3_ARATH
AC P35632; Q39003; Q8LE79; Q9S7Q3; Q9SQ14; Q9SQ15; Q9SQ16; Q9SQ17;
AC Q9SQ18; Q9SQ19; Q9SQ20; Q9SQ21; Q9SQ22; Q9SX13;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Floral homeotic protein APETALA3.
GN AP3 OR AT3G54340 OR T12E18_30.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Petal;
RX MEDLINE=92154682; PubMed=1346756;
RA Jack T., Brockman L.B., Meyerowitz E.M.;
RT "The homeotic gene APETALA3 of Arabidopsis thaliana encodes a MADS
RT box and is expressed in petals and stamens.";
RL Cell 68:683-697(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Landsberg erecta;
RX MEDLINE=95036018; PubMed=7948893;
RA Okamoto H., Yano A., Shiraishi H., Okada K., Shimura Y.;
RT "Genetic complementation of a floral homeotic mutation, apetal3,
RT with an Arabidopsis thaliana gene homologous to DEFICIENS of
RT Antirrhinum majus.";
RL Plant Mol. Biol. 26:465-472(1994).
RN [3]
RP SEQUENCE FROM N.A.; AND VARIANTS.
RC STRAIN=cv. Bla-1, cv. Bretagny, cv. Bs-1, cv. Bu-0, cv. Bu-2,
RC cv. Chi-1, cv. Co-1, cv. Columbia, cv. Corsacalla-1, cv. Cvi-0,
RC cv. Gr-3, cv. J1-1, cv. Kas-1, cv. Kent, cv. Landsberg erecta,
RC cv. Li-3, cv. Li-8, and cv. Lisse;
RX MEDLINE=99126449; PubMed=9927474;
RA Purugganan M.D., Suddith J.I.;
RT "Molecular population genetics of floral homeotic loci: departures
RT from the equilibrium-neutral model at the APETALA3 and PISTILLATA
RT genes of Arabidopsis thaliana.";
RL Genetics 151:839-848(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansoorge W., Unseld M.,
RA Fartmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA De Simone V., Choisne N., Artiguenave F., Robert C., Brottier P.,
RA Wincker P., Cattoi L., Weissbach J., Saurin W., Quetier F.,

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RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Brfle H., Jordan N., Baugert S.,
RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordsiek G.,
RA Reichelt J., Scharfe M., Schoen O., Barges M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
RA de Haan M., Mearse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Monfort A., Argiridou A., Flores M., Liguori R., Vitale D.,
RA Manhaupt G., Haase D., Schoof H., Rued S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White C., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:820-822(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RT "Full-length cDNA from Arabidopsis thaliana.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
RT SSP consortium (Salk/Stanford/PGECL).";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE OF 36-128 FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=99311297; PubMed=10382288;
RA Brunel D., Froger N., Pelletier G.;
RT "Development of amplified consensus genetic markers (ACGM) in Brassica
RT napus from Arabidopsis thaliana sequences of known biological
RT function.";
RL Genome 42:387-402(1999).
RN [8]
RP FUNCTION.
RX PubMed=8565821;
RA Krizek B.A., Meyerowitz E.M.;
RT "The Arabidopsis homeotic genes APETALA3 and PISTILLATA are sufficient
RT to provide the B class organ identity function.";
RL Development 122:11-22(1996).
RN [9]
RP CHARACTERIZATION.
RX PubMed=8643482;
RA Riechmann J.L., Krizek B.A., Meyerowitz E.M.;
RT "Dimerization specificity of Arabidopsis MADS domain homeotic proteins
RT APETALA1, APETALA3, PISTILLATA, and AGAMOUS.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:4793-4798(1996).
RN [10]
RP GENETIC REGULATION.
RX PubMed=11283333;
RA Ng M., Yanofsky M.F.;
RT "Activation of the Arabidopsis B class homeotic genes by APETALA1.";
RL Plant Cell 13:739-753(2001).
RN [11]
RP CHARACTERIZATION.
RX PubMed=11206550;
RA Honma T., Goto K.;
RT "Complexes of MADS-box proteins are sufficient to convert leaves into
RT floral organs.";
RL Nature 409:525-529(2001).

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Matches 10; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 2 LWAAQRYGRELRRMSDEFECSF 23
   ||| :||| :||| :|||
Db 784 LWKARAEKKLRMLRFEFEAF 805

RESULT 10
MATK_LEDPA
ID MATK_LEDPA STANDARD; PRT; 506 AA.
AC O62992;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DE Maturase K (Intron maturase).
GN MATK.
OS Ledum palustre (Wild rosemary).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
OX NCBI_TaxID=75583;
RN [1]
RP SEQUENCE FROM N.A.
RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
RA Yukawa T.;
RT "Investigation of sectional relationships in the genus
RT Rhododendron (Ericaceae) based on matk sequences.";
RL Shokubutsu Kenkyu Zasshi 73:143-154(1998).
CC -!- FUNCTION: Probably assists in splicing chloroplast group II
CC introns (By similarity).
CC -!- SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK
CC SUBFAMILY.
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CC or send an email to license@isb-sib.ch).
DR EMBL; AB012751; BAA25872.1; -
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_maturase2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW mRNA processing; Chloroplast.
SQ SEQUENCE 506 AA; 60412 MW; CFEA926307DAC85E CRC64;

Query Match 34.1%; Score 49.5; DB 1; Length 506;
Best Local Similarity 36.7%; Pred. No. 9;
Matches 11; Conservative 5; Mismatches 7; Indels 7; Gaps 1;

QY 2 LWAA-----QRYGRELRRMSDEFECSF 24
   ||| :||| :||| :|||
Db 393 VWAAALSDSIIEFGRIYRLSHVYSGSLK 422

RESULT 11
MATK_RHOFR
ID MATK_RHOFR STANDARD; PRT; 506 AA.
AC O62984;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Maturase K (Intron maturase).
GN MATK.
OS Rhododendron ferrugineum (Alpenrose).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.

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OX NCBI_TaxID=49622;
RN [1]
RP SEQUENCE FROM N.A.
RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
RA Yukawa T.;
RT "Investigation of sectional relationships in the genus
RT Rhododendron (Ericaceae) based on matk sequences.";
RL Shokubutsu Kenkyu Zasshi 73:143-154(1998).
CC -!- FUNCTION: Probably assists in splicing chloroplast group II
CC introns (By similarity).
CC -!- SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK
CC SUBFAMILY.
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DR EMBL; AB012741; BAA25862.1; -
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_maturase2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW mRNA processing; Chloroplast.
SQ SEQUENCE 506 AA; 60534 MW; ADA44B25E92436E8 CRC64;

Query Match 34.1%; Score 49.5; DB 1; Length 506;
Best Local Similarity 36.7%; Pred. No. 9;
Matches 11; Conservative 5; Mismatches 7; Indels 7; Gaps 1;

QY 2 LWAA-----QRYGRELRRMSDEFECSF 24
   ||| :||| :||| :|||
Db 393 VWAAALSDSIIEFGRIYRLSHVYSGSLK 422

RESULT 12
MATK_RHOTS
ID MATK_RHOTS STANDARD; PRT; 506 AA.
AC O62991;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Maturase K (Intron maturase).
GN MATK.
OS Rhododendron tsusiophyllum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
OX NCBI_TaxID=49629;
RN [1]
RP SEQUENCE FROM N.A.
RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
RA Yukawa T.;
RT "Investigation of sectional relationships in the genus
RT Rhododendron (Ericaceae) based on matk sequences.";
RL Shokubutsu Kenkyu Zasshi 73:143-154(1998).
CC -!- FUNCTION: Probably assists in splicing chloroplast group II
CC introns (By similarity).
CC -!- SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK
CC SUBFAMILY.
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CC -----
DR EMBL; U38616; AAC45355.1; -
DR EMBL; D89754; BAA20414.1; -
DR EMBL; AE000174; AAC73808.1; -
DR EMBL; D90710; BAA35378.1; -
DR PIR; A64807; A64807.
DR PDB; 1K3W; 04-OCT-02.
DR RcoGene; EGI3237; nei.
DR InterPro; IPR000191; Fapy_DNA_glyco.
DR InterPro; IPR000214; Fapy_DNAGlyco_zn.
DR Pfam; PF01149; Fapy_DNA_glyco; 1.
DR ProDom; PD003680; Fapy_DNA_glyco; 1.
DR PROSITE; PS01242; FPG; 1.
KW DNA repair; Hydrolase; Glycosidase; Endonuclease; Zinc; Zinc-finger;
KW Complete proteome; 3D-structure.
FT INIT_MET 0 0
FT ZN_FING 237 260 POTENTIAL.
SQ SEQUENCE 262 AA; 29714 MW; 5010961768ADC265 CRC64;

Query Match 33.8%; Score 49; DB 1; Length 262;
Best Local Similarity 47.4%; Pred. No. 5.2;
Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 9 GRELRMSDEFEGSKGLP 27
| :|:| :| :|:|
Db 3 GPEIRRAADNLEAAIKGKP 21

RESULT 15
END8_SALTI
ID END8_SALTI STANDARD; PRT; 262 AA.
AC Q8Z8D2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Endonuclease VIII (EC 3.2.-.-).
GN NEI OR STY0771 OR T2148.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagers K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18.";
RL J. Bacteriol. 185:2330-2337(2003).
CC -!- FUNCTION: DNA N-GLYCOSYLASE WITH AN AP LYASE ACTIVITY. REQUIRED
CC FOR THE REPAIR OF OXIDATIVE DNA DAMAGE. CLEAVES THE DNA BACKBONE
CC BY BETA-DELTA ELIMINATION AS WELL AS 5'DEOXYRIBOSE PHOSPHATE (By
CC similarity).
CC -!- SIMILARITY: BELONGS TO THE FPG FAMILY.
CC -----
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CC -----
DR EMBL; AL627268; CAD05190.1; -
DR EMBL; AE016841; AAO69762.1; -
DR InterPro; IPR000191; Fapy_DNA_glyco.
DR InterPro; IPR000214; Fapy_DNAGlyco_zn.
DR Pfam; PF01149; Fapy_DNA_glyco; 1.
DR ProDom; PD003680; Fapy_DNA_glyco; 1.
DR PROSITE; PS01242; FPG; 1.
KW DNA repair; Hydrolase; Glycosidase; Endonuclease; Zinc; Zinc-finger;
KW Complete proteome.
FT INIT_MET 0 0 BY SIMILARITY.
FT ZN_FING 237 260 POTENTIAL.
SQ SEQUENCE 262 AA; 29734 MW; 4E255C0CCF59A6A3 CRC64;

Query Match 33.8%; Score 49; DB 1; Length 262;
Best Local Similarity 47.4%; Pred. No. 5.2;
Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 9 GRELRMSDEFEGSKGLP 27
| :|:| :| :|:|
Db 3 GPEIRRAADNLEAAIKGKP 21

Search completed: September 15, 2003, 17:22:59
Job time : 6.36429 secs

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GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: September 15, 2003, 17:17:31 ; Search time 29.3143 Seconds  
(without alignments)  
237.680 Million cell updates/sec

Title: US-09-544-664-3  
Perfect score: 145  
Sequence: 1 NLWAAQRYGRELRRMSDEFGSKGLP 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	87	60.0	146	Q9I9N2	Q9I9N2 brachydanio
2	60	41.4	946	11 Q8K016	Q8K016 mus musculus
3	53	36.6	196	16 Q8VJS3	Q8VJS3 mycobacteri
4	53	36.6	223	16 Q10843	Q10843 mycobacteri
5	52	35.9	471	17 Q8ZY71	Q8ZY71 pyrobaculum
6	52	35.9	946	6 Q9GLY6	Q9GLY6 oryctolagus
7	51	35.2	231	10 Q8SEG0	Q8SEG0 arabidopsis
8	51	35.2	232	10 Q9SQ20	Q9SQ20 arabidopsis
9	51	35.2	232	10 Q9SQ22	Q9SQ22 arabidopsis
10	51	35.2	232	10 Q9SQ17	Q9SQ17 arabidopsis
11	51	35.2	232	10 Q9SQ19	Q9SQ19 arabidopsis
12	51	35.2	232	10 Q9SQ21	Q9SQ21 arabidopsis
13	51	35.2	232	10 Q8LB79	Q8LB79 arabidopsis
14	51	35.2	232	10 Q9SQ16	Q9SQ16 arabidopsis
15	51	35.2	232	10 Q9SQ15	Q9SQ15 arabidopsis
16	51	35.2	232	10 Q9S7Q3	Q9S7Q3 arabidopsis

17	51	35.2	232	10 Q9SQ18	Q9SQ18 arabidopsis
18	50.5	34.8	904	2 Q9KGW3	Q9KGW3 pseudomonas
19	50.5	34.8	909	16 Q8EI34	Q8EI34 shewanella
20	50.5	34.8	990	10 Q9C793	Q9C793 arabidopsis
21	50	34.5	168	11 Q8K316	Q8K316 mus musculus
22	50	34.5	283	15 Q37056	Q37056 chimpanzee
23	50	34.5	374	17 Q9HN29	Q9HN29 halobacteri
24	50	34.5	516	10 Q9SSP5	Q9SSP5 arabidopsis
25	50	34.5	851	11 Q8K2H3	Q8K2H3 mus musculus
26	49.5	34.1	153	5 Q9UB33	Q9UB33 anopheles g
27	49.5	34.1	401	5 Q97407	Q97407 anopheles g
28	49.5	34.1	505	8 Q47148	Q47148 menziesia c
29	49.5	34.1	506	8 Q47149	Q47149 rhododendro
30	49.5	34.1	506	8 Q47171	Q47171 rhododendro
31	49.5	34.1	506	8 Q63960	Q63960 rhododendro
32	49.5	34.1	506	8 Q62982	Q62982 rhododendro
33	49.5	34.1	506	8 Q62975	Q62975 rhododendro
34	49.5	34.1	506	8 Q62972	Q62972 rhododendro
35	49.5	34.1	506	8 Q62989	Q62989 rhododendro
36	49.5	34.1	506	8 Q62978	Q62978 rhododendro
37	49.5	34.1	506	8 Q47155	Q47155 rhododendro
38	49.5	34.1	506	8 Q47152	Q47152 rhododendro
39	49.5	34.1	506	8 Q47173	Q47173 rhododendro
40	49.5	34.1	506	8 Q62990	Q62990 rhododendro
41	49.5	34.1	506	8 Q62974	Q62974 rhododendro
42	49.5	34.1	506	8 Q62993	Q62993 menziesia m
43	49.5	34.1	506	8 Q47170	Q47170 rhododendro
44	49.5	34.1	506	8 Q47174	Q47174 rhododendro
45	49.5	34.1	506	8 Q62983	Q62983 rhododendro

ALIGNMENTS

RESULT 1

Q9I9N2 PRELIMINARY; PRT; 146 AA.  
ID Q9I9N2  
AC Q9I9N2;  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)  
DE Bad.  
GN BAD.  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20373792; PubMed=10917738;  
RA Inohara N., Nunez G.;  
RT "Genes with homology to mammalian apoptosis regulators identified in zebrafish."  
RL Cell Death Differ. 7:509-510(2000).  
DR EMBL; AF231017; AAF6962.2; -.  
DR HSSP; Q92934; 1G5J.  
DR ZFIN; ZDB-GENE-000616-1; bad.  
SQ SEQUENCE 146 AA; 16546 MW; 28A5650BBS107ECB CRC64;

Query Match 50.0%; Score 87; DB 13; Length 146;  
Best Local Similarity 55.2%; Pred. No. 6.7e-05;  
Matches 15; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 LWAAQRYGRELRRMSDEFGSKF 24  
|||||:|||||:  
Db 89 LWAAQYGGQLRRMSDEFGKMK 111

RESULT 2

Q8K016 PRELIMINARY; PRT; 946 AA.  
ID Q8K016  
AC Q8K016;

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Query Match          36.6%; Score 53; DB 16; Length 223;
Best Local Similarity 58.8%; Pred. No. 11;
Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0

QY      1 NLWAAQRYGREL RMSD 17
      ||||| || | : |
DB      165 NLWAADRYNRAIGHED 181

RESULT 5
ID      Q8ZY71      PRELIMINARY;      PRT;      471 AA.
AC      Q8ZY71;
DT      01-MAR-2002 (TRENBLrel. 20, Created)
DT      01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT      01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE      Hypothetical protein PAE0922.
GN      PAE0922.
OS      Pyrobaculum aerophilum.
OC      Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC      Thermoproteaceae; Pyrobaculum.
ON      NCBI_TaxID=13773;
RX      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX      PubMed=11792869;
RA      Fitz-gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA      Miller J.H.;
RT      "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT      aerophilum";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR      EMBL; AA009783; AAL63125.1; -.
DR      InterPro; IPR006638; E1p3.
DR      InterPro; IPR000182; GCM5acetyltransf.
DR      Pfam; PF00583; Acetyltransf. 1.
DR      SMART; SM00729; E1p3; 1.
DR      Hypothetical protein; Complete proteome.
SQ      SEQUENCE 471 AA; 52952 MW; 3B1E36E8AE2EFOA CRC64;
KW

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DR EMBL; AF143380; AAF25590.1; -,  
DR HSSP; P11746; 1MNM.  
DR InterPro; IPR002487; TF\_Kbox.  
DR InterPro; IPR002100; TF\_MADSbox.  
DR Pfam; PF01486; K-box; 1.

```

QY      6 QRYG-----RELRLMSDEFGSK 24
      |||      :|||: || :||
DB      107 QRLGCLDELDIQLRLLEDEMENTFK 133

RESULT 9
Q9SQ22
ID      Q9SQ22      PRELIMINARY;      PRT;      232 AA.
AC      Q9SQ22;
DT      01-MAY-2000 (TREMBLrel. 13, Created)
DT      01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT      01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE      Floral homeotic protein AP3.

```

```

GN APTALA3.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Li-8;
RX MEDLINE=99126449; PubMed=9927474;
RA Purugganan M.D., Suddith J.I.;
RT "Molecular population genetics of floral homeotic loci. Departures
RT from the equilibrium-neutral model at the APTALA3 and PISTILLATA
RT genes of Arabidopsis thaliana.";
RL Genetics 151:839-848(1999).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
DR EMBL; AF115801; AAD51890.1; -.
DR HSSP; P11746; 1NMN.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00432; MADS; 1.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SQ SEQUENCE 232 AA; 27267 MW; 42A852D697E22A65 CRC64;

Query Match 35.2%; Score 51; DB 10; Length 232;
Best Local Similarity 44.4%; Pred. No. 22;
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;

QY 6 QRYG-----RELRRMSDEFECSFK 24
||| :|||: ||| :||
Db 107 QRLGCLDELDIQELRLEDEMENTFK 133

RESULT 10
Q9SQ17 ID Q9SQ17 PRELIMINARY; PRT; 232 AA.
AC Q9SQ17;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Floral homeotic protein AP3.
GN APTALA3.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Lisse;
RX MEDLINE=99126449; PubMed=9927474;
RA Purugganan M.D., Suddith J.I.;
RT "Molecular population genetics of floral homeotic loci. Departures
RT from the equilibrium-neutral model at the APTALA3 and PISTILLATA
RT genes of Arabidopsis thaliana.";
RL Genetics 151:839-848(1999).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
DR EMBL; AF115809; AAD51896.1; -.
DR HSSP; P11746; 1NMN.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Lisse;
RX MEDLINE=99126449; PubMed=9927474;
RA Purugganan M.D., Suddith J.I.;
RT "Molecular population genetics of floral homeotic loci. Departures
RT from the equilibrium-neutral model at the APTALA3 and PISTILLATA
RT genes of Arabidopsis thaliana.";
RL Genetics 151:839-848(1999).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
DR EMBL; AF115809; AAD51896.1; -.
DR HSSP; P11746; 1NMN.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.

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DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SQ SEQUENCE 232 AA; 27284 MW; 04FCFC5B73C7729 CRC64;

Query Match 35.2%; Score 51; DB 10; Length 232;
Best Local Similarity 44.4%; Pred. No. 22;
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;

QY 6 QRYG-----RELRRMSDEFECSFK 24
||| :|||: ||| :||
Db 107 QRLGCLDELDIQELRLEDEMENTFK 133

RESULT 11
Q9SQ19 ID Q9SQ19 PRELIMINARY; PRT; 232 AA.
AC Q9SQ19;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Floral homeotic protein AP3.
GN APTALA3.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Bretagny;
RX MEDLINE=99126449; PubMed=9927474;
RA Purugganan M.D., Suddith J.I.;
RT "Molecular population genetics of floral homeotic loci. Departures
RT from the equilibrium-neutral model at the APTALA3 and PISTILLATA
RT genes of Arabidopsis thaliana.";
RL Genetics 151:839-848(1999).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
DR EMBL; AF115807; AAD51896.1; -.
DR HSSP; P11746; 1NMN.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SQ SEQUENCE 232 AA; 27311 MW; 71AE593FB8A67EC3 CRC64;

Query Match 35.2%; Score 51; DB 10; Length 232;
Best Local Similarity 44.4%; Pred. No. 22;
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;

QY 6 QRYG-----RELRRMSDEFECSFK 24
||| :|||: ||| :||
Db 107 QRLGCLDELDIQELRLEDEMENTFK 133

RESULT 12
Q9SQ21 ID Q9SQ21 PRELIMINARY; PRT; 232 AA.
AC Q9SQ21;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Floral homeotic protein AP3.
GN APTALA3.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Kent;
RX MEDLINE=99126449; PubMed=9927474;
RA Purugganan M.D., Suddith J.I.;
RT "Molecular population genetics of floral homeotic loci. Departures
RT from the equilibrium-neutral model at the APETALA3 and PISTILLATA
RT genes of Arabidopsis thaliana.";
RL Genetics 151:839-848(1999).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
DR EMBL; AF115805; AAD51894.1; -.
DR HSP; P11746; 1MNM.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS0066; MADS_BOX_2; 1.
DR DNA-binding; Nuclear protein; Transcription; Transcription regulation.
KW eurosids II; Brassicales; Brassicaceae; Arabidopsis.
SQ SEQUENCE 232 AA; 27286 MW; 66976305B88B63E3 CRC64;

Query Match 35.2%; Score 51; DB 10; Length 232;
Best Local Similarity 44.4%; Pred. No. 22;
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;

QY 6 QRYG-----RELRRMSDEFGSEK 24
||| :|||: ||| :||
Db 107 QRLGECLELDIQELRLREDEMENTFK 133

RESULT 13
Q8LB79
ID Q8LB79 PRELIMINARY; PRT; 232 AA.
AC Q8LB79;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-WAR-2003 (TREMELrel. 23, Last annotation update)
DE Floral homeotic protein APETALA3 (AP3).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Haas B.J., Volfovsky N., Town C.D., Troupkan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation.";
RL Genome Biol. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Brover V., Troupkan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RT "Full-length cDNA from Arabidopsis thaliana.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
DR EMBL; AY087369; AAM64919.1; -.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.

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DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS0066; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SQ SEQUENCE 232 AA; 27339 MW; CC90703F959CFAD5 CRC64;

Query Match 35.2%; Score 51; DB 10; Length 232;
Best Local Similarity 44.4%; Pred. No. 22;
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;

QY 6 QRYG-----RELRRMSDEFGSEK 24
||| :|||: ||| :||
Db 107 QRLGECLELDIQELRLREDEMENTFK 133

RESULT 14
Q9SQ16
ID Q9SQ16 PRELIMINARY; PRT; 232 AA.
AC Q9SQ16;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
DE Floral homeotic protein AP3.
GN APETALA3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Lisse;
RX MEDLINE=99126449; PubMed=9927474;
RA Purugganan M.D., Suddith J.I.;
RT "Molecular population genetics of floral homeotic loci. Departures
RT from the equilibrium-neutral model at the APETALA3 and PISTILLATA
RT genes of Arabidopsis thaliana.";
RL Genetics 151:839-848(1999).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
DR EMBL; AF115810; AAD51899.1; -.
DR HSP; P11746; 1MNM.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS0066; MADS_BOX_2; 1.
DR DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SQ SEQUENCE 232 AA; 27314 MW; DB8CALFC835557D6 CRC64;

Query Match 35.2%; Score 51; DB 10; Length 232;
Best Local Similarity 44.4%; Pred. No. 22;
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;

QY 6 QRYG-----RELRRMSDEFGSEK 24
||| :|||: ||| :||
Db 107 QRLGECLELDIQELRLREDEMENTFK 133

RESULT 15
Q9SQ15
ID Q9SQ15 PRELIMINARY; PRT; 232 AA.
AC Q9SQ15;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
DE Floral homeotic protein AP3.
GN APETALA3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Kas-1;  
RX MEDLINE=99126449; PubMed=9927474;  
RA Purugganan M.D.; Suddith J.I.;  
RT "Molecular population genetics of floral homeotic loci. Departures  
RT from the equilibrium-neutral model at the APETALA3 and PISTILLATA  
RT genes of Arabidopsis thaliana."; |  
RL Genetics 151:839-848(1999).  
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION  
CC FACTORS.  
DR EMBL; AF115812; AAD51901.1; -.  
DR HSSP; P11746; 1MNM.  
DR InterPro; IPR002487; TF\_Kbox.  
DR InterPro; IPR002100; TF\_MADSbox.  
DR Pfam; PF01486; K-box; 1.  
DR Pfam; PF00319; SRF-TF; 1.  
DR PRINTS; PR00404; MADSDOMAIN.  
DR SMART; SM00432; MADS; 1.  
DR PROSITE; PS00350; MADS\_BOX\_1; 1.  
DR PROSITE; PS50066; MADS\_BOX\_2; 1.  
KW DNA-binding; Nuclear protein; Transcription; Transcription regulation.  
SQ SEQUENCE 232 AA; 27300 MW; 5CA05FD44F824DF0 CRC64;  
  
Query Match 35.2%; Score 51; DB 10; Length 232;  
Best Local Similarity 44.4%; Pred. No. 22;  
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;  
  
QY 6 QRYG-----RELRLMSDEFGSFK 24  
Db 107 QRVGCLDELDIQELRLLEDEMENTFK 133  
  
Search completed: September 15, 2003, 17:25:46  
Job time : 30.3143 secs



XX New peptide conjugates for modulating apoptosis or for inhibiting B  
PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for  
PT treating neurodegenerative disorders, stroke, or cancer -  
XX  
PS Claim 18; Page 19; 74pp; English.  
XX  
CC The invention relates to a peptide conjugate having the formula:  
CC (R-X)n-peptide where n = 1-10; X = C=O, when the R-X group is attached  
CC to the N-terminus of the peptide, or a side chain of the peptide where  
CC the functional group of the side chain is NH2 or OH; or X = O or NH,  
CC when the R-X group is attached to the C-terminus of the peptide, or a  
CC side chain of the peptide, where the side chain functional group is COOH  
CC or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl optionally  
CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally  
CC monosubstituted with a 1-5C straight or branched chain alkyl group,  
CC phenyl optionally monosubstituted with a 1-5C straight or branched chain  
CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples  
CC of the peptide portion of the conjugate. The peptides represent analogues  
CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of  
CC the BH3 domain of the cell death agonist Bad. The peptide conjugate is  
CC useful for modulating apoptosis in the cells of a subject, or for  
CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of  
CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2  
CC function. In particular, the peptide conjugate is useful for treating a  
CC subject afflicted with a cancer characterized by cancer cells that  
CC express Bcl-2. The cancer includes prostate, colorectal, gastric,  
CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or  
CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide  
CC conjugate is also useful for treating disorders characterized by  
CC increased apoptosis, e.g. neurodegenerative disorders, acquired  
CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.  
XX  
SQ Sequence 28 AA;  
Query Match 100.0%; Score 148; DB 21; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.4e-15;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KNLWAAQRYGRELRRMSDEFGSGFKGLK 28  
Db 1 KNLWAAQRYGRELRRMSDEFGSGFKGLK 28  
RESULT 2  
AAB37056  
ID AAB37056 standard; peptide; 27 AA.  
AC AAB37056;  
XX  
XX 28-FEB-2001 (first entry)  
DT  
XX Bcl2 polypeptide BH3 domain peptide #56.  
DE  
XX Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;  
KW cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;  
KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;  
KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;  
KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;  
KW stroke; myocardial infarction.  
XX  
OS Homo sapiens.  
XX WO200059526-A1.  
PN  
XX 12-OCT-2000.  
PD  
XX 06-APR-2000; 2000WO-US09352.  
PF  
XX 07-APR-1999; 99US-0128202.  
PR  
XX (UIJE-) UNIV JEFFERSON THOMAS.  
PA  
XX

PI Huang Z, Wang J, Zhang Z, Shan S, Lu Z;  
XX WPI; 2000-679325/66.  
XX  
PT New peptide conjugates for modulating apoptosis or for inhibiting B  
PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for  
PT treating neurodegenerative disorders, stroke, or cancer -  
XX  
PS Claim 18; Page 19; 74pp; English.  
XX  
CC The invention relates to a peptide conjugate having the formula:  
CC (R-X)n-peptide where n = 1-10; X = C=O, when the R-X group is attached  
CC to the N-terminus of the peptide, or a side chain of the peptide where  
CC the functional group of the side chain is NH2 or OH; or X = O or NH,  
CC when the R-X group is attached to the C-terminus of the peptide, or a  
CC side chain of the peptide, where the side chain functional group is COOH  
CC or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl optionally  
CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally  
CC monosubstituted with a 1-5C straight or branched chain alkyl group,  
CC phenyl optionally monosubstituted with a 1-5C straight or branched chain  
CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples  
CC of the peptide portion of the conjugate. The peptides represent analogues  
CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of  
CC the BH3 domain of the cell death agonist Bad. The peptide conjugate is  
CC useful for modulating apoptosis in the cells of a subject, or for  
CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of  
CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2  
CC function. In particular, the peptide conjugate is useful for treating a  
CC subject afflicted with a cancer characterized by cancer cells that  
CC express Bcl-2. The cancer includes prostate, colorectal, gastric,  
CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or  
CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide  
CC conjugate is also useful for treating disorders characterized by  
CC increased apoptosis, e.g. neurodegenerative disorders, acquired  
CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.  
XX  
SQ Sequence 27 AA;  
Query Match 96.6%; Score 143; DB 21; Length 27;  
Best Local Similarity 100.0%; Pred. No. 8.1e-15;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KNLWAAQRYGRELRRMSDEFGSGFKGL 27  
Db 1 KNLWAAQRYGRELRRMSDEFGSGFKGL 27  
RESULT 3  
AAB37001  
ID AAB37001 standard; peptide; 26 AA.  
AC AAB37001;  
XX  
XX 28-FEB-2001 (first entry)  
DT  
XX Bcl2 polypeptide BH3 domain peptide #1.  
DE  
XX Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;  
KW cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;  
KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;  
KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;  
KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;  
KW stroke; myocardial infarction.  
XX  
OS Homo sapiens.  
XX WO200059526-A1.  
PN  
XX 12-OCT-2000.  
PD  
XX 06-APR-2000; 2000WO-US09352.  
PF  
XX 07-APR-1999; 99US-0128202.  
PR

XX PA (UYJE-) UNIV JEFFERSON THOMAS.  
XX PI Huang Z, Wang J, Zhang Z, Shan S, Lu Z;  
XX PI WPI; 2000-679325/66.  
XX DR New peptide conjugates for modulating apoptosis or for inhibiting B  
XX PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for  
XX PT treating neurodegenerative disorders, stroke, or cancer -  
XX PS Claim 18; Page 17; 74pp; English.  
XX SS The invention relates to a peptide conjugate having the formula:  
CC (R-X)n-peptide where n = 1-10; X = C=O, when the R-X group is attached  
CC to the N-terminus of the peptide, or a side chain of the peptide where  
CC the functional group of the side chain is NH2 or OH; or X = O or NH,  
CC when the R-X group is attached to the C-terminus of the peptide, or a  
CC side chain of the peptide, where the side chain functional group is COOH  
CC or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one  
CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally  
CC monosubstituted with a 1-5C straight or branched chain alkyl group,  
CC phenyl optionally monosubstituted with a 1-5C straight or branched chain  
CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples  
CC of the peptide portion of the conjugate. The peptides represent analogues  
CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of  
CC the BH3 domain of the cell death agonist Bad. The peptide conjugate is  
CC useful for modulating apoptosis in the cells of a subject, or for  
CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of  
CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2  
CC function. In particular, the peptide conjugate is useful for treating a  
CC subject afflicted with a cancer characterized by cancer cells that  
CC express Bcl-2. The cancer includes prostate, colorectal, gastric,  
CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or  
CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide  
CC conjugate is also useful for treating disorders characterized by  
CC increased apoptosis, e.g. neurodegenerative disorders, acquired  
CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.  
XX SS Sequence 26 AA;  
SQ Query Match 93.2%; Score 138; DB 21; Length 26;  
Best Local Similarity 100.0%; Pred. No. 4.6e-14;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 NLWAAQRYGRELRRMSDEFEGSFKGL 27  
Db 1 NLWAAQRYGRELRRMSDEFEGSFKGL 26  
RESULT 4  
AAB37002  
ID AAB37002 standard; peptide; 26 AA.  
XX AC AAB37002;  
XX DT 28-FEB-2001 (first entry)  
XX DE Bcl2 polypeptide BH3 domain peptide #2.  
XX KW Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;  
KW cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;  
KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;  
KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;  
KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;  
KW stroke; myocardial infarction.  
XX OS Homo sapiens.  
XX PN W0200059526-A1.  
XX PD 12-OCT-2000.  
XX

PF 06-APR-2000; 2000WO-US09352.  
XX 07-APR-1999; 99US-0128202.  
XX PA (UYJE-) UNIV JEFFERSON THOMAS.  
XX PI Huang Z, Wang J, Zhang Z, Shan S, Lu Z;  
XX PI WPI; 2000-679325/66.  
XX DR New peptide conjugates for modulating apoptosis or for inhibiting B  
XX PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for  
XX PT treating neurodegenerative disorders, stroke, or cancer -  
XX PS Claim 18; Page 17; 74pp; English.  
XX SS The invention relates to a peptide conjugate having the formula:  
CC (R-X)n-peptide where n = 1-10; X = C=O, when the R-X group is attached  
CC to the N-terminus of the peptide, or a side chain of the peptide where  
CC the functional group of the side chain is NH2 or OH; or X = O or NH,  
CC when the R-X group is attached to the C-terminus of the peptide, or a  
CC side chain of the peptide, where the side chain functional group is COOH  
CC or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one  
CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally  
CC monosubstituted with a 1-5C straight or branched chain alkyl group,  
CC phenyl optionally monosubstituted with a 1-5C straight or branched chain  
CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples  
CC of the peptide portion of the conjugate. The peptides represent analogues  
CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of  
CC the BH3 domain of the cell death agonist Bad. The peptide conjugate is  
CC useful for modulating apoptosis in the cells of a subject, or for  
CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of  
CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2  
CC function. In particular, the peptide conjugate is useful for treating a  
CC subject afflicted with a cancer characterized by cancer cells that  
CC express Bcl-2. The cancer includes prostate, colorectal, gastric,  
CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or  
CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide  
CC conjugate is also useful for treating disorders characterized by  
CC increased apoptosis, e.g. neurodegenerative disorders, acquired  
CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.  
XX SS Sequence 26 AA;  
SQ Query Match 93.2%; Score 138; DB 21; Length 26;  
Best Local Similarity 100.0%; Pred. No. 4.6e-14;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 NLWAAQRYGRELRRMSDEFEGSFKGL 27  
Db 1 NLWAAQRYGRELRRMSDEFEGSFKGL 26  
RESULT 5  
AAB37003  
ID AAB37003 standard; peptide; 27 AA.  
XX AC AAB37003;  
XX DT 28-FEB-2001 (first entry)  
XX DE Bcl2 polypeptide BH3 domain peptide #3.  
XX KW Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;  
KW cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;  
KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;  
KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;  
KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;  
KW stroke; myocardial infarction.  
XX OS Homo sapiens.  
XX PN W0200059526-A1.  
PN

XX PD 12-OCT-2000.  
 XX PF 06-APR-2000; 2000WO-US09352.  
 XX PR 07-APR-1999; 99US-0128202.  
 XX PA (UYJE-) UNIV JEFFERSON THOMAS.  
 XX PI Huang Z, Wang J, Zhang Z, Shan S, Lu Z;  
 XX WI; 2000-679325/66.  
 XX DR  
 XX PT New peptide conjugates for modulating apoptosis or for inhibiting B  
 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for  
 PT treating neurodegenerative disorders, stroke, or cancer -  
 XX PS Claim 18: Page 17; 74pp; English.  
 XX CC The invention relates to a peptide conjugate having the formula:  
 CC (R-X)<sub>n</sub>-peptide where n = 1-10; X = C=O, when the R-X group is attached  
 CC to the N-terminus of the peptide, or a side chain of the peptide where  
 CC the functional group of the side chain is NH<sub>2</sub> or OH; or X = O or NH,  
 CC when the R-X group is attached to the C-terminus of the peptide, or a  
 CC side chain of the peptide, where the side chain functional group is COOH  
 CC or CONH<sub>2</sub>; and R = 2-18C alkyl or alkoxy, 2-14C alkylene containing one  
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally  
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,  
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain  
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples  
 CC of the peptide portion of the conjugate. The peptides represent analogues  
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of  
 CC the BH3 domain of the cell death agonist Bad. The peptide conjugate is  
 CC useful for modulating apoptosis in the cells of a subject, or for  
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of  
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2  
 CC function. In particular, the peptide conjugate is useful for treating a  
 CC subject afflicted with a cancer characterized by cancer cells that  
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,  
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or  
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide  
 CC conjugate is also useful for treating disorders characterized by  
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired  
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.  
 XX SQ Sequence 27 AA;  
 Query Match 93.2%; Score 138; DB 21; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-14;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 NLWAAQRYGRELRRMSDEFGSFKGL 27  
 |||||  
 Db 1 NLWAAQRYGRELRRMSDEFGSFKGL 26  
 RESULT 6  
 AAB70370  
 ID AAB70370 standard; protein; 162 AA. 1  
 XX AC AAB70370;  
 XX DT 02-MAY-2001 (first entry)  
 XX DE Shorter murine BAD mutant amino acid sequence SEQ ID NO:3.  
 XX KW Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;  
 KW immunostimulant; neuroprotective; nootropic; antiischaemic; vulnary;  
 KW cytosolic; antiviral; antiarthritic; antiinflammatory; wound healing;  
 KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;  
 KW immunodeficiency disease; neurodegenerative disease; viral infection;  
 KW ischaemic cell death; reperfusion cell death; arthritis; infertility;  
 KW lymphoproliferative condition; inflammation; autoimmune disease.

XX OS Mus musculus.  
 OS Synthetic.  
 XX PN WO200110888-A1.  
 XX PD 15-FEB-2001.  
 XX PF 30-MAY-2000; 2000WO-US11864.  
 XX PR 28-MAY-1999; 99US-0136783.  
 XX PA (APOP-) APOPTOSIS TECHNOLOGY INC.  
 XX PI Zhou X;  
 XX WI; 2001-138734/14.  
 XX PT New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,  
 PT useful for screening for candidate compounds which induce or inhibit  
 PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or  
 PT Ser113 -  
 XX PS Claim 7; Page 148-149; 157pp; English.  
 XX CC The present invention describes an isolated or synthetic polypeptide  
 CC (I) comprising a less than full length amino acid sequence of a mutant  
 CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its  
 CC fragment, which contains amino acid substitutions at Ser118 of a human  
 CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine  
 CC BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,  
 CC nootropic, antiischaemic, vulnary, and immunosuppressive activities, and  
 CC antiarthritic, antiinflammatory and immunosuppressive activities, and  
 CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and  
 CC polynucleotides can be used for screening candidate compounds and drugs  
 CC for activity that promote cell survival or apoptosis. Other uses include  
 CC inducing or inhibiting apoptosis in a cell. Candidate compounds  
 CC identified and (mutant) BAD polypeptides are useful in treating  
 CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell  
 CC death, reperfusion cell death, wound healing, cancer, viral infections,  
 CC lymphoproliferative conditions, arthritis, infertility, inflammation and  
 CC autoimmune diseases. The present sequence represents a specifically  
 CC claimed shorter murine BAD mutant amino acid sequence from the present  
 CC invention.  
 XX SQ Sequence 162 AA;  
 Query Match 93.2%; Score 138; DB 22; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-13;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 NLWAAQRYGRELRRMSDEFGSFKGL 27  
 |||||  
 Db 98 NLWAAQRYGRELRRMSDEFGSFKGL 123  
 RESULT 7  
 AAR95168  
 ID AAR95168 standard; Protein; 204 AA.  
 XX AC AAR95168;  
 XX DT 06-JAN-1997 (first entry)  
 XX DE bcl-x(L)/bcl-2 associated death promoter protein.  
 XX KW Epitope; murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke;  
 KW polypeptide; bcl-x; cell death; regulate; BH1; BH2; apoptotic cell death;  
 KW cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS;  
 KW neurodegenerative disease; senescence; ischaemia; neoplasia.  
 XX OS Mus musculus.  
 XX SQ

FH Key Location/Qualifiers  
 FT Region 147..149  
 FT /note= "BH1 conserved amino acids"  
 FT Region 191..192  
 FT /note= "BH2 conserved amino acids"  
 FT Domain 38..61  
 FT /note= "PEST sequence"  
 FT Domain 111..130  
 FT /note= "PEST sequence"  
 FT  
 FT  
 PN W09613614-A1.  
 XX  
 XX 09-MAY-1996.  
 XX  
 PF 31-OCT-1995; 95WO-US14246.  
 XX  
 PR 31-OCT-1994; 94US-0333565.  
 XX  
 PA (UNIW ) UNIV WASHINGTON.  
 XX  
 PI Korsmeyer SJ;  
 XX  
 DR WPI; 1996-251465/25.  
 DR N-PSDB; AAT29479.  
 XX  
 XX Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter -  
 PT useful to treat neoplasia and apoptosis and to identify agents  
 PT inhibiting its binding to bcl-2 or bcl-x(L) to form heteromultimers  
 XX  
 PS Claim 3; Fig 1; 130pp; English.  
 XX  
 CC This sequence represents the murine bcl-x(L)/bcl-2 associated death  
 CC promoter (Bad) gene. Bad is a 22.1 kD protein which interacts with  
 CC bcl-2 and bcl-x proteins and regulates cell death. It has homology  
 CC to the bcl-2-related family clustered in the BH1 and BH2 domain. Bad  
 CC has been found to hybridise to bcl-x(L) and bcl-2 in yeast two-hybrid  
 CC assays and in vivo in mammalian cells. Overexpressed Bad counters the  
 CC death inhibitory activity of bcl-x(L), but is much less effective at  
 CC counteracting the death inhibitory activity of bcl-2. Bad expression can  
 CC accelerate apoptotic cell death induced by cytokine deprivation in an  
 CC IL-3 dependent cell line expressing bcl-x(L), and its also counters the  
 CC death repressor activity of bcl-x(L). Bad competes with Bax for binding  
 CC to bcl-x(L). Bad may be used to identify agents which inhibit its  
 CC binding to bcl-2 or bcl-x(L) to form heterodimers. Such agents may be  
 CC used to treat neurodegenerative diseases, immunodeficiency diseases,  
 CC e.g. AIDS, senescence or ischaemia.  
 XX  
 SQ Sequence 204 AA;  
 Query Match 93.2%; Score 138; DB 17; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-13;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 NLWAAQRYGRELRRMSDEFGSFKGL 27  
 |||||  
 Db 140 NLWAAQRYGRELRRMSDEFGSFKGL 165  
 RESULT 8  
 AAW61315  
 ID AAW61315 standard; Protein; 204 AA.  
 XX  
 AC AAW61315;  
 XX  
 XX 07-OCT-1998 (first entry)  
 DT  
 XX Murine BCL-XL/BCL-2 associated cell death regulator.  
 DE  
 XX Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;  
 KW serine substituted mutant; apoptosis; cancer; viral infection.  
 XX  
 OS Mus sp.  
 XX  
 PN W09613614-A1.

PN W09817682-A1.  
 XX  
 XX 30-APR-1998.  
 PD  
 XX  
 PF 17-OCT-1997; 97WO-US19175.  
 XX  
 XX 18-OCT-1996; 96US-0733505.  
 PR  
 XX (UNIW ) UNIV WASHINGTON.  
 PA  
 XX  
 PI Korsmeyer SJ;  
 XX  
 DR WPI; 1998-261422/23.  
 DR N-PSDB; AAV27833.  
 XX  
 XX New mutant BAD polypeptide with phosphorylatable serine replaced -  
 PT useful for, e.g. treating reduced apoptosis such as in cancer or  
 PT viral infection  
 XX  
 PS Claim 1; Fig 10; 95pp; English.  
 XX  
 CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell  
 CC death regulator) proteins, having an amino acid other than Ser at  
 CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The  
 CC present sequence is the murine BAD protein. Also described are: (1)  
 CC fragments of mutant BAD protein able to decrease cell viability; (2)  
 CC fusion proteins of mutant BAD with a heterologous polypeptide that  
 CC increases intracellular delivery. Mutant BAD proteins are used to treat  
 CC or prevent diseases associated with reduced apoptosis, e.g. cancer,  
 CC viral infection, lymphoproliferation, arthritis, infertility,  
 CC inflammation and autoimmune disease. Polynucleotide sequences encoding  
 CC mutant BAD proteins can be used similarly by gene therapy or to produce  
 CC transgenic animals for use as disease models or in drug screening. BAD  
 CC proteins phosphorylated at specified Ser are used to screen for enhancers  
 CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful  
 CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,  
 CC aging or ischaemic cell death. The apoptotic status of cells is  
 CC determined by measuring relative amounts of phosphorylated and non-  
 CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have  
 CC greater death-promoting activity than wild-type BAD which can become  
 CC phosphorylated on the specified Ser, forming a product that does not  
 CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family  
 CC proteins in the cytosol, thus promoting cell survival. The mutants with  
 CC Ser substituted cannot bind 14-3-3.  
 XX  
 SQ Sequence 204 AA;  
 Query Match 93.2%; Score 138; DB 19; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-13;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 NLWAAQRYGRELRRMSDEFGSFKGL 27  
 |||||  
 Db 140 NLWAAQRYGRELRRMSDEFGSFKGL 165  
 RESULT 9  
 AAW61316  
 ID AAW61316 standard; Protein; 204 AA.  
 XX  
 AC AAW61316;  
 XX  
 XX 07-OCT-1998 (first entry)  
 DT  
 XX  
 DE Mutant BCL-XL/BCL-2 associated cell death regulator #1.  
 XX  
 KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;  
 KW serine substituted mutant; apoptosis; cancer; viral infection.  
 XX  
 OS Mus sp.  
 OS Synthetic.  
 XX  
 PN W09817682-A1.



XX PF 17-OCT-1997; 97WO-US19175.  
 XX PR 18-OCT-1996; 96US-0733505.  
 XX PA (UNIW ) UNIV WASHINGTON.  
 XX PI Kormsmeier SJ;  
 XX DR WPI; 1998-261422/23.  
 XX DR N-PSDB; AAV27836.  
 XX PT New mutant BAD polypeptide with phosphorylatable serine replaced -  
 XX PT useful for, e.g. treating reduced apoptosis such as in cancer or  
 XX PT viral infection  
 XX PS Claim 7; Page 60-61; 95pp; English.  
 XX CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell  
 CC death regulator) proteins, having an amino acid other than Ser at  
 CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The  
 CC present sequence represents a mutant BAD protein. Also described are: (1)  
 CC fragments of mutant BAD protein able to decrease cell viability; (2)  
 CC fusion proteins of mutant BAD with a heterologous polypeptide that  
 CC increases intracellular delivery. Mutant BAD proteins are used to treat  
 CC or prevent diseases associated with reduced apoptosis, e.g. cancer,  
 CC viral infection, lymphoproliferation, arthritis, infertility,  
 CC inflammation and autoimmune disease. Polynucleotide sequences encoding  
 CC mutant BAD proteins can be used similarly by gene therapy or to produce  
 CC transgenic animals for use as disease models or in drug screening. BAD  
 CC proteins phosphorylated at specified Ser are used to screen for enhancers  
 CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful  
 CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,  
 CC aging or ischaemic cell death. The apoptotic status of cells is  
 CC determined by measuring relative amounts of phosphorylated and non-  
 CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have  
 CC greater death-promoting activity than wild-type BAD which can become  
 CC phosphorylated on the specified Ser, forming a product that does not  
 CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family  
 CC proteins in the cytosol, thus promoting cell survival. The mutants with  
 CC Ser substituted cannot bind 14-3-3.  
 XX SQ Sequence 204 AA;  
 Query Match 93.2%; Score 138; DB 19; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-13;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 NLWAAQRYGRELRRMSDEFGSFKGL 27  
 Db 140 NLWAAQRYGRELRRMSDEFGSFKGL 165  
 RESULT 12  
 AAW58832  
 ID AAW58832 standard; protein; 204 AA.  
 XX AC AAW58832;  
 XX DT 23-JUL-1998 (first entry)  
 XX DE Murine BAD protein.  
 XX KW BAD protein; Bcl-XL/Bcl-2 associated cell death regulator; 14-3-3;  
 KW serine phosphorylation; post-translational modification; apoptosis;  
 KW signal transduction regulator; phosphoserine phosphatase; senescence;  
 KW immunodeficiency disease; neurodegenerative disease; infertility;  
 KW cancer, viral infection; lymphoproliferative condition; arthritis;  
 KW inflammation; autoimmune diseases.  
 XX OS Mus sp.  
 XX WO9809643-A1.

XX PD 12-MAR-1998.  
 XX PF 09-SEP-1997; 97WO-US15871.  
 XX PR 09-SEP-1996; 96US-0707868.  
 XX PA (UNIW ) UNIV WASHINGTON.  
 XX PI Kormsmeier SJ;  
 XX DR WPI; 1998-207049/18.  
 XX PT Serine-phosphorylated Bcl-XL/Bcl-2 Associated cell Death regulator  
 XX PT polypeptide - useful for modulation of apoptosis associated with,  
 XX PT e.g. cancer and immunodeficiency diseases  
 XX PS Claim 3; Fig 8; 61pp; English.  
 XX CC This sequence represents a novel serine-phosphorylated protein, BAD  
 CC (Bcl-XL/Bcl-2 associated cell death regulator). The serine residue is  
 CC phosphorylated in a post-translational modification and allows binding  
 CC to the 14-3-3 protein which is a signal transduction regulator.  
 CC Modulators of phosphorylated BAD, which act through inhibition/activation  
 CC of a phosphoserine phosphatase, are useful for preventing/treating  
 CC increased/decreased apoptosis in a cell. The increased apoptosis may  
 CC result from immunodeficiency diseases, senescence, neurodegenerative  
 CC disease, ischaemic cell death, reperfusion cell death, infertility and  
 CC wound-healing. Decreased apoptosis may result from cancer, viral  
 CC infection, lymphoproliferative conditions, arthritis, infertility,  
 CC inflammation and autoimmune diseases. Measuring the amount of  
 CC phosphorylated compared to unphosphorylated BAD polypeptide and/or total  
 CC BAD in a cell is useful for determining the apoptotic state of a cell.  
 XX SQ Sequence 204 AA;  
 Query Match 93.2%; Score 138; DB 19; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-13;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 NLWAAQRYGRELRRMSDEFGSFKGL 27  
 Db 140 NLWAAQRYGRELRRMSDEFGSFKGL 165  
 RESULT 13  
 AAB70369  
 ID AAB70369 standard; protein; 204 AA.  
 XX AC AAB70369;  
 XX DT 02-MAY-2001 (first entry)  
 XX DE Longer murine BAD mutant amino acid sequence SEQ ID NO:2.  
 XX KW Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;  
 KW immunostimulant; neuroprotective; nootropic; antiischaemic; vulnery;  
 KW cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing;  
 KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;  
 KW immunodeficiency disease; neurodegenerative disease; viral infection;  
 KW ischaemic cell death; reperfusion cell death; arthritis; infertility;  
 KW lymphoproliferative condition; inflammation; autoimmune disease.  
 XX OS Mus musculus.  
 XX OS Synthetic.  
 XX PN WO200110888-A1.  
 XX PD 15-FEB-2001.  
 XX PF 30-MAY-2000; 2000WO-US11864.  
 XX PR 28-MAY-1999; 99US-0136783.

XX PA (APOP-) APOPTOSIS TECHNOLOGY INC.  
XX PI Zhou X;  
XX PT WPI; 2001-138734/14.  
XX DR  
XX PT New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,  
PT useful for screening for candidate compounds which induce or inhibit  
PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or  
PT Ser113 -  
XX PT  
XX PS Claim 4; Page 148; 157pp; English.  
XX CC The present invention describes an isolated or synthetic polypeptide  
CC (I) comprising a less than full length amino acid sequence of a mutant  
CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its  
CC fragment, which contains amino acid substitutions at Ser118 of a human  
CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine  
CC BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,  
CC nootropic, antiischaemic, vulnary, cytostatic, antiviral,  
CC antiarthritic, antiinflammatory and immunosuppressive activities, and  
CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and  
CC polynucleotides can be used for screening candidate compounds and drugs  
CC for activity that promote cell survival or apoptosis. Other uses include  
CC inducing or inhibiting apoptosis in a cell. Candidate compounds  
CC identified and (mutant) BAD polypeptides are useful in treating  
CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell  
CC death, reperfusion cell death, wound healing, cancer, viral infections,  
CC lymphoproliferative conditions, arthritis, infertility, inflammation and  
CC autoimmune diseases. The present sequence represents a specifically  
CC claimed longer murine BAD mutant amino acid sequence from the present  
CC invention.  
XX CC  
XX SQ Sequence 204 AA;  
Query Match 93.2%; Score 138; DB 22; Length 204;  
Best Local Similarity 100.0%; Pred. No. 4.5e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 NLWAAQRYGRELRLMSDEFEFGSKGL 27  
Db 140 NLWAAQRYGRELRLMSDEFEFGSKGL 165  
RESULT 14  
ABR39082  
ID ABR39082 standard; Protein; 204 AA.  
XX AC ABR39082;  
XX DT 10-MAY-2003 (first entry)  
XX DE Murine BAD protein SEQ ID NO:4.  
XX KW Murine; BAD; herpes simplex virus; HSV; US3; herpes virus; apoptosis;  
KW virucide; infection.  
XX OS Mus musculus.  
XX PN WO2003012049-A2.  
XX PD 13-FEB-2003.  
XX PF 31-JUL-2002; 2002WO-US241177.  
XX PR 31-JUL-2001; 2001US-308929P.  
XX PA (UYCH-) UNIV CHICAGO.  
XX PI Munger J, Roizman B;  
XX DR WPI; 2003-248168/24.

DR N-PSDB; AB281201.  
XX Inducing apoptosis in a cell infected with herpes simplex virus, HSV,  
PT by administering to the cell, a composition comprising an agent that  
PT inhibits phosphorylation of pro-apoptotic polypeptide BAD by HSV US3  
XX Claim 15; Page 168; 192pp; English.  
XX CC The present invention describes a method (M1) for inducing apoptosis in  
CC a cell infected with herpes simplex virus (HSV), which comprises  
CC administering to the cell, a composition having an agent that inhibits  
CC phosphorylation of pro-apoptotic polypeptide BAD by HSV US3. Also  
CC described is a method (M2) for treating a patient infected with HSV, by  
CC administering to the patient, a composition comprising a peptide  
CC comprising a sequence of 4-100 continuous amino acids of a 168 residue  
CC amino acid sequence (see ABR39081), where the peptide comprises Ser112,  
CC Ser135, or Ser155, or their combinations. BAD has virucide activity.  
CC M1 is useful for inducing apoptosis in a cell infected with HSV, where  
CC the cell is in a human. M2 is useful for treating a patient infected  
CC with HSV. The present sequence represents murine BAD, which is used in  
CC the exemplification of the present invention.  
XX SQ Sequence 204 AA;  
Query Match 93.2%; Score 138; DB 24; Length 204;  
Best Local Similarity 100.0%; Pred. No. 4.5e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 NLWAAQRYGRELRLMSDEFEFGSKGL 27  
Db 140 NLWAAQRYGRELRLMSDEFEFGSKGL 165  
RESULT 15  
AAU00220  
ID AAU00220 standard; Protein; 567 AA.  
XX AC AAU00220;  
XX DT 31-MAY-2001 (first entry)  
XX DE Bad-DTR apoptosis-modifying fusion protein.  
XX KW Mouse; Bad-DTR; apoptosis; cancer; spinal muscular atrophy;  
KW diphtheria toxin receptor binding domain; DTR; neoplasm; tumour;  
KW hyper-proliferation; Alzheimer's disease; neurodegenerative disorder;  
KW transient ischaemic neuronal injury; stroke; spinal cord injury;  
KW Huntington's disease.  
XX OS Chimeric - Mus sp.  
OS Chimeric - Corynebacterium diphtheriae.  
OS Chimeric - Synthetic.  
XX FH Key Location/Qualifiers  
FT Region 3..12 /note= "10x-histidine tag"  
XX PN WO200112661-A2.  
XX PD 22-FEB-2001.  
XX PF 15-AUG-2000; 2000WO-US22293.  
XX PR 16-AUG-1999; 99US-0149220.  
XX PA (HARD ) HARVARD COLLEGE.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX PI Youle RJ, Liu X, Collier RJ;  
XX DR WPI; 2001-218343/22.  
XX N-PSDB; AAS00248.



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OM protein - protein search, using sw model

Run on: September 15, 2003, 17:22:21 ; Search time 14.6 Seconds  
(without alignments)  
81.144 Million cell updates/sec

Title: US-09-544-664-55

Perfect score: 148

Sequence: 1 KNLWAAQRYGRELRRMSDFEGSKGLK 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	138	93.2	204	1	US-08-333-565-2
2	138	93.2	204	2	US-08-661-479-2
3	138	93.2	204	2	US-08-733-505A-1
4	138	93.2	204	2	US-08-733-505A-12
5	138	93.2	204	2	US-08-733-505A-13
6	138	93.2	204	2	US-08-733-505A-14
7	135	91.2	204	2	US-08-717-123-3
8	135	91.2	204	4	US-09-375-257-3
9	114	77.0	166	1	US-08-665-617-2
10	114	77.0	168	2	US-08-717-123-2
11	114	77.0	168	3	US-08-985-335-1
12	114	77.0	168	3	US-08-985-335-7
13	114	77.0	168	3	US-09-410-372-1
14	114	77.0	168	3	US-09-410-372-7
15	114	77.0	168	4	US-09-375-257-2
16	113	76.4	23	1	US-08-333-565-10
17	113	76.4	23	2	US-08-661-479-10
18	102	68.9	59	2	US-08-733-505A-55
19	102	68.9	59	2	US-08-733-505A-56
20	102	68.9	59	2	US-08-733-505A-57
21	102	68.9	59	2	US-08-733-505A-58
22	86	58.1	16	1	US-08-333-565-26
23	86	58.1	16	2	US-08-661-479-26
24	61	41.2	11	2	US-08-733-505A-34
25	61	41.2	11	2	US-08-706-741B-69
26	61	41.2	11	2	US-08-924-695A-59
27	51	34.5	66	2	US-08-867-087B-40

28	48.5	32.8	904	4	US-09-328-352-4656	Sequence 4656, Ap
29	46	31.1	610	4	US-09-252-991A-19594	Sequence 19594, A
30	46	31.1	946	3	US-09-074-579-3	Sequence 3, Appli
31	46	31.1	946	3	US-09-388-774-3	Sequence 3, Appli
32	46	31.1	946	4	US-09-546-153-1	Sequence 1, Appli
33	45.5	30.7	906	4	US-09-252-991A-31458	Sequence 31458, A
34	45	30.4	229	4	US-09-252-991A-23807	Sequence 23807, A
35	45	30.4	303	4	US-09-328-352-5164	Sequence 5164, Ap
36	45	30.4	356	4	US-09-235-103-2	Sequence 2, Appli
37	45	30.4	356	4	US-09-235-103-4	Sequence 4, Appli
38	45	30.4	1064	4	US-09-252-991A-17508	Sequence 17508, A
39	44.5	30.1	903	4	US-09-252-991A-28775	Sequence 28775, A
40	44	29.7	125	4	US-09-328-352-7449	Sequence 7449, Ap
41	44	29.7	263	4	US-09-651-656-27	Sequence 27, Appl
42	44	29.7	263	4	US-09-650-855-27	Sequence 27, Appl
43	44	29.7	277	4	US-09-252-991A-28581	Sequence 28581, A
44	44	29.7	877	4	US-09-206-551-20	Sequence 20, Appl
45	44	29.7	1125	4	US-09-252-991A-18729	Sequence 18729, A

ALIGNMENTS

RESULT 1  
US-08-333-565-2  
; Sequence 2, Application US/08333565  
; Patent No. 5622852  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, Stanley J.  
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH  
; TITLE OF INVENTION: REGULATOR  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Townsend and Townsend Kourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/333,565  
; FILING DATE: 31-OCT-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 15726A-000700  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 204 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..204  
; OTHER INFORMATION: /note= "Deduced amino acid sequence  
; OTHER INFORMATION: of mouse BAD."  
US-08-333-565-2

Query Match 93.2%; Score 138; DB 1; Length 204;  
Best Local Similarity 100.0%; Pred. No. 1.5e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NLWAAQRYGRELRRMSDEFEGSFKGL 27  
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Db 140 NLWAAQRYGRELRRMSDEFEGSFKGL 165

RESULT 2  
US-08-661-479-2  
; Sequence 2, Application US/08661479  
; Patent No. 5834209  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, STANLEY J.  
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH  
; TITLE OF INVENTION: REGULATOR  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/661,479  
; FILING DATE: 11-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/333,565  
; FILING DATE: 31-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 15726A-000700  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 204 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..204  
; OTHER INFORMATION: /note= "Deduced amino acid sequence  
; OTHER INFORMATION: of mouse BAD."  
US-08-661-479-2

Query Match 93.2%; Score 138; DB 2; Length 204;  
Best Local Similarity 100.0%; Pred. No. 1.5e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NLWAAQRYGRELRRMSDEFEGSFKGL 27  
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Db 140 NLWAAQRYGRELRRMSDEFEGSFKGL 165

RESULT 3  
US-08-733-505A-1  
; Sequence 1, Application US/08733505A  
; Patent No. 5856445  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, STANLEY J.  
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF  
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BLVD., SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: USA  
; ZIP: 63105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/733,505A  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 965458  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 727-5188  
; TELEFAX: (314) 727-6092  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 204 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-733-505A-1

Query Match 93.2%; Score 138; DB 2; Length 204;  
Best Local Similarity 100.0%; Pred. No. 1.5e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NLWAAQRYGRELRRMSDEFEGSFKGL 27  
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Db 140 NLWAAQRYGRELRRMSDEFEGSFKGL 165

RESULT 4  
US-08-733-505A-12  
; Sequence 12, Application US/08733505A  
; Patent No. 5856445  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, STANLEY J.  
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF  
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BLVD., SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: USA  
; ZIP: 63105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/733,505A  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 965458  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 727-5188  
; TELEFAX: (314) 727-6092  
; INFORMATION FOR SEQ ID NO: 12:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-733-505A-12

Query Match          93.2%; Score 138; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 NLWAAQRYGRELRLMSDEFEQSGFKGL 27
Db      140 NLWAAQRYGRELRLMSDEFEQSGFKGL 165

RESULT 5
US-08-733-505A-13
; Sequence 13, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,505A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-733-505A-13

Query Match          93.2%; Score 138; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 NLWAAQRYGRELRLMSDEFEQSGFKGL 27
Db      140 NLWAAQRYGRELRLMSDEFEQSGFKGL 165

RESULT 6
US-08-733-505A-14
; Sequence 14, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
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; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,505A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-733-505A-14

Query Match          93.2%; Score 138; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 NLWAAQRYGRELRLMSDEFEQSGFKGL 27
Db      140 NLWAAQRYGRELRLMSDEFEQSGFKGL 165

RESULT 7
US-08-717-123-3
; Sequence 3, Application US/08717123
; Patent No. 5965703
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
; TITLE OF INVENTION: Acids and Methods of Use
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/717,123
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
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; REFERENCE/DOCKET NUMBER: P-ID 1929
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-717-123-3

Query Match 91.2%; Score 135; DB 2; Length 204;
Best Local Similarity 96.2%; Pred. No. 4.2e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 NLWAAQRYGRELRRMSDEFEQSKGL 27
Db 140 NLWAAQRYGRELRRMTDEFEQSKGL 165

RESULT 8
US-09-375-257-3
; Sequence 3, Application US/09375257
; Patent No. 6504022
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
; FILE OF INVENTION: ACIDS AND METHODS OF USE
; FILE REFERENCE: 480140.428D1
; CURRENT APPLICATION NUMBER: US/09/375,257
; CURRENT FILING DATE: 1999-08-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-375-257-3

Query Match 91.2%; Score 135; DB 4; Length 204;
Best Local Similarity 96.2%; Pred. No. 4.2e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 NLWAAQRYGRELRRMSDEFEQSKGL 27
Db 140 NLWAAQRYGRELRRMTDEFEQSKGL 165

RESULT 9
US-08-665-617-2
; Sequence 2, Application US/08665617
; Patent No. 5663316
; GENERAL INFORMATION:
; APPLICANT: Xudong, Yin
; TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,617
; FILING DATE:
; CLASSIFICATION: 530

US-09-544-664-55.ra1

; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: CL-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-665-617-2

Query Match 77.0%; Score 114; DB 1; Length 166;
Best Local Similarity 91.7%; Pred. No. 5.4e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NLWAAQRYGRELRRMSDEFEQSKF 25
Db 101 NLWAAQRYGRELRRMSDEFEQSKF 124

RESULT 10
US-08-717-123-2
; Sequence 2, Application US/08717123
; Patent No. 5965703
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
; TITLE OF INVENTION: Acids and Methods of Use
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/717,123
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 1929
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-717-123-2

Query Match 77.0%; Score 114; DB 2; Length 168;
Best Local Similarity 91.7%; Pred. No. 5.5e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NLWAAQRYGRELRRMSDEFEQSKF 25
Db 103 NLWAAQRYGRELRRMSDEFEQSKF 126
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RESULT 11
US-08-985-335-1
; Sequence 1, Application US/08985335
; Patent No. 6080847
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,335
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0421 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-845-4166
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SYNORAB01
; CLONE: 358673
; US-08-985-335-1

Query Match 77.0%; Score 114; DB 3; Length 168;
Best Local Similarity 91.7%; Pred. No. 5.5e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NLWAAQRYGRELRRMSDEFSGFK 25
|||||
Db 103 NLWAAQRYGRELRRMSDEFVDSFK 126

RESULT 12
US-08-985-335-7
; Sequence 7, Application US/08985335
; Patent No. 6080847
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION
; NUMBER OF SEQUENCES: 9

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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,335
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0421 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-845-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1683637
; US-08-985-335-7

Query Match 77.0%; Score 114; DB 3; Length 168;
Best Local Similarity 91.7%; Pred. No. 5.5e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NLWAAQRYGRELRRMSDEFSGFK 25
|||||
Db 103 NLWAAQRYGRELRRMSDEFVDSFK 126

RESULT 13
US-09-410-372-1
; Sequence 1, Application US/09410372
; Patent No. 6281334
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/410,372
; FILING DATE:

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;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/985,335  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Billings, Lucy J.  
;; REGISTRATION NUMBER: 36,749  
;; REFERENCE/DOCKET NUMBER: PF-0421 US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 650-855-0555  
;; TELEFAX: 650-845-4166  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 168 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; IMMEDIATE SOURCE:  
;; LIBRARY: SYNORAB01  
;; CLONE: 358673  
US-09-410-372-1

Query Match 77.0%; Score 114; DB 3; Length 168;  
Best Local Similarity 91.7%; Pred. No. 5.5e-10;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 NLWAAQRYGRELRRMSDEFVDSFK 25  
|||||  
Db 103 NLWAAQRYGRELRRMSDEFVDSFK 126

RESULT 14  
US-09-410-372-7  
; Sequence 7, Application US/09410372  
; Patent No. 6281334  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Yue, Henry  
; APPLICANT: Lal, Preeti  
; APPLICANT: Shah, Purvi  
; APPLICANT: Corley, Neil C.  
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Dr.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/410,372  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/985,335  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0421 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 168 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single

;; TOPOLOGY: linear  
;; IMMEDIATE SOURCE:  
;; LIBRARY: GenBank  
;; CLONE: 1683637  
US-09-410-372-7

Query Match 77.0%; Score 114; DB 3; Length 168;  
Best Local Similarity 91.7%; Pred. No. 5.5e-10;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 NLWAAQRYGRELRRMSDEFVDSFK 25  
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Db 103 NLWAAQRYGRELRRMSDEFVDSFK 126

RESULT 15  
US-09-375-257-2  
; Sequence 2, Application US/09375257  
; Patent No. 6504022  
; GENERAL INFORMATION:  
; APPLICANT: Horne, William A.  
; APPLICANT: Oltersdorf, Tilman  
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC  
; FILE OF INVENTION: ACIDS AND METHODS OF USE  
; FILE REFERENCE: 480140.428D1  
; CURRENT APPLICATION NUMBER: US/09/375,257  
; CURRENT FILING DATE: 1999-08-16  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 168  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-375-257-2

Query Match 77.0%; Score 114; DB 4; Length 168;  
Best Local Similarity 91.7%; Pred. No. 5.5e-10;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 NLWAAQRYGRELRRMSDEFVDSFK 25  
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Db 103 NLWAAQRYGRELRRMSDEFVDSFK 126

Search completed: September 15, 2003, 17:45:06  
Job time : 14.6 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 15, 2003, 17:25:56 ; Search time 22.2 Seconds  
(without alignments)  
184,034 Million cell updates/sec

Title: US-09-544-664-55  
Perfect score: 148  
Sequence: 1 KNLWAAQRYGRELRRMSDEFGSKGLK 28

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 541936 seqs, 145912426 residues

Total number of hits satisfying chosen parameters: 541936

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
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9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	Query Match	Length	DB	ID	Description
1	135	91.2	204	9	US-09-922-378-3	Sequence 3, Appli
2	135	91.2	204	14	US-10-066-179-3	Sequence 3, Appli
3	114	77.0	25	15	US-10-059-261-258	Sequence 258, App
4	114	77.0	168	9	US-09-922-378-2	Sequence 2, Appli
5	114	77.0	168	9	US-09-894-657-1	Sequence 1, Appli
6	114	77.0	168	9	US-09-894-657-7	Sequence 7, Appli
7	114	77.0	168	14	US-10-066-179-2	Sequence 2, Appli
8	71	48.0	15	15	US-10-174-105A-147	Sequence 147, App
9	52	35.1	215	15	US-10-156-761-9145	Sequence 9145, Ap
10	51	34.5	682	12	US-10-238-075-1077	Sequence 1077, Ap
11	47	31.8	35	15	US-10-092-750-1	Sequence 1, Appli
12	47	31.8	138	15	US-10-092-750-241	Sequence 241, App
13	46	31.1	946	9	US-09-828-423-3	Sequence 3, Appli
14	44	29.7	270	11	US-09-934-455-162	Sequence 162, App
15	44	29.7	272	15	US-10-156-761-11541	Sequence 11541, A

15	44	29.7	426	9	US-09-815-242-5704	Sequence 5704, Ap			
17	44	29.7	699	14	US-10-008-355-8	Sequence 8, Appli			
18	44	29.7	705	9	US-09-815-242-12463	Sequence 12463, A			
19	44	29.7	712	14	US-10-008-355-2	Sequence 2, Appli			
20	44	29.7	877	12	US-10-369-294-20	Sequence 20, Appl			
21	43	29.1	94	9	US-09-864-761-39540	Sequence 39540, A			
22	43	29.1	164	11	US-09-986-480-395	Sequence 395, App			
23	43	29.1	213	9	US-09-843-846-18	Sequence 18, Appl			
24	43	29.1	232	10	US-09-881-752A-238	Sequence 238, App			
25	43	29.1	380	9	US-09-149-045-2	Sequence 2, Appli			
26	43	29.1	380	15	US-10-166-359-2	Sequence 2, Appli			
27	43	29.1	380	15	US-10-166-113-2	Sequence 2, Appli			
28	43	29.1	380	15	US-10-166-357-2	Sequence 2, Appli			
29	43	29.1	380	15	US-10-166-372-2	Sequence 2, Appli			
30	43	29.1	380	15	US-10-184-722-3	Sequence 3, Appli			
31	43	29.1	380	15	US-10-251-385-62	Sequence 62, Appl			
32	43	29.1	380	15	US-10-251-385-198	Sequence 198, App			
33	43	29.1	380	15	US-10-225-567A-233	Sequence 233, App			
34	43	29.1	543	15	US-10-156-761-13485	Sequence 13485, A			
35	43	29.1	571	9	US-09-815-242-11813	Sequence 11813, A			
36	43	29.1	582	10	US-09-331-631A-22	Sequence 22, Appl			
37	43	29.1	640	9	US-09-989-722-501	Sequence 501, App			
38	43	29.1	640	9	US-09-989-723-501	Sequence 501, App			
39	43	29.1	640	9	US-09-989-279-501	Sequence 501, App			
40	43	29.1	640	9	US-09-989-727-501	Sequence 501, App			
41	43	29.1	640	10	US-09-989-731-501	Sequence 501, App			
42	43	29.1	640	10	US-09-989-732-501	Sequence 501, App			
43	43	29.1	640	10	US-09-991-073-501	Sequence 501, App			
44	43	29.1	640	10	US-09-909-320-292	Sequence 292, App			
45	43	29.1	640	10	US-09-990-442-501	Sequence 501, App			

ALIGNMENTS

RESULT 1  
US-09-922-378-3  
; Sequence 3, Application US/09922378  
; Patent No. US20020037869A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, William A.  
; APPLICANT: Oltersdorf, Tilman  
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC  
; TITLE OF INVENTION: ACIDS AND METHODS OF USE  
; FILE REFERENCE: 480140.428D3  
; CURRENT APPLICATION NUMBER: US/09/922,378  
; CURRENT FILING DATE: 2001-08-03  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 204  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-922-378-3

Query Match 91.2%; Score 135; DB 9; Length 204;  
Best Local Similarity 96.2%; Pred. No. 8.2e-12;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	2	NLWAAQRYGRELRRMSDEFGSKGL 27
DB	140	NLWAAQRYGRELRRMTDEFGSKGL 165

RESULT 2  
US-10-066-179-3  
; Sequence 3, Application US/10066179  
; Publication No. US20020115631A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, William A.  
; APPLICANT: Oltersdorf, Tilman  
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC  
; TITLE OF INVENTION: ACIDS AND METHODS OF USE

; FILE REFERENCE: 480140.428C1  
; CURRENT APPLICATION NUMBER: US/10/066,179  
; CURRENT FILING DATE: 2002-02-01  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 204  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; US-10-066-179-3

Query Match 91.2%; Score 135; DB 14; Length 204;  
Best Local Similarity 96.2%; Pred. No. 8.2e-12;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 NLWAAQRYGRELRRMSDEFECSFKL 27  
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Db 140 NLWAAQRYGRELRRMTDEFECSFKL 165

RESULT 3  
US-10-059-261-258  
; Sequence 258, Application US/10059261  
; Publication No. US20030077826a1  
; GENERAL INFORMATION:  
; APPLICANT: EDELMAN, LENA  
; APPLICANT: JACOTOT, ETIENNE DANIEL FRANCOIS  
; APPLICANT: BRIAND, JEAN-PAUL  
; TITLE OF INVENTION: CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET  
; TITLE OF INVENTION: SPECIFIC CELLS AND A MODULE REGULATING THE APOPTOGENIC  
; TITLE OF INVENTION: FUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX  
; TITLE OF INVENTION: (PTPC)  
; FILE REFERENCE: 03495,0216  
; CURRENT APPLICATION NUMBER: US/10/059,261  
; CURRENT FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: 60/265,594  
; PRIOR FILING DATE: 2001-02-02  
; NUMBER OF SEQ ID NOS: 325  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 258  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: TOX peptide  
US-10-059-261-258

Query Match 77.0%; Score 114; DB 15; Length 25;  
Best Local Similarity 91.7%; Pred. No. 1e-09;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NLWAAQRYGRELRRMSDEFECSFK 25  
|||||  
Db 1 NLWAAQRYGRELRRMSDEFECSFK 24

RESULT 4  
US-09-922-378-2  
; Sequence 2, Application US/09922378  
; Patent No. US20020037869A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, William A.  
; APPLICANT: Oltersdorf, Tilman  
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC  
; TITLE OF INVENTION: ACIDS AND METHODS OF USE  
; FILE REFERENCE: 480140.428D3  
; CURRENT APPLICATION NUMBER: US/09/922,378  
; CURRENT FILING DATE: 2001-08-03  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 168  
; TYPE: PRT

; ORGANISM: Homo sapiens  
US-09-922-378-2

Query Match 77.0%; Score 114; DB 9; Length 168;  
Best Local Similarity 91.7%; Pred. No. 7.2e-09;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NLWAAQRYGRELRRMSDEFECSFK 25  
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Db 103 NLWAAQRYGRELRRMSDEFECSFK 126

RESULT 5  
US-09-894-657-1  
; Sequence 1, Application US/09894657  
; Patent No. US20020098569A1  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; Yue, Henry  
; Lal, Preeti  
; Shah, Purvi  
; Corley, Neil C.  
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL  
; PROLIFERATION  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Dr.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/894,657  
; FILING DATE: 28-Jun-2001  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/410,372  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0421 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 168 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: SYNORAB01  
; CLONE: 358673  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-894-657-1

Query Match 77.0%; Score 114; DB 9; Length 168;  
Best Local Similarity 91.7%; Pred. No. 7.2e-09;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NLWAAQRYGRELRRMSDEFECSFK 25  
|||||  
Db 103 NLWAAQRYGRELRRMSDEFECSFK 126

RESULT 6  
US-09-894-657-7

```
/ Sequence 7, Application US/09894557
/ Patent No. US20020098569A1
/ GENERAL INFORMATION:
/ APPLICANT: Hillman, Jennifer L.
/ Yue, Henry
/ Lal, Preeti
/ Shah, Purvi
/ Corley, Neil C.
/ TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
/ PROLIFERATION
/ NUMBER OF SEQUENCES: 9
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Dr.
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/894,657
/ FILING DATE: 28-Jun-2001
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/410,372
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0421 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-855-0535
/ TELEFAX: 650-845-4166
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 168 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GenBank
/ CLONE: 1683637
/ SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-894-657-7

Query Match 77.0%; Score 114; DB 9; Length 168;
Best Local Similarity 91.7%; Pred. No. 7.2e-09;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NLWAAQRYGRELRRMSDEFESEFK 25
Db 103 NLWAAQRYGRELRRMSDEFESEFK 126

RESULT 7
US-10-066-179-2
/ Sequence 2, Application US/10066179
/ Publication No. US20020115631A1
/ GENERAL INFORMATION:
/ APPLICANT: Horne, William A.
/ APPLICANT: Oltersdorf, Tilman
/ TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
/ ACIDS AND METHODS OF USE
/ FILE REFERENCE: 480140.428C1
/ CURRENT APPLICATION NUMBER: US/10/066.179
/ CURRENT FILING DATE: 2002-02-01
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 163

Query Match 77.0%; Score 114; DB 14; Length 168;
Best Local Similarity 91.7%; Pred. No. 7.2e-09;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NLWAAQRYGRELRRMSDEFESEFK 25
Db 103 NLWAAQRYGRELRRMSDEFESEFK 126

RESULT 8
US-10-174-105A-147
/ Sequence 147, Application US/10174105A
/ Publication No. US2003006852A1
/ GENERAL INFORMATION:
/ APPLICANT: Cell Signaling Technology, Inc.
/ APPLICANT: ZHANG, Hui
/ APPLICANT: COMB, Michael J.
/ APPLICANT: TAN, Yi
/ TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPECIF
/ CONTEXT-INDEPENDENT ANTIBODIES COUPLED WITH DATABASE SEARCHIN
/ FILE REFERENCE: CST-138 CIP3
/ CURRENT APPLICATION NUMBER: US/10/174,105A
/ CURRENT FILING DATE: 2002-06-18
/ PRIOR APPLICATION NUMBER: US 09/148,712
/ PRIOR FILING DATE: 1998-09-04
/ PRIOR APPLICATION NUMBER: US 09/535,364
/ PRIOR FILING DATE: 2000-03-24
/ NUMBER OF SEQ ID NOS: 193
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 147
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic Peptide
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (8)..(8)
/ OTHER INFORMATION: PHOSPHORYLATION; serine at position 8 is phosphorylated
US-10-174-105A-147

Query Match 48.0%; Score 71; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00097;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GRELRRMSDEFESE 23
Db 1 GRELRRMSDEFESE 14

RESULT 9
US-10-156-761-9145
/ Sequence 9145, Application US/10156761
/ Publication No. US20030119018A1
/ GENERAL INFORMATION:
/ APPLICANT: OMURA, SATOSHI
/ APPLICANT: IKEDA, HARUO
/ APPLICANT: ISHIKAWA, JUN
/ APPLICANT: HORIKAWA, HIROSHI
/ APPLICANT: SHIBA, TADAYOSHI
/ APPLICANT: SAKAKI, YOSHIYUKI
/ APPLICANT: HATTORI, MASAHIRA
/ TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
/ FILE REFERENCE: 249-262
/ CURRENT APPLICATION NUMBER: US/10/156,761
/ CURRENT FILING DATE: 2002-05-29
/ PRIOR APPLICATION NUMBER: JP 2001-204089
/ PRIOR FILING DATE: 2001-05-30
/ PRIOR APPLICATION NUMBER: JP 2001-272697
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;
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 946 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENEBAK
; CLONE: g133985
; SEQUENCE DESCRIPTION: SEQ ID NO: 3 :
US-09-828-423-3

Query Match      31.1%; Score 46; DB 9; Length 946;
Best Local Similarity 30.8%; Pred. No. 2.7e+02;
Matches 8; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

QY      2 NLWAAQRYGRELRRMSDEFGSKGL 27
Db      212 DVWVIEPQGLRFLHVPDTFEGHFDGV 237

RESULT 14
US-09-934-455-162
; Sequence 162, Application US/09934455
; Publication No. US20030121070A1
; GENERAL INFORMATION:
; APPLICANT: Adam, Luc
; APPLICANT: Creelman, Robert
; APPLICANT: Dubell, Arnold
; APPLICANT: Heard, Jacqueline
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Keddle, James
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Reuber, Lynne
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Pineda, Omaira
; TITLE OF INVENTION: Genes for Modifying Plant Traits IV
; FILE REFERENCE: MBI-0025
; CURRENT APPLICATION NUMBER: US/09/934,455
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227439
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: MBI-0022
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: MBI-0023
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 516
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 162
; LENGTH: 270
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-934-455-162

Query Match      29.7%; Score 44; DB 11; Length 270;
Best Local Similarity 40.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 8; Indels 4; Gaps 1;

QY      2 NLWAAQRYGRELRRMSDEFGSKGLK 28
Db      78 NMFQPIYGRDFKRSS----SSMVGLK 100

RESULT 15
US-10-156-761-11541
; Sequence 11541, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
```

```

; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 11541
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-11541

Query Match      29.7%; Score 44; DB 15; Length 272;
Best Local Similarity 53.3%; Pred. No. 1.5e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      4 WAAQRYGRELRRMSD 18
Db      29 WIAAHGAEELRRAD 43

Search completed: September 15, 2003, 17:47:53
Job time : 22.2 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 15, 2003, 17:18:16 : Search time 12.6 Seconds  
(without alignments)  
213.708 Million cell updates/sec

Title: US-09-544-664-55  
Perfect score: 148  
Sequence: 1 KNLWAAQRYGRELRRMSDEFGSKGLK 28

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues  
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	138	93.2	204	2 A55671	bad protein - mous
2	54	36.5	946	2 JC5575	inter-alpha-trypsi
3	53	35.8	223	2 D70760	hypothetical prote
4	53	35.8	946	2 S54354	inter-alpha-inhibi
5	52	35.1	370	2 S38185	2-dehydro-3-deoxy-
6	51	34.5	232	2 A42095	floral homeotic pr
7	50	33.8	374	2 C84338	spermidine/putresc
8	50	33.8	516	2 A96753	probable threonine
9	50	33.8	1378	2 A81393	DNA-directed RNA p
10	49.5	33.4	127	2 A11210	glycerol-3-phospha
11	49	33.1	453	2 E83517	conserved hypothet
12	48.5	32.8	134	2 S40376	Ig kappa chain - h
13	48.5	32.8	314	2 T02975	annexin p35 - maiz
14	48	32.4	206	2 C36365	transforming prote
15	48	32.4	220	2 F72289	oxidoreductase, so
16	48	32.4	526	2 T08545	threonine synthase
17	48	32.4	1164	2 T24806	hypothetical prote
18	47.5	32.1	334	2 A39172	Antho-RFamide neur
19	47.5	32.1	1140	2 T09486	hypothetical prote
20	47	31.8	287	2 S43852	neuropeptide Pol-R
21	47	31.8	597	2 G82308	oxaloacetate decar
22	47	31.8	967	2 F82668	hypothetical prote
23	47	31.8	5138	2 B96695	annexin p33 - maiz
24	46.5	31.4	435	2 A4308	Antho-RFamide prec
25	46.5	31.4	165	2 S59899	chlorocruorin chai
26	46	31.1	399	2 T35440	probable polyamine
27	46	31.1	946	1 IYHU2	inter-alpha-trypsi
28	46	31.1	261	2 G69510	conserved hypothet
29	45.5	30.7			

30	45.5	30.7	327	2 AF2859	conserved hypothet
31	45.5	30.7	327	2 D97636	probable secreted
32	45.5	30.7	562	2 C71473	hypothetical prote
33	45.5	30.7	905	2 G83314	NADH dehydrogenase
34	45.5	30.7	1014	2 T36031	exonuclease ABC c
35	45	30.4	273	2 S06736	photosystem II oxy
36	45	30.4	273	2 AG2287	manganese-stabiliz
37	45	30.4	295	2 F83201	conserved hypothet
38	45	30.4	346	2 H95406	conserved hypothet
39	45	30.4	486	2 T31294	hypothetical prote
40	45	30.4	591	2 E44465	sodium ion pump ox
41	45	30.4	591	2 AB0509	oxaloacetate decar
42	45	30.4	591	2 AB0909	oxaloacetate decar
43	45	30.4	596	2 A28088	oxaloacetate decar
44	45	30.4	715	2 S52675	probable membrane
45	45	30.4	864	1 VCLJG4	env polyprotein -

ALIGNMENTS

RESULT 1

A55671  
bad protein - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 03-Mar-1995 #sequence\_revision 03-Mar-1995 #text\_change 05-Nov-1999  
C:Accession: A55671  
R:Yang, E.; Zha, J.; Jockel, J.; Boise, L.H.; Thompson, C.B.; Korsmeyer, S.J.  
Cell 80, 285-291, 1995  
A:Title: Bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promot  
A:Reference number: A55671; MUID:95136361; PMID:7834748  
A:Accession: A55671  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-204 <YAN>  
A:Cross-references: GB:L37296; NID:g639778; PIDN:AAA64465.1; PID:g639779  
C:Keywords: heterodimer

Query Match 93.2%; Score 138; DB 2; Length 204;  
Best Local Similarity 100.0%; Pred. No. 1.2e-12;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NLWAAQRYGRELRRMSDEFGSKGL 27

|||||  
Db 140 NLWAAQRYGRELRRMSDEFGSKGL 165

RESULT 2

JC5575  
inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster  
C:Species: Mesocricetus auratus (golden hamster)  
C:Date: 23-Sep-1997 #sequence\_revision 23-Sep-1997 #text\_change 20-Jun-2000  
C:Accession: JC5575; PC4485  
R:Nakatani, T.; Suzuki, Y.; Yamamoto, T.; Sinohara, H.  
J. Biochem. 122, 71-82, 1997  
A:Title: Molecular cloning and sequencing of cDNAs encoding three heavy-chain precurs  
sin inhibitor heavy chain family.  
A:Reference number: JC5574; MUID:97420688; PMID:9276673  
A:Accession: JC5575  
A:Molecule type: mRNA  
A:Residues: 1-946 <NAK>  
A:Cross-references: DDBJ:D89286; NID:g1694689; PIDN:BAA13939.1; PID:g1694690  
A:Experimental source: liver  
A:Accession: PC4485  
A:Molecule type: protein  
A:Residues: 55-64;140-146;151-156;424-447;500-528;577-605 <NA2>  
C:Comment: In the plasma three inter-alpha-trypsin inhibitor heavy chains 1, 2 and 3  
that the complexes play important role for pancreatic cancer.  
C:Superfamily: inter-alpha-trypsin inhibitor complex component II  
F:261-264,717-916/Disulfide bonds: #status predicted  
Query Match 36.5%; Score 54; DB 2; Length 946;  
Best Local Similarity 34.6%; Pred. No. 11;



C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C;Accession: A96753  
R:Theologias, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Al-Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marzi,Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; MUID:21016719; PMID:11130712  
A;Accession: A96753  
A>Status: preliminary  
A:Molecule type: DNA  
A;Residues: 1-516 <STO>  
A;Cross-references: GB:AEO05173; NID:g5903070; PIDN:AAAD55628.1; GSFDDB:GN00141  
C;Genetics:  
A;Gene: F3N23.1  
A;Map position: 1

Query Match 33.8%; Score 50; DB 2; Length 516;  
Best Local Similarity 35.3%; Pred. No. 23;  
Matches 12; Conservative 7; Mismatches 7; Indels 8; Gaps 1;

QY 2 NLWAQRGGRLEFRMSD-----EFGSGFKGL 27  
||| : ||| : ||| :  
Db 163 NLWAEPRGKQLQNMDLWKHCGISHTGSFSDL 196

RESULT 9  
A81393  
DNA-directed RNA polymerase (EC 2.7.7.6) beta chain Cj0478 [imported] - Campylobacte  
C;Species: Campylobacter jejuni  
C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 03-Jun-2002  
C;Accession: A81393  
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chi  
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Ba  
Nature 403, 665-668, 2000  
A>Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals  
A;Reference number: A81250; MUID:20150912; PMID:10688204  
A;Accession: A81393  
A>Status: preliminary  
A:Molecule type: DNA  
A;Residues: 1-1378 <PAR>  
A;Cross-references: GB:AL139075; GB:AL111168; NID:g6967817; PIDN:CAB75116.1; PID:g6967817  
A;Experimental source: serotype O2, strain NCTC 11168  
C;Genetics:  
A;Gene: rpoB; Cj0478  
C;Superfamily: DNA-directed RNA polymerase beta chain  
C;Keywords: nucleotidylyltransferase

Query Match 33.8%; Score 50; DB 2; Length 1378;  
Best Local Similarity 40.8%; Pred. No. 53;  
Matches 13; Conservative 3; Mismatches 10; Indels 6; Gaps 2;

QY 3 LWAAQRYG--RELRRM----SDEFECSFKGLK 28  
:||| : ||| : ||| :  
Db 1306 VWALEAYGAHTLRMLTIKSDDVEGESAYK 1337

RESULT 10  
A11210  
glycerol-3-phosphate cytidyltransferase (gct), CDP-glycerol pyrophosphorylase (tel  
C;Species: Listeria monocytogenes  
C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 01-Mar-2002  
C;Accession: A11210  
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Blo  
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi  
D.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournan, A.

Ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria* species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: A11210  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-127 <GLA>  
A:Cross-references: GB:NC\_003210; PIDN:CAC99167.1; PID:gl6410491; GSPDB:GN00177  
A:Experimental source: strain EGD-e  
C:Genetics:  
A:Gene: tagD  
C:Superfamily: *Bacillus subtilis* glycerol-3-phosphate cytidylyltransferase tagD

Query Match 33.4%; Score 49.5; DB 2; Length 127;  
Best Local Similarity 36.4%; Pred. No. 6.5;  
Matches 12; Conservative 6; Mismatches 10; Indels 5; Gaps 1;

QY 1 KNLWAAQR-----YGRELRMSDEFFGSFKGLK 28  
Db 71 ENNWEQRDDIEKYIDVFVGMGDWEGEFDFLK 103

RESULT 11  
E83517  
conserved hypothetical protein PA1031 [imported] - *Pseudomonas aeruginosa* (strain PA01)  
C:Species: *Pseudomonas aeruginosa*  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Accession: E83517  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen  
A:Reference number: A82950; MUID:20437337; PMID:10984043  
A:Accession: E83517  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-453 <STO>  
A:Cross-references: GB:AE004535; GB:AE004091; NID:g9946936; PIDN:AA604420.1; GSPDB:GN00177  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA1031

Query Match 33.1%; Score 49; DB 2; Length 453;  
Best Local Similarity 55.6%; Pred. No. 28;  
Matches 10; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

QY 4 WAAQRYGR--ELRRMSDE 19  
Db 65 WASERQREELRLRLASE 82

RESULT 12  
S40376  
Ig kappa chain - human  
C:Species: *Homo sapiens* (man)  
C:Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40376  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341  
A:Accession: S40376  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-134 <KLE>  
A:Cross-references: EMBL:X72486; NID:g441440; PIDN:CAA51154.1; PID:g441441  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-113/Domain: immunoglobulin homology <IM>

Query Match 32.8%; Score 48.5; DB 2; Length 134;  
Best Local Similarity 38.2%; Pred. No. 9.7;

Matches 13; Conservative 1; Mismatches 9; Indels 11; Gaps 1;

QY 4 WAAQRYGRELRM-----SDEFECSFKG 26  
Db 58 WFRQPRGSRRLIYNVSKRDSGVSDRFSGSG 91

RESULT 13  
T02975  
annexin p35 - maize  
C:Species: *Zea mays* (maize)  
C:Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 21-Jul-2000  
C:Accession: T02975  
R:Battey, N.H.; James, N.C.; Greenland, A.J.  
Plant Physiol. 112, 1391-1396, 1996  
A:Title: CDNA isolation and gene expression of maize annexins P33 and P35.  
A:Reference number: Z14796; MUID:97092863; PMID:8938425  
A:Accession: T02975  
A:Status: preliminary; translated from GB/EMBL/DDBU  
A:Molecule type: mRNA  
A:Residues: 1-314 <BAT>  
A:Cross-references: EMBL:X98245; NID:gl370602; PIDN:CAA66901.1; PID:gl370603  
A:Experimental source: cultivar clipper; root tip  
C:Superfamily: annexin I; annexin repeat homology  
F:14-85/Domain: annexin repeat homology <AXR>

Query Match 32.8%; Score 48.5; DB 2; Length 314;  
Best Local Similarity 47.6%; Pred. No. 23;  
Matches 10; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 6 AQRGREGRELRMSDEFFGSFK 25  
Db 54 ABAYGKELLRALGDEIHGKFE 74

RESULT 14  
C36365  
transforming protein homolog MRAS3 - *Rhizomucor racemosus*  
C:Species: *Rhizomucor racemosus*  
C:Date: 28-Mar-1991 #sequence\_revision 28-Mar-1991 #text\_change 19-Jan-2001  
C:Accession: C36365  
R:Casale, W.L.; McConnell, D.G.; Wang, S.Y.; Lee, Y.J.; Linz, J.E.  
Mol. Cell. Biol. 10, 6654-6663, 1990  
A:Title: Expression of a gene family in the dimorphic fungus *Mucor racemosus* which encodes a protein homologous to the human MRAS3 protein.  
A:Reference number: A36365; MUID:91061774; PMID:1701021  
A:Accession: C36365  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-206 <CAS>  
A:Cross-references: GB:M55177  
C:Superfamily: ras transforming protein; translation elongation factor Tu homology  
C:Keywords: GTP binding; nucleotide binding; P-loop  
F:11-126/Domain: translation elongation factor Tu homology <ETU>  
F:17-24/Region: nucleotide-binding motif A (P-loop)  
F:123-126/Region: GTP-binding NKXD motif  
F:153-155/Region: GTP-binding SAK/L motif  
F:23,24,42,123,124,126,153/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser) #

Query Match 32.4%; Score 48; DB 2; Length 206;  
Best Local Similarity 62.5%; Pred. No. 18;  
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 11 RELRRMSDEFFGSFKG 26  
Db 169 REIRRMKEQEGRSKG 184

RESULT 15  
F72289  
oxidoreductase, sol/devB family - *Thermotoga maritima* (strain MS80)  
C:Species: *Thermotoga maritima*  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000  
C:Accession: F72289

R; Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey  
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.  
 C.M.  
 Nature 399, 323-329, 1999  
 A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq  
 A:Reference number: A72200; MUID:99287316; PMID:10360571  
 A:Accession: F72289  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-220 <ARN>  
 A:Cross-references: GB:AE001772; GB:AE000512; NID:g4981693; PIDN:AAD36230.1; PID:g498170  
 A:Experimental source: strain MSB8  
 C:Genetics:  
 A:Gene: TW1154  
 C:Superfamily: yeast SOL3 protein

Query Match 32.4%; Score 48; DB 2; Length 220;  
Best Local Similarity 34.8%; Pred. No. 19;  
Matches 8; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

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QY      5 AAQRYGRELRRMSDEFEGSFKGL 27
      | : : | | | : | : | : | : | :
Db     111 ACEKYEREIRSATDQFDLAILGM 133
```

Search completed: September 15, 2003, 17:27:03  
Job time : 12.6 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: September 15, 2003, 17:16:55 ; Search time 6.6 Seconds  
(without alignments)  
199.507 Million cell updates/sec

Title: US-09-544-664-55  
Perfect score: 148  
Sequence: 1 KNLWAAQRYGRELRRMSDEFGFKGLX 28

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	138	93.2	204	1	BAD_MOUSE
2	138	93.2	205	1	BAD_RAT
3	114	77.0	168	1	BAD_HUMAN
4	54	36.5	946	1	ITH2_MESAU
5	53	35.8	946	1	ITH2_MOUSE
6	52.5	35.5	506	1	MATK_LEDPA
7	52.5	35.5	506	1	MATK_RHOPR
8	52.5	35.5	506	1	MATK_RHOTS
9	52	35.1	370	1	AROG_YEAST
10	51	34.5	232	1	AP3_ARATH
11	51	34.5	851	1	CE05_MOUSE
12	50	33.8	1378	1	RPOB_CAMJE
13	49	33.1	453	1	RWOC_PSEAE
14	48	32.4	205	1	RAS3_RHIRA
15	48	32.4	220	1	6PGL_THEMA
16	48	32.4	519	1	THRC_SOLTU
17	48	32.4	526	1	THRC_ARATH
18	47.5	32.1	334	1	FKRA_CALPA
19	47.5	32.1	507	1	MATK_LOIPR
20	47	31.8	198	1	BIM_MOUSE
21	47	31.8	287	1	PRFA_POLPE
22	46.5	31.4	429	1	FMK2_ATEL
23	46.5	31.4	435	1	FMK1_ATEL
24	46	31.1	946	1	ITH2_HUMAN
25	45.5	30.7	1014	1	UVRA_STRCO
26	45	30.4	273	1	P8BO_ANASP
27	45	30.4	328	1	SNF4_KLULA
28	45	30.4	590	1	DCOA_SALTY
29	45	30.4	595	1	DCOA_KLEPN
30	45	30.4	653	1	HT2A_HUMAN
31	45	30.4	865	1	ENV_SIVAT
32	45	30.4	915	1	CE05_HUMAN
33	45	30.4	1535	1	LMML_CAEEL

34	45	30.4	5596	1	MDN1_HUMAN	Q9nu22 homo sapien
35	44.5	30.1	506	1	MATK_GAUPR	Q95g10 gaultheria
36	44.5	30.1	512	1	MATK_LILTS	Q9gi33 lillium tsin
37	44.5	30.1	907	1	NUOG_ECOLI	P33602 escherichia
38	44.5	30.1	907	1	NUOG_SALTY	P33900 salmonella
39	44	29.7	196	1	BIM_MOUSE	O54918 mus musculus
40	44	29.7	196	1	BIM_RAT	O88498 rattus norv
41	44	29.7	262	1	END8_ECO57	O8x9c6 escherichia
42	44	29.7	262	1	END8_ECOLI	P50465 escherichia
43	44	29.7	262	1	END8_SALTY	O8z8d2 salmonella
44	44	29.7	262	1	END8_SALTY	O8zqu6 salmonella
45	44	29.7	629	1	SYM_THEMA	O33925 thermotoga

ALIGNMENTS

RESULT 1  
BAD\_MOUSE  
ID BAD\_MOUSE STANDARD; PRT; 204 AA.  
AC Q61337;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component 6) (Bcl-xL/Bcl-2 associated death promoter).  
GN BAD OR BCL6.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain, and Thymus;  
RX MEDLINE=95136361; PubMed=7834748;  
RA Yang E., Zha J., Jockel J., Boise L.H., Thompson C.B., Korsmeyer S.J.;  
RT "Bad, a heterodimeric partner for Bcl-XL and Bcl-2, displaces Bax and promotes cell death.";  
RL Cell 80:285-291(1995).  
RN [2]  
RP PHOSPHORYLATION, AND MUTAGENESIS OF SER-112 AND SER-136.  
RX MEDLINE=98022383; PubMed=9381178;  
RA Del Peso L., Gonzalez-Garcia M., Page C., Herrera R., Nunez G.;  
RT "Interleukin-3-induced phosphorylation of BAD through the protein kinase Akt.";  
RL Science 278:687-689(1997).  
RN [3]  
RP MUTAGENESIS OF SERINE RESIDUES.  
RX MEDLINE=20403302; PubMed=10949026;  
RA Datta S.R., Katsov A., Hu L., Petros A., Fesik S.W., Yaffe M.B., Greenberg M.E.;  
RT "14-3-3 proteins and survival kinases cooperate to inactivate BAD by BH3 domain phosphorylation.";  
RL Mol. Cell 6:41-51(2000).  
CC -I- FUNCTION: Promotes cell death. Successfully competes for the binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level of heterodimerization of these proteins with BAX. Can reverse the death repressor activity of Bcl-x(L), but not that of Bcl-2. Appears to act as a link between growth factor receptor signaling and the apoptotic pathways.  
CC -I- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-x(L), Bcl-2 and Bcl-w. Also binds protein S100A10 (by similarity). The Ser-112/Ser-136 phosphorylated form binds 14-3-3 proteins.  
CC -I- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon phosphorylation, locates to the cytoplasm.  
CC -I- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the Bcl-2 family.  
CC -I- PTM: Phosphorylated on Ser-112 in response to survival stimuli. Subsequent phosphorylation on Ser-136 promotes heterodimerization with 14-3-3 proteins. This interaction then facilitates the phosphorylation at Ser-155, a site within the BH3 domain, leading to the release of Bcl-x(L) and the promotion of cell survival.



Query Match 93.2%; Score 138; DB 1; Length 205;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-13;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NLWAAQRYGRELRRMSDFEGSFKGL 27  
 Db 141 NLWAAQRYGRELRRMSDFEGSFKGL 166

RESULT 3  
 BAD\_HUMAN STANDARD; PRT; 168 AA.  
 ID Q92934; O14803;  
 AC 01-NOV-1997 (Rel. 35, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component 6) (Bcl-XL/Bcl-2 associated death promoter) (BCL2-like 8 protein).  
 GN BAD OR BCL2L8.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Yin D.X., Li Z., Huang B., Chen S., Zhou H.;  
 RT "A human protein that interacts with Bcl-2 and have homology to mouse BAD.";  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A., AND PHOSPHORYLATION BY RAF-1.  
 RX MEDLINE=97083574; PubMed=8929532;  
 RA Wang H.-G., Rapp U.R., Reed J.C.;  
 RT "Bcl-2 targets the protein kinase Raf-1 to mitochondria.";  
 RL Cell 87:629-638(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Takayama S., Reed J.C.;  
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A., AND DIMERIZATION.  
 RX TISSUE=Bone marrow;  
 MEDLINE=98049554; PubMed=9388232;  
 RA Chang S., Weeks S., Fritz L.C., Oltersdorf T.;  
 RT "Dimerization properties of human BAD.";  
 RL J. Biol. Chem. 272:30866-30872(1997).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshitoki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fritch D., Winkler D., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzyzanski M.I., Skalska U., Marra M.A.;  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [6]

RP STRUCTURE BY NMR OF 103-127.  
 RX MEDLINE=21073561; PubMed=11206074;  
 RA Petros A.M., Nettesheim D.G., Wang Y., Olejniczak E.T., Meadows R.P., Mack J., Swift K., Matayoshi E.D., Zhang H., Thompson C.B., Esik S.W.;  
 RT "Rationale for Bcl-xL/Bad peptide complex formation from structure, mutagenesis, and biophysical studies.";  
 RL Protein Sci. 9:2528-2534(2000).  
 CC -!- FUNCTION: Promotes cell death. Successfully competes for the binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level of heterodimerization of these proteins with BAX. Can reverse the death repressor activity of Bcl-x(L), but not that of Bcl-2 (By similarity). Appears to act as a link between growth factor receptor signaling and the apoptotic pathways.  
 CC -!- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-x(L), Bcl-2 and Bcl-w. Also binds protein S100A10 (By similarity). The Ser-75/Ser-99 phosphorylated form binds 14-3-3 proteins (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon phosphorylation, locates to the cytoplasm.  
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.  
 CC -!- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the Bcl-2 family.  
 CC -!- PTM: Phosphorylated on Ser-75 in response to survival stimuli. Subsequent phosphorylation on Ser-99 promotes heterodimerization with 14-3-3 proteins. This interaction then facilitates the phosphorylation at Ser-118, a site within the BH3 domain, leading to the release of Bcl-x(L) and the promotion of cell survival. Ser-99 is the major site of AKT/PKB phosphorylation, Ser-118 the major site of protein kinase A (CAK) phosphorylation (By similarity).  
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.  
 CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -!- CAUTION: Ref.1 sequence differs from that shown due to frameshifts in position 64 and 91.  
 CC -----  
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 CC -----  
 CC EMBL; U66879; AAB36516.1; ALT\_FRAME.  
 CC EMBL; AF021792; AAB72092.1; -.  
 CC EMBL; AF031523; AAB88124.1; -.  
 CC EMBL; BC001901; AAB01901.1; -.  
 CC PDB; 1G5J; 07-FEB-01.  
 CC Genew; HGNC:936; BAD.  
 CC MTM; 503167; -.  
 CC GO; GO:0005737; Cytoplasm; NAS.  
 CC GO; GO:0005741; Mitochondrial outer membrane; NAS.  
 CC GO; GO:0005515; Protein binding activity; NAS.  
 CC GO; GO:0008632; Apoptotic program; TAS.  
 CC GO; GO:0006917; Induction of apoptosis; NAS.  
 CC InterPro; IPR000712; BCL2-BH.  
 CC PROSITE; PS01259; BH3; FALSE\_NEG.  
 CC Apoptosis; Phosphorylation; Polymorphism; 3D-structure.  
 CC DOMAIN 110 124 BH3.  
 CC MOD\_RES 75 75 PHOSPHORYLATION (BY PKA AND PKB) (BY SIMILARITY).  
 CC MOD\_RES 99 99 PHOSPHORYLATION (BY PKA AND PKB) (BY SIMILARITY).  
 CC MOD\_RES 118 118 PHOSPHORYLATION (BY PKA AND PKB) (BY SIMILARITY).  
 CC VARIANT 107 107 A -> S (in dbSNP:3729933).  
 CC HELIX 106 121 /FTid-VAR\_015380.  
 CC SEQUENCE 168 AA; 18392 MW; 69FD8D27DDEE3241 CRC64;  
 Query Match 77.0%; Score 114; DB 1; Length 168;

DR SMART; SM00609; VIT; 1.

CC and between

CC and between

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CC -----
DR EMBL; X70392; CAA49842.1; -.
DR PIR; S54354; S54354.
DR MGI; MGI:96619; Itih2.
DR InterPro; IPR006587; VIT.
DR InterPro; IPR002035; VME_A.
DR Pfam; PF00092; vwa; 1.
DR SMART; SM00609; VIT; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS00234; VWFA; 1.
KW Serine protease inhibitor; Repeat; Signal; Multigene family;
KW Glycoprotein.
FT SIGNAL 1 18 POTENTIAL.
FT PROPEP 19 54 BY SIMILARITY.
FT CHAIN 55 702 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN
H2.
FT PROPEP 703 946 BY SIMILARITY.
FT DOMAIN 308 468 VWFA.
FT CARBOHYD 118 118 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT BINDING 702 702 CHONDROITIN 4-SULFATE, CROSS-LINK SITE
(BY SIMILARITY).
FT SEQUENCE 946 AA; 105927 MW; 40DB6716433ED9DC CRC64;
Query Match 35.8%; Score 53; DB 1; Length 946;
Best Local Similarity 34.6%; Pred. No. 6;
Matches 9; Conservative 5; Mismatches 12; Indels 0; Gaps 0;
QY 2 NLWAAQRYGRELRRMSDFEGSGKL 27
Db 212 NWLIEPQGMRFHLVPTDFEGHFGV 237
RESULT 6
MATK_LEDPA
ID MATK_LEDPA STANDARD; PRT; 506 AA.
AC O62992;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Maturase K (Intron maturase).
GN MATK.
OS Leducum palustre (Wild rosemary).
OG Chloroplast.
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
CC Asteridae; Ericales; Ericaceae; Ericoidae; Rhodoreae; Rhododendron.
CC NCBI_TaxID=75583;
RN [1]
RP SEQUENCE FROM N.A.
RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
RA Yukawa T.;
RT "Investigation of sectional relationships in the genus
RT Rhododendron (Ericaceae) based on matk sequences.";
RL Shokubutsu Kenkyu Zasshi 73:143-154(1998).
CC -!- FUNCTION: Probably assists in splicing chloroplast group II
CC introns (By similarity).
CC -!- SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK
CC SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X70392; CAA49842.1; -.
DR PIR; S54354; S54354.
DR MGI; MGI:96619; Itih2.
DR InterPro; IPR006587; VIT.
DR InterPro; IPR002035; VME_A.
DR Pfam; PF00092; vwa; 1.
DR SMART; SM00609; VIT; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS00234; VWFA; 1.
KW Serine protease inhibitor; Repeat; Signal; Multigene family;
KW Glycoprotein.
FT SIGNAL 1 18 POTENTIAL.
FT PROPEP 19 54 BY SIMILARITY.
FT CHAIN 55 702 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN
H2.
FT PROPEP 703 946 BY SIMILARITY.
FT DOMAIN 308 468 VWFA.
FT CARBOHYD 118 118 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT BINDING 702 702 CHONDROITIN 4-SULFATE, CROSS-LINK SITE
(BY SIMILARITY).
FT SEQUENCE 946 AA; 105927 MW; 40DB6716433ED9DC CRC64;
Query Match 35.8%; Score 53; DB 1; Length 946;
Best Local Similarity 34.6%; Pred. No. 6;
Matches 9; Conservative 5; Mismatches 12; Indels 0; Gaps 0;
QY 2 NLWAAQRYGRELRRMSDFEGSGKL 27
Db 212 NWLIEPQGMRFHLVPTDFEGHFGV 237

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DR EMBL; AB012751; BAA25872.1; -.
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_maturase2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW mRNA processing; Chloroplast.
SQ SEQUENCE 506 AA; 60412 MW; CFEA926307DAC85E CRC64;
Query Match 35.5%; Score 52.5; DB 1; Length 506;
Best Local Similarity 37.5%; Pred. No. 3.6;
Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;
QY 1 KNLWAA-----QRYGRELRRMSDFEGSGK 25
Db 391 KPWWAALSDSDIIFRGRIYRNLSHYSGSLK 422
RESULT 7
MATK_RHOFR
ID MATK_RHOFR STANDARD; PRT; 506 AA.
AC O62984;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Maturase K (Intron maturase).
GN MATK.
OS Rhododendron ferrugineum (Alpenrose).
OG Chloroplast.
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
CC Asteridae; Ericales; Ericaceae; Ericoidae; Rhodoreae; Rhododendron.
CC NCBI_TaxID=49622;
RN [1]
RP SEQUENCE FROM N.A.
RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
RA Yukawa T.;
RT "Investigation of sectional relationships in the genus
RT Rhododendron (Ericaceae) based on matk sequences.";
RL Shokubutsu Kenkyu Zasshi 73:143-154(1998).
CC -!- FUNCTION: Probably assists in splicing chloroplast group II
CC introns (By similarity).
CC -!- SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK
CC SUBFAMILY.
CC -----
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CC -----
DR EMBL; AB012741; BAA25862.1; -.
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_maturase2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW mRNA processing; Chloroplast.
SQ SEQUENCE 506 AA; 60534 MW; ADA44B25E92436E8 CRC64;
Query Match 35.5%; Score 52.5; DB 1; Length 506;
Best Local Similarity 37.5%; Pred. No. 3.6;
Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;
QY 1 KNLWAA-----QRYGRELRRMSDFEGSGK 25
Db 391 KPWWAALSDSDIIFRGRIYRNLSHYSGSLK 422
RESULT 8
MATK_RHOTS
ID MATK_RHOTS STANDARD; PRT; 506 AA.
AC O62991;

```



OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Petal;  
RX MEDLINE=92154682; PubMed=1346756;  
RA Jack T., Brockman L.L., Meyerowitz E.M.;  
RT "The homeotic gene APETALA3 of Arabidopsis thaliana encodes a MADS  
RT box and is expressed in petals and stamens.";  
RL Cell 68:683-697(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Landsberg erecta;  
RX MEDLINE=95036018; PubMed=7948893;  
RA Okamoto H., Yano A., Shiraishi H., Okada K., Shimura Y.;  
RT "Genetic complementation of a floral homeotic mutation, apetal3,  
RT with an Arabidopsis thaliana gene homologous to DEFICIENS of  
RT Antirrhinum majus.";  
RL Plant Mol. Biol. 26:465-472(1994).  
RN [3]  
RP SEQUENCE FROM N.A. AND VARIANTS.  
RC STRAIN=cv. Bla-1, cv. Bretagny, cv. Bs-1, cv. Bu-0, cv. Bu-2,  
RC cv. Chi-1, cv. Co-1, cv. Columbia, cv. Corsacalla-1, cv. Cvi-0,  
RC cv. Gr-3, cv. JI-1, cv. Kas-1, cv. Kent, cv. Landsberg erecta,  
RC cv. Li-3, cv. Li-8, and cv. Lisse;  
RX MEDLINE=99126449; PubMed=9927474;  
RA Purugganan M.D., Suddith J.I.;  
RT "Molecular population genetics of floral homeotic loci: departures  
RT from the equilibrium-neutral model at the APETALA3 and PISTILLATA  
RT genes of Arabidopsis thaliana.";  
RL Genetics 151:839-848(1999).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RX MEDLINE=21016720; PubMed=11130713;  
RA Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unseld M.,  
RA Farmanb B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,  
RA Delseny M., Boutry M., Griwell L.A., Mache R., Puigdomenech P.,  
RA De Simone V., Choise N., Artiguenave F., Robert C., Brottier P.,  
RA Wincker P., Catolico L., Weissbach J., Saurin W., Quetier F.,  
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,  
RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,  
RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,  
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,  
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordsiek G.,  
RA Reichelt J., Scharfe M., Schoen O., Barges M., Terol J., Climent J.,  
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,  
RA Cooke R., Laude M., Berger-Llauro C., Purnelle B., Masuy D.,  
RA de Haan M., Maarise A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,  
RA Monfort A., Argirou A., Flores M., Liguori R., Vitale D.,  
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,  
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,  
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,  
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,  
RA Pai G., Millscher J., Sellers P., Gill J.E., Feldblyum T.V.,  
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,  
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,  
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,  
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,  
RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,  
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;  
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis  
RT thaliana.";  
RL Nature 408:820-822(2000).  
RN [5]  
RP SEQUENCE FROM N.A.  
RA Brover V., Troughan M., Alexandrov N., Lu Y.-P., Flavell R.,  
RA Feldmann K.;  
RT "Full-length cDNA from Arabidopsis thaliana.";  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;  
RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the  
RT SSP consortium (Salk/Stanford/PGECC).";  
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE OF 36-128 FROM N.A.  
RC STRAIN=cv. Columbia;  
RX MEDLINE=99311297; PubMed=10382288;  
RA Brunel D., Froger N., Pelletier G.;  
RT "Development of amplified consensus genetic markers (ACGM) in Brassica  
RT napus from Arabidopsis thaliana sequences of known biological  
RT function.";  
RL Genome 42:387-402(1999).  
RN [8]  
RP FUNCTION.  
RX PubMed=8565821;  
RA Krizek B.A., Meyerowitz E.M.;  
RT "The Arabidopsis homeotic genes APETALA3 and PISTILLATA are sufficient  
RT to provide the B class organ identity function.";  
RL Development 122:11-22(1996).  
RN [9]  
RP CHARACTERIZATION.  
RX PubMed=8643482;  
RA Riechmann J.B., Krizek B.A., Meyerowitz E.M.;  
RT "Dimerization specificity of Arabidopsis MADS domain homeotic proteins  
RT APETALA1, APETALA3, PISTILLATA, and AGAMOUS.";  
RL Proc. Natl. Acad. Sci. U.S.A. 93:4793-4798(1996).  
RN [10]  
RP GENETIC REGULATION.  
RX PubMed=11283333;  
RA Ng M., Yanofsky M.F.;  
RT "Activation of the Arabidopsis B class homeotic genes by APETALA1.";  
RL Plant Cell 13:739-753(2001).  
RN [11]  
RP CHARACTERIZATION.  
RX PubMed=11206550;  
RA Honma T., Goto K.;  
RT "Complexes of MADS-box proteins are sufficient to convert leaves into  
RT floral organs.";  
RL Nature 409:525-529(2001).  
CC -!- FUNCTION: Probable transcription factor involved in the genetic  
CC control of flower development. Is required for normal development  
CC of petals and stamens in the wild-type flower. Forms an  
CC heterodimer with PISTILLATA that is required for autoregulation of  
CC both AP3 and PI genes. AP3/PI heterodimer interacts with APETALA1  
CC or SPALATA3 to form a ternary complex that could be responsible  
CC for the regulation of the genes involved in the flower  
CC development.  
CC -!- SUBUNIT: Forms a heterodimer with PISTILLATA, capable of binding  
CC to CArG-box sequences. AP3/PI heterodimer binds AP1 or SEP3 to  
CC form complexes.  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- TISSUE SPECIFICITY: Expressed in petals and stamens.  
CC -!- INDUCTION: Positively regulated by the meristem identity proteins  
CC APETALA1 and LEAFY with the cooperation of UFO.  
CC -!- MISCELLANEOUS: Mutations in AP3 cause transformation of petals  
CC into sepals and stamens into carpels.  
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION  
CC FACTORS.  
CC -!- SIMILARITY: Contains 1 K-box dimerization domain.  
CC -----  
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CC -----  
DR EMBL; M86357; AAA32740.1; -.  
DR EMBL; D21125; BAR04665.1; -.  
DR EMBL; AF115798; AAD51887.1; -.  
DR EMBL; AF115799; AAD51888.1; -.



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RN [2]
RP SEQUENCE OF 338-1031 FROM N.A.
RX MEDLINE=96084944; PubMed=7489896;
RA Bustanante V.H., Puente J.L., Sanchez-Lopez F., Bobadilla M.,
RA Calva E.;
RT "Identification of Campylobacter jejuni and C.coli using the rpoB
RT gene and a cryptic DNA fragment from C.jejuni.";
RL Gene 165:1-8(1995).
CC -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC [RNA]{N}.
CC -!- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
CC ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
CC BETA' CHAIN.
CC -!- SIMILARITY: Belongs to the RNA polymerase beta chain family.
CC -----
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CC -----
DR EMBL; AL139075; CAB75116.1; -.
DR EMBL; X77304; CAA54509.1; -.
DR PIR; A81393; A81393.
DR PIR; S41868; S41868.
DR HSP; Q9KWU7; 1HOM.
DR InterPro; IPR001572; RNA_pol_B.
DR Pfam; PF04563; RNA_pol_Rpb2_1; 1.
DR Pfam; PF04561; RNA_pol_Rpb2_2; 1.
DR Pfam; PF04565; RNA_pol_Rpb2_3; 1.
DR Pfam; PF00562; RNA_pol_Rpb2_6; 1.
DR Pfam; PF04560; RNA_pol_Rpb2_7; 1.
DR PROSITE; PS01166; RNA_POL_BETA; 1.
KW Transferase; Transcription; DNA-directed RNA polymerase;
KW Complete proteome.
FT CONFLICT 338 347 NDLANGVDA -> NTLWMALMQP (IN REF. 2).
FT CONFLICT 558 558 A -> R (IN REF. 2).
FT CONFLICT 671 671 C -> S (IN REF. 2).
FT CONFLICT 691 691 A -> R (IN REF. 2).
SQ SEQUENCE 1378 AA; 155915 MW; AB7467C305028EB5 CRC64;

Query Match 33.8%; Score 50; DB 1; Length 1378;
Best Local Similarity 40.6%; Pred. No. 25;
Matches 13; Conservative 3; Mismatches 10; Indels 6; Gaps 2;

QY 3 LWAAQRYG--RELRRM---SDEFEGSPKGLK 28
:|: | | | | | | | | | | | | | |
Db 1306 VWALEAYGRAHTLREMLTIKSDVGEGRFSAYK 1337

RESULT 13
RMUC_PSEAE
ID RMUC_PSEAE STANDARD; PRT; 453 AA.
AC Q914U3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA recombination protein rmuc homolog.
GN RMUC OR PA1031.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,

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RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garby R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.A., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
CC -!- FUNCTION: Involved in DNA recombination (By similarity).
CC -!- SIMILARITY: BELONGS TO THE RMUC FAMILY.
CC -----
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CC -----
DR EMBL; AE004535; AAG04420.1; -.
DR PIR; E83517; E83517.
DR InterPro; IPR003798; DUF195.
DR Pfam; PF02646; Rmuc; 1.
KW DNA recombination; Coiled coil; Complete proteome.
FT DOMAIN 16 201 COILED COIL (POTENTIAL).
FT SEQUENCE 453 AA; 51539 MW; 1E7EA97E82EC5E4B CRC64;

Query Match 33.1%; Score 49; DB 1; Length 453;
Best Local Similarity 55.6%; Pred. No. 11;
Matches 10; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

QY 4 WAAQRYGR--ELRRMSDE 19
:|: | | | | | | | | | |
Db 65 WASERQGREELRLASE 82

RESULT 14
RAS3_RHRA
ID RAS3_RHRA STANDARD; PRT; 205 AA.
AC P22280;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ras-like protein 3.
GN RAS3.
OS Rhizomucor racemosus (Mucor circinelloides f. lusitanicus).
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
OC Mucor.
OX NCBI_TaxID=4841;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 1216B;
RX MEDLINE=91061774; PubMed=1701021;
RA Casale W.L., McConnell D.G., Wang S.-Y., Lee Y.-J., Linz J.E.;
RT "Expression of a gene family in the dimorphic fungus Mucor racemosus
RT which exhibits striking similarity to human ras genes.";
RL Mol. Cell. Biol. 10:6654-6663(1990).
CC -!- ENZYME REGULATION: ALTERNATE BETWEEN AN INACTIVE FORM BOUND TO GDP
CC AND AN ACTIVE FORM BOUND TO GTP. ACTIVATED BY A GUANINE
CC NUCLEOTIDE-EXCHANGE FACTOR (GEF) AND INACTIVATED BY A GTPASE-
CC ACTIVATING PROTEIN (GAP).
CC -!- SUBCELLULAR LOCATION: Plasma membrane.
CC -!- DEVELOPMENTAL STAGE: IN SPORULATING MYCELIUM AND MUCH LESS IN
CC GERMLING AND YEAST.
CC -!- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RAS FAMILY.
CC -----
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OM protein - protein search, using sw model

Run on: September 15, 2003, 17:17:31 ; Search time 30.4 Seconds  
(without alignments)  
237.680 Million cell updates/sec

Title: US-09-544-664-55  
Perfect score: 148  
Sequence: 1 KNLWAAQRYGRELRRMSDEFEGSPKGLK 28

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL23:\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriaph.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	91	61.5	146	13	Q9I9N2
2	57	38.5	471	17	Q8ZY71
3	53	35.8	196	16	Q8VJ53
4	53	35.8	223	16	Q10843
5	53	35.8	946	11	Q8K016
6	52.5	35.5	505	8	Q47148
7	52.5	35.5	506	8	Q47149
8	52.5	35.5	506	8	Q47171
9	52.5	35.5	506	8	Q63960
10	52.5	35.5	506	8	Q62982
11	52.5	35.5	506	8	Q62975
12	52.5	35.5	506	8	Q62972
13	52.5	35.5	506	8	Q62989
14	52.5	35.5	506	8	Q62978
15	52.5	35.5	506	8	Q47155
16	52.5	35.5	506	8	Q47152

17	52.5	35.5	506	8	Q47173	047173 rhododendro
18	52.5	35.5	506	8	Q62990	062990 rhododendro
19	52.5	35.5	506	8	Q62974	062974 rhododendro
20	52.5	35.5	506	8	Q62993	062993 menziesia m
21	52.5	35.5	506	8	Q47170	047170 rhododendro
22	52.5	35.5	506	8	Q47174	047174 rhododendro
23	52.5	35.5	506	8	Q62983	062983 rhododendro
24	52.5	35.5	506	8	Q62980	062980 rhododendro
25	52.5	35.5	506	8	Q62981	062981 rhododendro
26	52.5	35.5	506	8	Q62977	062977 rhododendro
27	52.5	35.5	506	8	Q47168	047168 menziesia p
28	52.5	35.5	506	8	Q62988	062988 rhododendro
29	52.5	35.5	506	8	Q62973	062973 rhododendro
30	52.5	35.5	506	8	Q62992	062992 ledum palus
31	52.5	35.5	506	8	Q47175	047175 rhododendro
32	52.5	35.5	506	8	Q8HSP1	Q8HSP1 rhododendro
33	52.5	35.5	506	8	Q8HSP0	Q8HSP0 rhododendro
34	52.5	35.5	506	8	Q8HSP9	Q8HSP9 rhododendro
35	52.5	35.5	506	8	Q8HSP8	Q8HSP8 rhododendro
36	52.5	35.5	506	8	Q8HSP7	Q8HSP7 rhododendro
37	52.5	35.5	506	8	Q8HSP6	Q8HSP6 rhododendro
38	52.5	35.5	506	8	Q8HSP5	Q8HSP5 rhododendro
39	52.5	35.5	506	8	Q8HSP4	Q8HSP4 rhododendro
40	52.5	35.5	507	8	Q62985	062985 rhododendro
41	52.5	35.5	507	8	Q62986	062986 rhododendro
42	52.5	35.5	508	8	Q62979	062979 rhododendro
43	51.5	34.8	506	8	Q47153	047153 rhododendro
44	51.5	34.8	506	8	Q47160	047160 rhododendro
45	51.5	34.8	506	8	Q8HSP4	Q8HSP4 rhododendro

#### ALIGNMENTS

RESULT 1  
Q9I9N2  
ID Q9I9N2 PRELIMINARY; PRT; 146 AA.  
AC Q9I9N2;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
DE Bad.  
GN BAD.  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20373792; PubMed=10917738;  
RA Inohara N., Nunez G.;  
RT "Genes with homology to mammalian apoptosis regulators identified in zebrafish."  
RL Cell Death Differ. 7:509-510(2000).  
DR EMBL; AF231017; AAF66962.2; -;  
DR HSSP; Q92934; 1G5J.  
DR ZFIN; ZDB-GENE-000616-1; bad.  
SQ SEQUENCE 146 AA; 16546 MW; 28A5650B5107ECB CRC64;  
Query Match 61.5%; Score 91; DB 13; Length 146;  
Best Local Similarity 61.5%; Pred. No. 2.1e-05;  
Matches 16; Conservative 6; Mismatches 4; Indels 0; Gaps 0;  
QY 3 LWAQRYGRELRRMSDEFEGSPKGLK 28  
||||:||||:||||:|  
Db 89 LWAQRYGRELRRMSDEFEGSPKGLK 114  
RESULT 2  
Q8ZY71  
ID Q8ZY71 PRELIMINARY; PRT; 471 AA.  
AC Q8ZY71;

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DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein PAE0922.
GN PAE0922.
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
NCBI_TaxID=13773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX PubMed=11792869;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT aerophilum."
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR EMBL; AE009793; AAL63125.1; -.
DR InterPro; IPR006638; Elp3.
DR InterPro; IPR000182; GCN5acetyltransf.
DR Pfam; PF00583; Acetyltransf; 1.
DR SMART; SM00729; Elp3; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 471 AA; 52952 MW; 3B1E3E8AE2EF0A CRC64;

Query Match 38.5%; Score 57; DB 17; Length 471;
Best Local Similarity 44.0%; Pred. No. 7;
Matches 11; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 4 WAAQRYGRLRMSDEFGSKGLK 28
Db | ||||| : : : | | | |
404 WQSGMGRLMRLAEETAGEFGALK 428

RESULT 3
Q8VJS3
ID Q8VJS3 PRELIMINARY; PRT; 196 AA.
AC Q8VJS3;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE IS1607, transposase.
GN MT2070.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
CX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE007058; AAK46348.1; -.
DR TIGR; MT2070; -.
DR InterPro; IPR003346; Transposase_20.
DR Pfam; PF02371; Transposase_20; 1.
SQ SEQUENCE 196 AA; 21349 MW; C145A8D836FD9C2D CRC64;

Query Match 35.8%; Score 53; DB 16; Length 196;
Best Local Similarity 58.8%; Pred. No. 10;
Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 NLWAAQRYGRELRRMSD 18
Db ||||| | : | |
134 NLWADRYNRAIARGHD 150

Query Match 35.8%; Score 53; DB 16; Length 223;
Best Local Similarity 58.8%; Pred. No. 12;
Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 NLWAAQRYGRELRRMSD 18
Db ||||| | : | |
165 NLWADRYNRAIARGHD 181

RESULT 5
Q8K016
ID Q8K016 PRELIMINARY; PRT; 946 AA.
AC Q8K016;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Inter-alpha trypsin inhibitor, heavy chain 2.
GN ITIH2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034341; AAH34341.1; -.
DR MGI; MGI:96619; Itih2.
DR InterPro; IPR006587; VIT.
DR InterPro; IPR002035; VWF_A.
DR SMART; SM00609; VIT; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS50234; VWF_A; 1.
SQ SEQUENCE 946 AA; 105945 MW; 8B17DBA71B85BC5C CRC64;

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RESULT 4
Q10843
ID Q10843 PRELIMINARY; PRT; 223 AA.
AC Q10843;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Hypothetical protein RV2014.
GN RV2014 OR MTCY39.03C.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
CX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
CC -!- SIMILARITY: TO M.PARATUBERCULOSIS IS900.
DR EMBL; Z74025; CAA98415.1; -.
DR Tuberculist; RV2014; -.
DR InterPro; IPR003346; Transposase_20.
DR Pfam; PF02371; Transposase_20; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 223 AA; 24132 MW; 70456750017FEF37 CRC64;

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Query Match 35.8%; Score 53; DB 16; Length 223;
Best Local Similarity 58.8%; Pred. No. 12;
Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 NLWAAQRYGRELRRMSD 18
Db ||||| | : | |
165 NLWADRYNRAIARGHD 181

RESULT 5
Q8K016
ID Q8K016 PRELIMINARY; PRT; 946 AA.
AC Q8K016;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Inter-alpha trypsin inhibitor, heavy chain 2.
GN ITIH2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034341; AAH34341.1; -.
DR MGI; MGI:96619; Itih2.
DR InterPro; IPR006587; VIT.
DR InterPro; IPR002035; VWF_A.
DR SMART; SM00609; VIT; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS50234; VWF_A; 1.
SQ SEQUENCE 946 AA; 105945 MW; 8B17DBA71B85BC5C CRC64;

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Query Match      35.8%; Score 53; DB 11; Length 946;
Best Local Similarity 34.6%; Pred. No. 58;
Matches 9; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 2 NLWAAQRYGRELRRMSDEFGSKGL 27
DB 212 NVWNEPQGRFLHPDTEFGHQGV 237

RESULT 6
O47148
ID O47148 PRELIMINARY; PRT; 505 AA.
AC O47148;
DT 01-JUN-1998 (TRENBLrel. 06, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Ribosomal maturase (Intron maturase) (Maturase K) (Fragment).
GN MATK.
OS Menziesia ciliocalyx.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Menziesia.
OX NCBI_TaxID=49154;
RN [1]
RP SEQUENCE FROM N.A.
RA Kron K.A.;
RT "Phylogenetics of Rhododendroideae (Ericaceae).";
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
CC INTRONS (BY SIMILARITY).
CC -!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
CC AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
CC MITOCHONDRIAL INTRONS.
DR EMBL; U61331; AAC15245.2; -.
DR InterPro; IPR000442; Intron_maturase2.
DR Pfam; PF01348; Intron_maturas2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW mRNA processing; Chloroplast.
FT NON_TER 1
SQ SEQUENCE 505 AA; 60233 MW; EE5F927AD2E57DE5 CRC64;

Query Match      35.5%; Score 52.5; DB 8; Length 505;
Best Local Similarity 37.5%; Pred. No. 34;
Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

QY 1 KNLWAA-----ORYGRELRRMSDEFGSKF 25
DB 390 KPVWAALSDSDIIEFGRIYRLSHYSGSLK 421

RESULT 7
O47149
ID O47149 PRELIMINARY; PRT; 506 AA.
AC O47149;
DT 01-JUN-1998 (TRENBLrel. 06, Created)
DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Ribosomal maturase (Intron maturase) (Maturase K).
GN MATK.
OS Rhododendron kiusianum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
OX NCBI_TaxID=49167;
RN [1]
RP SEQUENCE FROM N.A.
RA Kron K.A.;
RT "Phylogenetics of Rhododendroideae (Ericaceae).";
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II

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CC INTRONS (BY SIMILARITY).
CC -!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
CC AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
CC MITOCHONDRIAL INTRONS.
DR EMBL; U61332; AAB93753.1; -.
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_maturas2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW mRNA processing; Chloroplast.
SQ SEQUENCE 506 AA; 60502 MW; 0009EA88CD28549F CRC64;

Query Match      35.5%; Score 52.5; DB 8; Length 506;
Best Local Similarity 37.5%; Pred. No. 34;
Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

QY 1 KNLWAA-----ORYGRELRRMSDEFGSKF 25
DB 391 KPVWAALSDSDIIEFGRIYRLSHYSGSLK 422

RESULT 8
O47171
ID O47171 PRELIMINARY; PRT; 506 AA.
AC O47171;
DT 01-JUN-1998 (TRENBLrel. 06, Created)
DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Ribosomal maturase (Intron maturase) (Maturase K).
GN MATK.
OS Rhododendron edgeworthii.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
OX NCBI_TaxID=49162;
RN [1]
RP SEQUENCE FROM N.A.
RA Kron K.A.;
RT "Phylogenetics of Rhododendroideae (Ericaceae).";
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
CC INTRONS (BY SIMILARITY).
CC -!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
CC AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
CC MITOCHONDRIAL INTRONS.
DR EMBL; U61354; AAB93748.1; -.
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_maturas2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW mRNA processing; Chloroplast.
SQ SEQUENCE 506 AA; 60485 MW; 8A6353BFC5F4DC85 CRC64;

Query Match      35.5%; Score 52.5; DB 8; Length 506;
Best Local Similarity 37.5%; Pred. No. 34;
Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

QY 1 KNLWAA-----ORYGRELRRMSDEFGSKF 25
DB 391 KPVWAALSDSDIIEFGRIYRLSHYSGSLK 422

RESULT 9
O63960
ID O63960 PRELIMINARY; PRT; 506 AA.
AC O63960;
DT 01-AUG-1998 (TRENBLrel. 07, Created)
DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Ribosomal maturase (Intron maturase) (Maturase K).
GN MATK OR YCF14.
OS Rhododendron tashiroi, and

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OS Rhododendron farrerae.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Ericales; Ericaceae; Ericoidae; Rhodoreae; Rhododendron.
OX NCBI_TaxID=75582, 75580;
RN [1]
RP SEQUENCE FROM N.A.
RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
RA Yukawa T.;
RL J. Jpn. Bot. 0:0-0(1998).
CC -!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
CC INTRONS (BY SIMILARITY).
CC -!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS.
CC AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
CC MITOCHONDRIAL INTRONS.
DR EMBL; AB012749; BAA25870.1; -.
DR EMBL; AB012745; BAA25866.1; -.
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_maturase2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW mRNA processing; Chloroplast.
SQ SEQUENCE 506 AA; 60389 MW; DE0C07AE5608B787 CRC64;

Query Match 35.5%; Score 52.5; DB 8; Length 506;
Best Local Similarity 37.5%; Pred. No. 34;
Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

QY 1 KNLWAA-----QRYGRELRLRMSDEFGSGFK 25
Db 391 KPWWAALSDDIERFGRIRYLNLSHYSGSLK 422

RESULT 10
O62982
ID O62982 PRELIMINARY; PRT; 506 AA.
AC O62982;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Ribosomal maturase (Intron maturase) (Maturase K).
GN MATK.
OS Rhododendron nipponicum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Ericales; Ericaceae; Ericoidae; Rhodoreae; Rhododendron.
OX NCBI_TaxID=75577;
RN [1]
RP SEQUENCE FROM N.A.
RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
RA Yukawa T.;
RL J. Jpn. Bot. 0:0-0(1998).
CC -!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
CC INTRONS (BY SIMILARITY).
CC -!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS.
CC AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
CC MITOCHONDRIAL INTRONS.
DR EMBL; AB012739; BAA25860.1; -.
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_maturase2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW mRNA processing; Chloroplast.
SQ SEQUENCE 506 AA; 60419 MW; 1F95132CCF4F6B40 CRC64;

Query Match 35.5%; Score 52.5; DB 8; Length 506;
Best Local Similarity 37.5%; Pred. No. 34;
Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

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QY 1 KNLWAA-----QRYGRELRLRMSDEFGSGFK 25
Db 391 KPWWAALSDDIERFGRIRYLNLSHYSGSLK 422

RESULT 11
O62975
ID O62975 PRELIMINARY; PRT; 506 AA.
AC O62975;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Ribosomal maturase (Intron maturase) (Maturase K).
GN MATK.
OS Rhododendron ponticum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Ericales; Ericaceae; Ericoidae; Rhodoreae; Rhododendron.
OX NCBI_TaxID=49628;
RN [1]
RP SEQUENCE FROM N.A.
RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
RA Yukawa T.;
RL J. Jpn. Bot. 0:0-0(1998).
CC -!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
CC INTRONS (BY SIMILARITY).
CC -!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS.
CC AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
CC MITOCHONDRIAL INTRONS.
DR EMBL; AB012732; BAA25853.1; -.
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_maturase2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW mRNA processing; Chloroplast.
SQ SEQUENCE 506 AA; 60449 MW; 21DFF700B071B5B8 CRC64;

Query Match 35.5%; Score 52.5; DB 8; Length 506;
Best Local Similarity 37.5%; Pred. No. 34;
Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

QY 1 KNLWAA-----QRYGRELRLRMSDEFGSGFK 25
Db 391 KPWWAALSDDIERFGRIRYLNLSHYSGSLK 422

RESULT 12
O62972
ID O62972 PRELIMINARY; PRT; 506 AA.
AC O62972;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Ribosomal maturase (Intron maturase) (Maturase K).
GN MATK.
OS Rhododendron ovatum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Ericales; Ericaceae; Ericoidae; Rhodoreae; Rhododendron.
OX NCBI_TaxID=49169;
RN [1]
RP SEQUENCE FROM N.A.
RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
RA Yukawa T.;
RL J. Jpn. Bot. 0:0-0(1998).
CC -!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
CC INTRONS (BY SIMILARITY).

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CC -!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
CC AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
CC MITOCHONDRIAL INTRONS.
DR EMBL; AB012729; BAA25850.1; -.
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_maturas2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW mRNA processing; Chloroplast.
SQ SEQUENCE 506 AA; 60493 MW; D230E54B8C20FEF0 CRC64;

Query Match 35.5%; Score 52.5; DB 8; Length 506;
Best Local Similarity 37.5%; Pred. No. 34;
Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

QY 1 KNLWAA-----QRYGRELRRMSDEFEFSFK 25
| : ||| : ||| : ||| : ||| : |||
Db 391 KPVWAALSDSDIIEFRGRIYRNLSHYSGSLK 422

RESULT 13
O62989 PRELIMINARY; PRT; 506 AA.
AC O62989;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Ribosomal maturase (Intron maturase) (Maturase K).
GN MATK.
OS Rhododendron indicum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
OX NCBI_TaxID=75381;
RN [1]
RP SEQUENCE FROM N.A.
RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
RA Yukawa T.;
RT "Investigation of Sectional Relationships in the Genus
RT Rhododendron(Ericaceae) based on matK Sequences.";
RL J. Jpn. Bot. 0:0-0(1998).
CC -!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
CC INTRONS (BY SIMILARITY).
CC -!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
CC AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
CC MITOCHONDRIAL INTRONS.
DR EMBL; AB012747; BAA25868.1; -.
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_maturas2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW mRNA processing; Chloroplast.
SQ SEQUENCE 506 AA; 60489 MW; 6D38A1D4D6FEC9BF CRC64;

Query Match 35.5%; Score 52.5; DB 8; Length 506;
Best Local Similarity 37.5%; Pred. No. 34;
Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

QY 1 KNLWAA-----QRYGRELRRMSDEFEFSFK 25
| : ||| : ||| : ||| : ||| : |||
Db 391 KPVWAALSDSDIIEFRGRIYRNLSHYSGSLK 422

RESULT 14
O62978 PRELIMINARY; PRT; 506 AA.
AC O62978;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Ribosomal maturase (Intron maturase) (Maturase K).
GN MATK.

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OS Rhododendron canadense.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
OX NCBI_TaxID=49465;
RN [1]
RP SEQUENCE FROM N.A.
RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
RA Yukawa T.;
RT "Investigation of Sectional Relationships in the Genus
RT Rhododendron(Ericaceae) based on matK Sequences.";
RL J. Jpn. Bot. 0:0-0(1998).
CC -!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
CC INTRONS (BY SIMILARITY).
CC -!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
CC AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
CC MITOCHONDRIAL INTRONS.
DR EMBL; AB012735; BAA25856.1; -.
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_maturas2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW mRNA processing; Chloroplast.
SQ SEQUENCE 506 AA; 60350 MW; 5E832589ED64EA25 CRC64;

Query Match 35.5%; Score 52.5; DB 8; Length 506;
Best Local Similarity 37.5%; Pred. No. 34;
Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

QY 1 KNLWAA-----QRYGRELRRMSDEFEFSFK 25
| : ||| : ||| : ||| : ||| : |||
Db 391 KPVWAALSDSDIIEFRGRIYRNLSHYSGSLK 422

RESULT 15
O47155 PRELIMINARY; PRT; 506 AA.
AC O47155;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Ribosomal maturase (intron maturase) (Maturase K).
GN MATK.
OS Rhododendron hongkongense.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
OX NCBI_TaxID=49165;
RN [1]
RP SEQUENCE FROM N.A.
RA Kron K.A.;
RT "Phylogenetics of Rhododendroideae (Ericaceae).";
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
CC INTRONS (BY SIMILARITY).
CC -!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
CC AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
CC MITOCHONDRIAL INTRONS.
DR EMBL; U61338; AAB93751.1; -.
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_maturas2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW mRNA processing; Chloroplast.
SQ SEQUENCE 506 AA; 60406 MW; 4B5C675CE32218D8 CRC64;

Query Match 35.5%; Score 52.5; DB 8; Length 506;
Best Local Similarity 37.5%; Pred. No. 34;
Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

QY 1 KNLWAA-----QRYGRELRRMSDEFEFSFK 25

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Db 391 KPWAAALSDSDIERFGRIYRNLSHYSGSLK 422

Search completed: September 15, 2003, 17:25:50  
Job time : 31.4 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2003, 17:16:01 ; Search time 38.1857 Seconds  
(without alignments)  
112.231 Million cell updates/sec

Title: US-09-544-664-56  
Perfect score: 143  
Sequence: 1 KNLWAQRVGRLERRMSDEFSGPKGL (27)

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_19Jun03.\*

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- 2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*
- 3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*
- 4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*
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- 13: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*
- 14: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.\*
- 15: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.\*
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- 19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*
- 20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*
- 21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*
- 22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*
- 23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*
- 24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	143	100.0	27	21 AAB37056	Bcl2 polypeptide B
2	143	100.0	28	21 AAB37055	Bcl2 polypeptide B
3	138	96.5	26	21 AAB37001	Bcl2 polypeptide B
4	138	96.5	26	21 AAB37002	Bcl2 polypeptide B
5	138	96.5	27	21 AAB37003	Bcl2 polypeptide B
6	138	96.5	162	22 AAB70370	Shorter murine BAD
7	138	96.5	204	17 AAR95168	bcl-x(L)/bcl-2 ass
8	138	96.5	204	19 AAW61315	Murine BCL-XL/BCL-
9	138	96.5	204	19 AAW61316	Mutant BCL-XL/BCL-

10	138	96.5	204	19 AAW61317	Mutant BCL-XL/BCL-
11	138	96.5	204	19 AAW61318	Mutant BCL-XL/BCL-
12	138	96.5	204	19 AAW58832	Murine BAD protein
13	138	96.5	204	22 AAB70369	Longer murine BAD
14	138	96.5	204	24 ABR39082	Murine BAD protein
15	138	96.5	567	22 AAU00220	Bad-DTR apoptosis
16	114	79.7	24	23 AAU78627	Human BAD peptide
17	114	79.7	25	23 ABP56161	PTPC-interacting T
18	114	79.7	25	23 ABG78484	Mutant Bcl2 compet
19	114	79.7	25	23 ABG78493	Mutant Bcl2 compet
20	114	79.7	25	23 AAU78610	Human BAD peptide
21	114	79.7	25	23 AAU78620	Human BAD peptide
22	114	79.7	166	18 AAU32476	BBC6 protein for r
23	114	79.7	168	19 AAW55779	Human Bcl-XL/Bcl-2
24	114	79.7	168	21 AAB13512	Human cell prolife
25	114	79.7	168	22 AAB70368	Human BAD mutant a
26	114	79.7	168	22 AAB48287	Human BAD protein.
27	114	79.7	168	22 AAG67688	Amino acid sequenc
28	114	79.7	168	24 ABR39081	Human BAD protein
29	114	79.7	201	23 ABP41630	Human ovarian anti
30	113	79.0	23	17 AAR95166	bcl-x(L)/bcl-2 ass
31	111	77.6	25	23 ABG78490	Mutant Bcl2 compet
32	111	77.6	25	23 AAU78617	Human BAD peptide
33	110	76.9	25	23 ABG78488	Mutant Bcl2 compet
34	110	76.9	25	23 ABG78489	Mutant Bcl2 compet
35	110	76.9	25	23 AAU78615	Human BAD peptide
36	110	76.9	25	23 AAU78616	Human BAD peptide
37	109	76.2	23	23 AAU78628	Human BAD peptide
38	109	76.2	25	23 ABG78486	Mutant Bcl2 compet
39	109	76.2	25	23 ABG78492	Mutant Bcl2 compet
40	109	76.2	25	23 ABG78497	Mutant Bcl2 compet
41	109	76.2	25	23 AAU78612	Human BAD peptide
42	109	76.2	25	23 AAU78619	Human BAD peptide
43	109	76.2	25	23 AAU78624	Human BAD peptide
44	108	75.5	25	23 ABG78485	Mutant Bcl2 compet
45	108	75.5	25	23 AAU78611	Human BAD peptide

ALIGNMENTS

RESULT 1

AAB37056  
ID AAB37056 standard; peptide; 27 AA.  
XX  
AC AAB37056;  
XX  
DT 28-FEB-2001 (first entry)  
XX  
DE Bcl2 polypeptide BH3 domain peptide #56.

Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;  
cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;  
KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;  
KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;  
KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;  
KW stroke; myocardial infarction.

OS Homo sapiens.

XX WO200059526-A1.

XX 12-OCT-2000.

PD 06-APR-2000; 2000WC-US09352.

PF 07-APR-1999; 99US-0128202.

XX (UJJE-) UNIV JEFFERSON THOMAS.

XX Huang Z, Wang J, Zhang Z, Shan S, Lu Z;

XX WPI; 2000-679325/66.

XX New peptide conjugates for modulating apoptosis or for inhibiting B  
 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for  
 PT treating neurodegenerative disorders, stroke, or cancer  
 XX  
 PS Claim 18; Page 19; 74pp; English.  
 XX  
 CC The invention relates to a peptide conjugate having the formula:  
 CC (R-X)<sub>n</sub>-peptide where n = 1-10; X = C=O, when the R-X group is attached  
 CC to the N-terminus of the peptide, or a side chain of the peptide where  
 CC the functional group of the side chain is NH<sub>2</sub> or OH; or X = O or NH,  
 CC when the R-X group is attached to the C-terminus of the peptide, or a  
 CC side chain of the peptide, where the side chain functional group is COOH  
 CC or CONH<sub>2</sub>; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one  
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally  
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,  
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain  
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples  
 CC of the peptide portion of the conjugate. The peptides represent analogues  
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of  
 CC the BH3 domain of the cell death agonist Bad. The peptide conjugate is  
 CC useful for modulating apoptosis in the cells of a subject, or for  
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of  
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2  
 CC function. In particular, the peptide conjugate is useful for treating a  
 CC subject afflicted with a cancer characterized by cancer cells that  
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,  
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or  
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide  
 CC conjugate is also useful for treating disorders characterized by  
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired  
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.  
 XX Sequence 27 AA;  
 SQ

Query Match 100.0%; Score 143; DB 21; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 7.3e-15;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNLWAAQRYGRELRLMSDEFECSFKGL 27  
 |||||  
 Db 1 KNLWAAQRYGRELRLMSDEFECSFKGL 27

RESULT 2  
 AAB37055  
 ID AAB37055 standard; peptide: 28 AA.  
 AC AAB37055;  
 XX  
 DT 28-FEB-2001 (first entry)  
 XX  
 DE Bcl2 polypeptide BH3 domain peptide #55.  
 KW Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;  
 KW cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;  
 KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;  
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;  
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;  
 KW stroke; myocardial infarction.  
 XX  
 OS Homo sapiens.  
 XX WO200059526-A1.  
 PN 12-OCT-2000.  
 XX  
 PD 06-APR-2000; 2000WO-US09352.  
 PF 07-APR-1999; 99US-0128202.  
 XX  
 PR (UYJE-) UNIV JEFFERSON THOMAS.  
 PA  
 XX

PI Huang Z, Wang J, Zhang Z, Shan S, Lu Z;  
 XX WPI; 2000-679325/66.  
 DR  
 XX  
 PT New peptide conjugates for modulating apoptosis or for inhibiting B  
 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for  
 PT treating neurodegenerative disorders, stroke, or cancer  
 XX  
 PS Claim 18; Page 19; 74pp; English.  
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 CC The invention relates to a peptide conjugate having the formula:  
 CC (R-X)<sub>n</sub>-peptide where n = 1-10; X = C=O, when the R-X group is attached  
 CC to the N-terminus of the peptide, or a side chain of the peptide where  
 CC the functional group of the side chain is NH<sub>2</sub> or OH; or X = O or NH,  
 CC when the R-X group is attached to the C-terminus of the peptide, or a  
 CC side chain of the peptide, where the side chain functional group is COOH  
 CC or CONH<sub>2</sub>; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one  
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally  
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,  
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain  
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples  
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 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or  
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide  
 CC conjugate is also useful for treating disorders characterized by  
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired  
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.  
 XX Sequence 28 AA;  
 SQ

Query Match 100.0%; Score 143; DB 21; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 7.6e-15;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNLWAAQRYGRELRLMSDEFECSFKGL 27  
 |||||  
 Db 1 KNLWAAQRYGRELRLMSDEFECSFKGL 27

RESULT 3  
 AAB37001  
 ID AAB37001 standard; peptide: 26 AA.  
 AC AAB37001;  
 XX  
 DT 28-FEB-2001 (first entry)  
 XX  
 DE Bcl2 polypeptide BH3 domain peptide #1.  
 KW Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;  
 KW cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;  
 KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;  
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;  
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;  
 KW stroke; myocardial infarction.  
 XX  
 OS Homo sapiens.  
 XX WO200059526-A1.  
 PN 12-OCT-2000.  
 XX  
 PD 06-APR-2000; 2000WO-US09352.  
 PF 07-APR-1999; 99US-0128202.  
 XX  
 PR

XX PA (UYJE-) UNIV JEFFERSON THOMAS.  
 XX PI Huang Z, Wang J, Zhang Z, Shan S, Lu Z;  
 XX DR WPI; 2000-679325/66.  
 XX  
 XX New peptide conjugates for modulating apoptosis or for inhibiting B  
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 CC (R-X)n-peptide where n = 1-10; X = C=O, when the R-X group is attached  
 CC to the N-terminus of the peptide, or a side chain of the peptide where  
 CC the functional group of the side chain is NH2 or OH; or X = O or NH,  
 CC when the R-X group is attached to the C-terminus of the peptide, or a  
 CC side chain of the peptide, where the side chain functional group is COOH  
 CC or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylene containing one  
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally  
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,  
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain  
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples  
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of  
 CC the BH3 domain of the cell death agonist Bad. The peptide conjugate is  
 CC useful for modulating apoptosis in the cells of a subject, or for  
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 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2  
 CC function. In particular, the peptide conjugate is useful for treating a  
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 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or  
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide  
 CC conjugate is also useful for treating disorders characterized by  
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired  
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.  
 XX  
 XX Sequence 26 AA;  
 SQ  
 Query Match 96.5%; Score 138; DB 21; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-14;  
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 Db 1 NLWAAQRYGRELRRMSDEFEGSKGL 26  
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 ID AAB37002 standard; peptide; 26 AA.  
 XX  
 AC AAB37002;  
 XX  
 DT 28-FEB-2001 (first entry)  
 XX  
 DE Bcl2 polypeptide BH3 domain peptide #2.  
 XX  
 KW Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;  
 KW cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;  
 KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;  
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;  
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;  
 KW stroke; myocardial infarction.  
 XX  
 OS Homo sapiens.  
 XX WO200059526-A1.  
 XX  
 PD 12-OCT-2000.  
 XX

PF 06-APR-2000; 2000WO-US09352.  
 XX  
 PR 07-APR-1999; 99US-0128202.  
 XX  
 PA (UYJE-) UNIV JEFFERSON THOMAS.  
 XX  
 PI Huang Z, Wang J, Zhang Z, Shan S, Lu Z;  
 XX WPI; 2000-679325/66.  
 XX  
 XX New peptide conjugates for modulating apoptosis or for inhibiting B  
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 CC to the N-terminus of the peptide, or a side chain of the peptide where  
 CC the functional group of the side chain is NH2 or OH; or X = O or NH,  
 CC when the R-X group is attached to the C-terminus of the peptide, or a  
 CC side chain of the peptide, where the side chain functional group is COOH  
 CC or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylene containing one  
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally  
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,  
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 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples  
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 XX  
 XX Sequence 26 AA;  
 SQ  
 Query Match 96.5%; Score 138; DB 21; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-14;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 NLWAAQRYGRELRRMSDEFEGSKGL 27  
 Db 1 NLWAAQRYGRELRRMSDEFEGSKGL 26  
 RESULT 5  
 AAB37003  
 ID AAB37003 standard; peptide; 27 AA.  
 XX  
 AC AAB37003;  
 XX  
 DT 28-FEB-2001 (first entry)  
 XX  
 DE Bcl2 polypeptide BH3 domain peptide #3.  
 XX  
 KW Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;  
 KW cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;  
 KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;  
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;  
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;  
 KW stroke; myocardial infarction.  
 XX  
 OS Homo sapiens.  
 XX WO200059526-A1.  
 PN

XX PD 12-OCT-2000.  
 XX OS  
 PF 06-APR-2000; 2000WO-US09352.  
 XX PN  
 PR 07-APR-1999; 99US-0128202.  
 XX PD  
 XX (UYJE-) UNIV JEFFERSON THOMAS.  
 XX PA  
 XX Huang Z, Wang J, Zhang Z, Shan S, Lu Z;  
 PI WPI; 2000-679325/66.  
 XX DR  
 XX New peptide conjugates for modulating apoptosis or for inhibiting B  
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 CC the functional group of the side chain is NH<sub>2</sub> or OH; or X = O or NH,  
 CC when the R-X group is attached to the C-terminus of the peptide, or a  
 CC side chain of the peptide, where the side chain functional group is COOH  
 CC or CONH<sub>2</sub>; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl containing one  
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally  
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,  
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain  
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 CC conjugate is also useful for treating disorders characterized by  
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired  
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.  
 XX  
 SQ Sequence 27 AA;  
 Query Match 96.5%; Score 138; DB 21; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-14;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 NLWAAQRYGRELRRMSDEFGSPKGL 27  
 |||||  
 DB 1 NLWAAQRYGRELRRMSDEFGSPKGL 26  
 RESULT 6  
 AAB70370  
 ID AAB70370 standard; protein; 162 AA.  
 XX  
 AC AAB70370;  
 XX  
 DT 02-MAY-2001 (first entry)  
 XX  
 DE Shorter murine BAD mutant amino acid sequence SEQ ID NO:3.  
 XX  
 KW Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;  
 KW immunostimulant; neuroprotective; nontropic; antiischaemic; vulnary;  
 KW cytosolic; antiviral; antiarthritic; antiinflammatory; wound healing;  
 KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;  
 KW immunodeficiency disease; neurodegenerative disease; viral infection;  
 KW ischaemic cell death; reperfusion cell death; arthritis; infertility;  
 KW lymphoproliferative condition; inflammation; autoimmune disease.

XX Mus musculus.  
 OS Synthetic.  
 XX WO200110888-A1.  
 XX PD 15-FEB-2001.  
 XX 30-MAY-2000; 2000WO-US11864.  
 XX PF 28-MAY-1999; 99US-0136783.  
 PR (APOP-) APOPTOSIS TECHNOLOGY INC.  
 XX PA  
 XX Zhou X;  
 PI WPI; 2001-138734/14.  
 XX DR  
 XX New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,  
 PT useful for screening for candidate compounds which induce or inhibit  
 PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or  
 PT Ser113 -  
 XX  
 PS Claim 7; Page 148-149; 157pp; English.  
 XX  
 CC The present invention describes an isolated or synthetic polypeptide  
 CC (I) comprising a less than full length amino acid sequence of a mutant  
 CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its  
 CC fragment, which contains amino acid substitutions at Ser118 of a human  
 CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine  
 CC BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,  
 CC nontropic, antiischaemic, vulnary, cytostatic, antiviral,  
 CC antiarthritic, antiinflammatory and immunosuppressive activities, and  
 CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and  
 CC polynucleotides can be used for screening candidate compounds and drugs  
 CC for activity that promote cell survival or apoptosis. Other uses include  
 CC inducing or inhibiting apoptosis in a cell. Candidate compounds  
 CC identified and (mutant) BAD polypeptides are useful in treating  
 CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell  
 CC death, reperfusion cell death, wound healing, cancer, viral infections,  
 CC lymphoproliferative conditions, arthritis, infertility, inflammation and  
 CC autoimmune diseases. The present sequence represents a specifically  
 CC claimed shorter murine BAD mutant amino acid sequence from the present  
 CC invention.  
 XX  
 SQ Sequence 162 AA;  
 Query Match 96.5%; Score 138; DB 22; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-13;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 NLWAAQRYGRELRRMSDEFGSPKGL 27  
 |||||  
 DB 98 NLWAAQRYGRELRRMSDEFGSPKGL 123  
 RESULT 7  
 AAR95168  
 ID AAR95168 standard; Protein; 204 AA.  
 XX  
 AC AAR95168;  
 XX  
 DT 06-JAN-1997 (first entry)  
 XX  
 DE bcl-x(L)/bcl-2 associated death promoter protein.  
 XX  
 KW Epitope; murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke;  
 KW polypeptide; bcl-x; cell death; regulate; Bcl1; BH2; apoptotic cell death;  
 KW cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS;  
 KW neurodegenerative disease; senescence; ischaemia; neoplasia.  
 XX  
 OS Mus musculus.  
 XX

FH Key Location/Qualifiers  
 FT Region 147..149  
 FT /note= "BH1 conserved amino acids"  
 FT Region 191..192  
 FT /note= "BH2 conserved amino acids"  
 FT Domain 38..61  
 FT /note= "PEST sequence"  
 FT Domain 111..130  
 FT /note= "PEST sequence"  
 XX  
 XX  
 PN WO9613614-A1.  
 XX  
 XX 09-MAY-1996.  
 PD  
 XX  
 PF 31-OCT-1995; 95WO-US14246.  
 XX  
 XX 31-OCT-1994; 94US-0333565.  
 PR  
 XX (UNIW ) UNIV WASHINGTON.  
 PA  
 XX Korsmeyer SJ;  
 PI  
 XX WPI; 1996-251465/25.  
 DR N-PSDB; RAT29479.  
 DR  
 XX Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter -  
 PT useful to treat neoplasia and apoptosis and to identify agents  
 PT inhibiting its binding to bcl-2 or bcl-x(L) to form heteromultimers  
 XX  
 PS Claim 3; Fig 1; 130pp; English.  
 XX  
 CC This sequence represents the murine bcl-x(L)/bcl-2 associated death  
 CC promoter (Bad) gene. Bad is a 22.1 kD protein which interacts with  
 CC bcl-2 and bcl-x proteins and regulates cell death. It has homology  
 CC to the bcl-2-related family clustered in the BH1 and BH2 domain. Bad  
 CC has been found to hybridise to bcl-x(L) and bcl-2 in yeast two-hybrid  
 CC assays and in vivo in mammalian cells. Overexpressed Bad counters the  
 CC death inhibitory activity of bcl-x(L), but is much less effective at  
 CC countering the death inhibitory activity of bcl-2. Bad expression can  
 CC accelerate apoptotic cell death induced by cytokine deprivation in an  
 CC IL-3 dependent cell line expressing bcl-x(L), and its also counters the  
 CC death repressor activity of bcl-x(L). Bad competes with Bax for binding  
 CC to bcl-x(L). Bad may be used to identify agents which inhibit its  
 CC binding to bcl-2 or bcl-x(L) to form heterodimers. Such agents may be  
 CC used to treat neurodegenerative diseases, immunodeficiency diseases,  
 CC e.g. AIDS, senescence or ischaemia.  
 XX  
 SQ Sequence 204 AA;  
 Query Match 96.5%; Score 138; DB 17; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 4e-13;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 NLWAAQRYGRELRRMSDEFGSFKGL 27  
 ||||||||||||||||||||||||||||  
 Db 140 NLWAAQRYGRELRRMSDEFGSFKGL 165  
 RESULT 8  
 AAW61315  
 ID AAW61315 standard; Protein; 204 AA.  
 XX  
 AC AAW61315;  
 XX  
 XX 07-OCT-1998 (first entry)  
 DT  
 XX  
 DE Murine BCL-XL/BCL-2 associated cell death regulator.  
 XX  
 KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;  
 KW serine substituted mutant; apoptosis; cancer; viral infection.  
 XX  
 OS Mus sp.  
 OS  
 XX  
 PN

PN WO9817682-A1.  
 XX  
 XX 30-APR-1998.  
 PD  
 XX  
 PF 17-OCT-1997; 97WO-US19175.  
 XX  
 XX 18-OCT-1996; 96US-0733505.  
 PR  
 XX (UNIW ) UNIV WASHINGTON.  
 PA  
 XX Korsmeyer SJ;  
 PI  
 XX WPI; 1998-261422/23.  
 DR N-PSDB; AAV27833.  
 DR  
 XX New mutant BAD polypeptide with phosphorylatable serine replaced -  
 PT useful for, e.g. treating reduced apoptosis such as in cancer or  
 PT viral infection  
 XX  
 PS Claim 1; Fig 10; 95pp; English.  
 XX  
 CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell  
 CC death regulator) proteins, having an amino acid other than Ser at  
 CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The  
 CC present sequence is the murine BAD protein. Also described are: (1)  
 CC fragments of mutant BAD protein able to decrease cell viability; (2)  
 CC fusion proteins of mutant BAD with a heterologous polypeptide that  
 CC increases intracellular delivery. Mutant BAD proteins are used to treat  
 CC or prevent diseases associated with reduced apoptosis, e.g. cancer,  
 CC viral infection, lymphoproliferation, arthritis, infertility,  
 CC inflammation and autoimmune disease. Polynucleotide sequences encoding  
 CC mutant BAD proteins can be used similarly by gene therapy or to produce  
 CC transgenic animals for use as disease models or in drug screening. BAD  
 CC proteins phosphorylated at specified Ser are used to screen for enhancers  
 CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful  
 CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,  
 CC aging or ischaemic cell death. The apoptotic status of cells is  
 CC determined by measuring relative amounts of phosphorylated and non-  
 CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have  
 CC greater death-promoting activity than wild-type BAD which can become  
 CC phosphorylated on the specified Ser, forming a product that does not  
 CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family  
 CC proteins in the cytosol, thus promoting cell survival. The mutants with  
 CC Ser substituted cannot bind 14-3-3.  
 XX  
 SQ Sequence 204 AA;  
 Query Match 96.5%; Score 138; DB 19; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 4e-13;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 NLWAAQRYGRELRRMSDEFGSFKGL 27  
 ||||||||||||||||||||||||||||  
 Db 140 NLWAAQRYGRELRRMSDEFGSFKGL 165  
 RESULT 9  
 AAW61316  
 ID AAW61316 standard; Protein; 204 AA.  
 XX  
 AC AAW61316;  
 XX  
 XX 07-OCT-1998 (first entry)  
 DT  
 XX  
 DE Mutant BCL-XL/BCL-2 associated cell death regulator #1.  
 XX  
 KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;  
 KW serine substituted mutant; apoptosis; cancer; viral infection.  
 XX  
 OS Mus sp.  
 OS Synthetic.  
 XX  
 XX WO9817682-A1.  
 PN

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XX 30-APR-1998.
PD
XX
XX 17-OCT-1997; 97WO-US19175.
PF
XX
XX 18-OCT-1996; 96US-0733505.
PR
XX
XX (UNIW ) UNIV WASHINGTON.
PA
XX
XX Korsmeyer SJ;
PI
XX
XX WPI; 1998-261422/23.
DR
XX N-PSDB; AAV27834.
DR
XX
XX New mutant BAD polypeptide with phosphorylatable serine replaced -
PT useful for, e.g. treating reduced apoptosis such as in cancer or
PT viral infection
PT
XX
XX Claim 7; Page 59; 95pp; English.
PS
XX
XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
CC death regulator) proteins, having an amino acid other than Ser at
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
CC present sequence represents a mutant BAD protein. Also described are: (1)
CC fragments of mutant BAD protein able to decrease cell viability; (2)
CC fusion proteins of mutant BAD with a heterologous polypeptide that
CC increases intracellular delivery. Mutant BAD proteins are used to treat
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,
CC viral infection, lymphoproliferation, arthritis, infertility,
CC inflammation and autoimmune disease. Polynucleotide sequences encoding
CC mutant BAD proteins can be used similarly by gene therapy or to produce
CC transgenic animals for use as disease models or in drug screening. BAD
CC proteins phosphorylated at specified Ser are used to screen for enhancers
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
CC aging or ischaemic cell death. The apoptotic status of cells is
CC determined by measuring relative amounts of phosphorylated and non-
CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
CC greater death-promoting activity than wild-type BAD which can become
CC phosphorylated on the specified Ser, forming a product that does not
CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
CC proteins in the cytosol, thus promoting cell survival. The mutants with
CC Ser substituted cannot bind 14-3-3.
XX
XX Sequence 204 AA;
SQ
Query Match 96.5%; Score 138; DB 19; Length 204;
Best Local Similarity 100.0%; Pred. No. 4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 NLWAAQRYGRELRRMSDEFGSKGL 27
Db 140 NLWAAQRYGRELRRMSDEFGSKGL 165
RESULT 10
AAW61317
ID AAW61317 standard; Protein; 204 AA.
XX
XX AAW61317;
AC
XX
XX 07-OCT-1998 (first entry)
DT
XX
XX Mutant BCL-XL/BCL-2 associated cell death regulator #2.
DE
XX
XX Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
KW serine substituted mutant; apoptosis; cancer; viral infection.
KW
XX
XX Mus sp.
OS
XX Synthetic.
OS
XX
XX WO9817682-A1.
PN
XX
XX

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PD 30-APR-1998.
XX
XX 17-OCT-1997; 97WO-US19175.
PF
XX
XX 18-OCT-1996; 96US-0733505.
PR
XX
XX (UNIW ) UNIV WASHINGTON.
PA
XX
XX Korsmeyer SJ;
PI
XX
XX WPI; 1998-261422/23.
DR
XX N-PSDB; AAV27835.
DR
XX
XX New mutant BAD polypeptide with phosphorylatable serine replaced -
PT useful for, e.g. treating reduced apoptosis such as in cancer or
PT viral infection
PT
XX
XX Claim 7; Page 60; 95pp; English.
PS
XX
XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
CC death regulator) proteins, having an amino acid other than Ser at
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
CC present sequence represents a mutant BAD protein. Also described are: (1)
CC fragments of mutant BAD protein able to decrease cell viability; (2)
CC fusion proteins of mutant BAD with a heterologous polypeptide that
CC increases intracellular delivery. Mutant BAD proteins are used to treat
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,
CC viral infection, lymphoproliferation, arthritis, infertility,
CC inflammation and autoimmune disease. Polynucleotide sequences encoding
CC mutant BAD proteins can be used similarly by gene therapy or to produce
CC transgenic animals for use as disease models or in drug screening. BAD
CC proteins phosphorylated at specified Ser are used to screen for enhancers
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
CC aging or ischaemic cell death. The apoptotic status of cells is
CC determined by measuring relative amounts of phosphorylated and non-
CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
CC greater death-promoting activity than wild-type BAD which can become
CC phosphorylated on the specified Ser, forming a product that does not
CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
CC proteins in the cytosol, thus promoting cell survival. The mutants with
CC Ser substituted cannot bind 14-3-3.
XX
XX Sequence 204 AA;
SQ
Query Match 96.5%; Score 138; DB 19; Length 204;
Best Local Similarity 100.0%; Pred. No. 4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 NLWAAQRYGRELRRMSDEFGSKGL 27
Db 140 NLWAAQRYGRELRRMSDEFGSKGL 165
RESULT 11
AAW61318
ID AAW61318 standard; Protein; 204 AA.
XX
XX AAW61318;
AC
XX
XX 07-OCT-1998 (first entry)
DT
XX
XX Mutant BCL-XL/BCL-2 associated cell death regulator #3.
DE
XX
XX Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
KW serine substituted mutant; apoptosis; cancer; viral infection.
KW
XX
XX Mus sp.
OS
XX Synthetic.
OS
XX
XX WO9817682-A1.
PN
XX
XX 30-APR-1998.
PD

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XX PF 17-OCT-1997; 97WO-US19175.
XX PR 18-OCT-1996; 96US-0733505.
XX PA (UNIW ) UNIV WASHINGTON.
XX PI Kormsmeier SJ;
XX DR WPI; 1998-261422/23.
XX DR N-PSDB; AAV27836.
XX PT New mutant BAD polypeptide with phosphorylatable serine replaced -
XX useful for, e.g. treating reduced apoptosis such as in cancer or
XX viral infection
XX PS Claim 7; Page 60-61; 95pp; English.
XX CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
CC death regulator) proteins, having an amino acid other than Ser at
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
CC present sequence represents a mutant BAD protein. Also described are: (1)
CC fragments of mutant BAD protein able to decrease cell viability; (2)
CC fusion proteins of mutant BAD with a heterologous polypeptide that
CC increases intracellular delivery. Mutant BAD proteins are used to treat
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,
CC viral infection, lymphoproliferation, arthritis, infertility,
CC inflammation and autoimmune disease. Polynucleotide sequences encoding
CC mutant BAD proteins can be used similarly by gene therapy or to produce
CC transgenic animals for use as disease models or in drug screening. BAD
CC proteins phosphorylated at specified Ser are used to screen for enhancers
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
CC aging or ischaemic cell death. The apoptotic status of cells is
CC determined by measuring relative amounts of phosphorylated and non-
CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
CC greater death-promoting activity than wild-type BAD which can become
CC phosphorylated on the specified Ser, forming a product that does not
CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
CC proteins in the cytosol, thus promoting cell survival. The mutants with
CC Ser substituted cannot bind 14-3-3.
XX SQ Sequence 204 AA;
Query Match 96.5%; Score 138; DB 19; Length 204;
Best Local Similarity 100.0%; Pred. No. 4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
Db 140 NLWAAQRYGRELRRMSDEFEGSFKGL 165
RESULT 12
AAW58832
ID AAW58832 standard; protein; 204 AA.
AC AAW58832;
XX 23-JUL-1998 (first entry)
DT Murine BAD protein.
XX BAD protein; Bcl-XL/Bcl-2 associated cell death regulator; 14-3-3;
KW serine phosphorylation; post-translational modification; apoptosis;
KW signal transduction regulator; phosphoserine phosphatase; senescence;
KW immunodeficiency disease; neurodegenerative disease; infertility;
KW cancer, viral infection; lymphoproliferative condition; arthritis;
XX inflammation; autoimmune diseases.
XX Mus sp.
XX W09809643-A1.

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XX PD 12-MAR-1998.
XX PF 09-SEP-1997; 97WO-US15871.
XX PR 09-SEP-1996; 96US-0707868.
XX PA (UNIW ) UNIV WASHINGTON.
XX PI Kormsmeier SJ;
XX DR WPI; 1998-207049/18.
XX PT Serine-phosphorylated Bcl-X-l/Bcl-2 Associated cell Death regulator
XX polypeptide - useful for modulation of apoptosis associated with,
XX e.g. cancer and immunodeficiency diseases
XX PS Claim 3; Fig 8; 61pp; English.
XX CC This sequence represents a novel serine-phosphorylated protein, BAD
XX (Bcl-XL/Bcl-2 associated cell death regulator). The serine residue is
XX phosphorylated in a post-translational modification and allows binding
XX to the 14-3-3 protein which is a signal transduction regulator.
XX Modulators of phosphorylated BAD, which act through inhibition/activation
XX of a phosphoserine phosphatase, are useful for preventing/treating
XX increased/decreased apoptosis in a cell. The increased apoptosis may
XX result from immunodeficiency diseases, senescence, neurodegenerative
XX disease, ischaemic cell death, reperfusion cell death, infertility and
XX wound-healing. Decreased apoptosis may result from cancer, viral
XX infection, lymphoproliferative conditions, arthritis, infertility,
XX inflammation and autoimmune diseases. Measuring the amount of
XX phosphorylated compared to unphosphorylated BAD polypeptide and/or total
XX BAD in a cell is useful for determining the apoptotic state of a cell.
XX SQ Sequence 204 AA;
Query Match 96.5%; Score 138; DB 19; Length 204;
Best Local Similarity 100.0%; Pred. No. 4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
Db 140 NLWAAQRYGRELRRMSDEFEGSFKGL 165
RESULT 13
AAB70369
ID AAB70369 standard; protein; 204 AA.
XX AAB70369;
AC AAB70369;
XX 02-MAY-2001 (first entry)
DT Longer murine BAD mutant amino acid sequence SEQ ID NO:2.
XX Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
KW immunostimulant; neuroprotective; nootropic; antiischaemic; vulnerary;
KW cytosolic; antiviral; antiarthritic; antiinflammatory; wound healing;
KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;
KW immunodeficiency disease; neurodegenerative disease; viral infection;
KW ischaemic cell death; reperfusion cell death; arthritis; infertility;
KW lymphoproliferative condition; inflammation; autoimmune disease.
XX Mus musculus.
XX Synthetic.
XX W0200110888-A1.
XX 15-FEB-2001.
XX 30-MAY-2000; 2000WO-US11864.
XX 28-MAY-1999; 99US-0136783.

```

XX PA (APOP-) APOPTOSIS TECHNOLOGY INC.  
 XX PI Zhou X;  
 XX WPI; 2001-138734/14.  
 XX  
 XX New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,  
 PT useful for screening for candidate compounds which induce or inhibit  
 PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or  
 PT Ser113 -  
 XX  
 XX Claim 4; Page 148; 157pp; English.  
 XX  
 XX The present invention describes an isolated or synthetic polypeptide  
 CC (I) comprising a less than full length amino acid sequence of a mutant  
 CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its  
 CC fragment, which contains amino acid substitutions at Ser118 of a human  
 CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine  
 CC BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,  
 CC neurotropic, antiischaemic, vulnerary, cytostatic, antiviral,  
 CC antiarthritic, antiinflammatory and immunosuppressive activities, and  
 CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and  
 CC polynucleotides can be used for screening candidate compounds and drugs  
 CC for activity that promote cell survival or apoptosis. Other uses include  
 CC inducing or inhibiting apoptosis in a cell. Candidate compounds  
 CC identified and (mutant) BAD polypeptides are useful in treating  
 CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell  
 CC death, reperfusion cell death, wound healing, cancer, viral infections,  
 CC lymphoproliferative conditions, arthritis, infertility, inflammation and  
 CC autoimmune diseases. The present sequence represents a specifically  
 CC claimed longer murine BAD mutant amino acid sequence from the present  
 CC invention.  
 XX  
 XX Sequence 204 AA;  
 SQ  
 Query Match 96.5%; Score 138; DB 22; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 4e-13;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 NLWAAQRYGRELRRMSDEFGSFKGL 27  
 Db 140 NLWAAQRYGRELRRMSDEFGSFKGL 165  
 |||||  
 RESULT 14  
 ABR39082  
 ID ABR39082 standard; Protein; 204 AA.  
 XX  
 XX ABR39082;  
 AC  
 XX 10-MAY-2003 (first entry)  
 DT  
 XX Murine BAD protein SEQ ID NO:4.  
 DE  
 XX Murine; BAD; herpes simplex virus; HSV; US3; herpes virus; apoptosis;  
 KW virucide; infection.  
 KW  
 XX Mus musculus.  
 OS  
 XX WO2003012049-A2.  
 PN  
 PD 13-FEB-2003.  
 XX  
 XX 31-JUL-2002; 2002WO-US24177.  
 PF  
 XX 31-JUL-2001; 2001US-308929P.  
 PR  
 XX (UYCH-) UNIV CHICAGO.  
 PA  
 XX Munger J, Roizman B;  
 PI  
 XX WPI; 2003-248168/24.  
 DR

DR N-PSDB; ABZ81201.  
 XX  
 XX Inducing apoptosis in a cell infected with herpes simplex virus, HSV,  
 PT by administering to the cell, a composition comprising an agent that  
 PT inhibits phosphorylation of pro-apoptotic polypeptide BAD by HSV US3 -  
 XX  
 XX Claim 15; Page 168; 192pp; English.  
 XX  
 XX The present invention describes a method (M1) for inducing apoptosis in  
 CC a cell infected with herpes simplex virus (HSV), which comprises  
 CC administering to the cell, a composition having an agent that inhibits  
 CC phosphorylation of pro-apoptotic polypeptide BAD by HSV US3. Also  
 CC described is a method (M2) for treating a patient infected with HSV, by  
 CC administering to the patient, a composition comprising a peptide  
 CC comprising a sequence of 4-100 continuous amino acids of a 168 residue  
 CC amino acid sequence (see ABR39081), where the peptide comprises Ser112,  
 CC Ser135, or Ser155, or their combinations. BAD has virucide activity.  
 CC M1 is useful for inducing apoptosis in a cell infected with HSV, where  
 CC the cell is in a human. M2 is useful for treating a patient infected  
 CC with HSV. The present sequence represents murine BAD, which is used in  
 CC the exemplification of the present invention.  
 XX  
 XX Sequence 204 AA;  
 SQ  
 Query Match 96.5%; Score 138; DB 24; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 4e-13;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 NLWAAQRYGRELRRMSDEFGSFKGL 27  
 Db 140 NLWAAQRYGRELRRMSDEFGSFKGL 165  
 |||||  
 RESULT 15  
 AAU00220  
 ID AAU00220 standard; Protein; 567 AA.  
 XX  
 XX AAU00220;  
 AC  
 XX 31-MAY-2001 (first entry)  
 DT  
 XX Bad-DTRR apoptosis-modifying fusion protein.  
 DE  
 XX Mouse; Bad-DTRR; apoptosis; cancer; spinal muscular atrophy;  
 KW diphtheria toxin receptor binding domain; DTR; neoplasm; tumour;  
 KW hyper-proliferation; Alzheimer's disease; neurodegenerative disorder;  
 KW transient ischaemic neuronal injury; stroke; spinal cord injury;  
 KW Huntington's disease.  
 XX  
 XX Chimeric - Mus sp.  
 OS  
 OS Chimeric - Corynebacterium diphtheriae.  
 OS Chimeric - Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FT Region 3..12  
 FT /note= "10x histidine tag"  
 XX  
 XX WO200112661-A2.  
 PN  
 PD 22-FEB-2001.  
 XX  
 XX 15-AUG-2000; 2000WO-US22293.  
 PF  
 XX 16-AUG-1999; 99US-0149220.  
 PR  
 XX (HARD ) HARVARD COLLEGE.  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA  
 XX Youle RJ, Liu X, Collier RJ;  
 PI  
 XX WPI; 2001-218343/22.  
 DR  
 XX N-PSDB; AAS00248.  
 DR

PT Novel fusion protein for modifying apoptosis in target cell and  
PT reducing apoptosis after transient ischaemic neuronal injury, has two  
PT domains which targets protein to a cell and modifies apoptotic response  
PT of cell

XX  
PS Claim 4; Page 59-61; 65pp; English.

XX  
CC The sequence represents the amino acid sequence of Bad-DTRR apoptosis-  
CC modifying fusion protein comprising Bad gene sequence fused via a short  
CC linker to diphtheria toxin translocation domain (DTRR). The  
CC functional apoptosis-modifying fusion protein is capable of binding a  
CC target cell and integrating into or crossing a cellular membrane of the  
CC target cell. The apoptosis-modifying fusion protein comprises at least  
CC two domains: the DTR domain, which targets the fusion protein to the  
CC target cell and the Bcl-XL domain, which modifies an apoptotic response  
CC of the target cell. The fusion protein is useful for modifying  
CC (inhibiting or enhancing) apoptosis in a target cell, such as neuron,  
CC lymphocyte, cancer, neoplasm, macrophage, epithelial, stem, tumour or  
CC hyper-proliferative cell or an adipocyte. It is also useful for reducing  
CC apoptosis in a subject after transient ischaemic neuronal injury,  
CC especially spinal cord injury. The fusion protein may be used to treat  
CC various diseases and injury conditions through inhibition or enhancement  
CC of apoptotic cellular response, including neurodegenerative disorders  
CC such as Alzheimer's disease, Huntington's disease, spinal muscular  
CC atrophy, stroke episodes and unregulated cell growth as in tumours and  
CC various cancers. The apoptosis-modifying fusion protein can be delivered  
CC effectively throughout the body and targeted to selective tissue and  
CC cells.

XX  
SQ Sequence 567 AA;

Query Match 96.5%; Score 138; DB 22; Length 567;  
Best Local Similarity 100.0%; Pred. No. 1.2e-12;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NLWAAQRYGRELRRMSDEFEGSKGL 27  
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Db 161 NLWAAQRYGRELRRMSDEFEGSKGL 186

Search completed: September 15, 2003, 17:22:14  
Job time : 38.1857 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2003, 17:22:21 ; Search time 14.0786 Seconds  
(without alignments)  
81.144 Million cell updates/sec

Title: US-09-544-664-56  
Perfect score: 143  
Sequence: 1 KNLWAAQRYGRLRRMSDEFGSKGL 27

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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2	138	96.5	204	2	US-08-661-479-2
3	138	96.5	204	2	US-08-733-505A-1
4	138	96.5	204	2	US-08-733-505A-12
5	138	96.5	204	2	US-08-733-505A-13
6	138	96.5	204	2	US-08-733-505A-14
7	135	94.4	204	2	US-08-717-123-3
8	135	94.4	204	4	US-09-375-257-3
9	114	79.7	166	1	US-08-665-617-2
10	114	79.7	166	2	US-08-717-123-2
11	114	79.7	168	3	US-08-985-335-1
12	114	79.7	168	3	US-08-985-335-7
13	114	79.7	168	3	US-09-410-372-1
14	114	79.7	168	3	US-09-410-372-7
15	114	79.7	168	4	US-09-375-257-2
16	113	79.0	23	1	US-08-333-565-10
17	113	79.0	23	2	US-08-661-479-10
18	102	71.3	59	2	US-08-733-505A-55
19	102	71.3	59	2	US-08-733-505A-56
20	102	71.3	59	2	US-08-733-505A-57
21	102	71.3	59	2	US-08-733-505A-58
22	86	60.1	16	1	US-08-333-565-26
23	86	60.1	16	2	US-08-661-479-26
24	61	42.7	11	2	US-08-733-505A-34
25	61	42.7	11	2	US-08-706-741B-69
26	61	42.7	11	2	US-08-924-695A-69
27	51	35.7	66	2	US-08-867-087B-40

28	48.5	33.9	904	4	US-09-328-352-4656	Sequence 4656, Ap
29	46	32.2	610	4	US-09-252-991A-19594	Sequence 19594, A
30	46	32.2	946	3	US-09-074-579-3	Sequence 3, Appl
31	46	32.2	946	3	US-09-388-774-3	Sequence 3, Appl
32	46	32.2	946	4	US-09-546-153-1	Sequence 1, Appl
33	45.5	31.8	906	4	US-09-252-991A-31458	Sequence 31458, A
34	45	31.5	229	4	US-09-252-991A-23807	Sequence 23807, A
35	45	31.5	303	4	US-09-328-352-5164	Sequence 5164, Ap
36	45	31.5	356	4	US-09-235-103-2	Sequence 2, Appl
37	45	31.5	356	4	US-09-235-103-4	Sequence 4, Appl
38	45	31.5	1064	4	US-09-252-991A-17508	Sequence 17508, A
39	44.5	31.1	903	4	US-09-328-352-7449	Sequence 7449, Ap
40	44	30.8	125	4	US-09-651-656-27	Sequence 27, Appl
41	44	30.8	263	4	US-09-650-855-27	Sequence 27, Appl
42	44	30.8	263	4	US-09-252-991A-28581	Sequence 28581, A
43	44	30.8	277	4	US-09-206-551-20	Sequence 20, Appl
44	44	30.8	877	4	US-09-252-991A-18729	Sequence 18729, A
45	44	30.8	1125	4		

ALIGNMENTS

RESULT 1  
US-08-333-565-2  
; Sequence 2, Application US/08333565  
; Patent No. 5622852  
; GENERAL INFORMATION:  
; APPLICANT: KORMEYER, Stanley J.  
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH  
; TITLE OF INVENTION: REGULATOR  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/333,565  
; FILING DATE: 31-OCT-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 15726A-000700  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 204 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: Single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..204  
; OTHER INFORMATION: /note= "Deduced amino acid sequence  
; OTHER INFORMATION: of mouse BAD."  
US-08-333-565-2

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Best Local Similarity 100.0%; Pred. No. 1e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: CL-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-665-617-2

Query Match 79.7%; Score 114; DB 1; Length 166;
Best Local Similarity 91.7%; Pred. No. 4e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NLWAAQRYGRELRRMSDEFGSPK 25
Db 101 NLWAAQRYGRELRRMSDEFGVDSFK 124
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RESULT 10
US-08-717-123-2
; Sequence 2, Application US/08717123
; Patent No. 5965703
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
; TITLE OF INVENTION: Acids and Methods of Use
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/717,123
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 1929
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-717-123-2

Query Match 79.7%; Score 114; DB 2; Length 168;
Best Local Similarity 91.7%; Pred. No. 4e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NLWAAQRYGRELRRMSDEFGSPK 25
Db 103 NLWAAQRYGRELRRMSDEFGVDSFK 126
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RESULT 11
US-08-985-335-1
; Sequence 1, Application US/08985335
; Patent No. 6080847
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,335
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0421 US
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SYNORAB01
; CLONE: 358673
US-08-985-335-1

Query Match 79.7%; Score 114; DB 3; Length 168;
Best Local Similarity 91.7%; Pred. No. 4e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NLWAAQRYGRELRRMSDEFEGSFK 25
|||||
Db 103 NLWAAQRYGRELRRMSDEFVDSFK 126

RESULT 12
US-08-985-335-7
; Sequence 7, Application US/08985335
; Patent No. 6080847
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION
; NUMBER OF SEQUENCES: 9
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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,335
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0421 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1683637
US-08-985-335-7

Query Match 79.7%; Score 114; DB 3; Length 168;
Best Local Similarity 91.7%; Pred. No. 4e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NLWAAQRYGRELRRMSDEFEGSFK 25
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Db 103 NLWAAQRYGRELRRMSDEFVDSFK 126

RESULT 13
US-09-410-372-1
; Sequence 1, Application US/09410372
; Patent No. 6281334
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/410,372
; FILING DATE:
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; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/985,335  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0421 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 168 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: SYNORAB01  
; CLONE: 358673  
; US-09-410-372-1

Query Match 79.7%; Score 114; DB 3; Length 168;  
Best Local Similarity 91.7%; Pred. No. 4e-10;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NLWAAQRYGRELRRMSDEFEGSFK 25  
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Db 103 NLWAAQRYGRELRRMSDEFVDSFK 126

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US-09-410-372-7  
; Sequence 7, Application US/09410372  
; Patent No. 6281334  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Yue, Henry  
; APPLICANT: Lal, Preeti  
; APPLICANT: Shah, Purvi  
; APPLICANT: Corley, Neil C.  
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL  
; TITLE OF INVENTION: PROLIFERATION  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Dr.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/410,372  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/985,335  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0421 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 168 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single

; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 1683637  
; US-09-410-372-7

Query Match 79.7%; Score 114; DB 3; Length 168;  
Best Local Similarity 91.7%; Pred. No. 4e-10;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NLWAAQRYGRELRRMSDEFEGSFK 25  
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Db 103 NLWAAQRYGRELRRMSDEFVDSFK 126

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; Sequence 2, Application US/09375257  
; Patent No. 6504022  
; GENERAL INFORMATION:  
; APPLICANT: Horne, William A.  
; APPLICANT: Oltersdorf, Tilman  
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC  
; TITLE OF INVENTION: ACIDS AND METHODS OF USE  
; FILE REFERENCE: 480140.428D1  
; CURRENT APPLICATION NUMBER: US/09/375,257  
; CURRENT FILING DATE: 1999-08-16  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 168  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-375-257-2

Query Match 79.7%; Score 114; DB 4; Length 168;  
Best Local Similarity 91.7%; Pred. No. 4e-10;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NLWAAQRYGRELRRMSDEFEGSFK 25  
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Db 103 NLWAAQRYGRELRRMSDEFVDSFK 126

Search completed: September 15, 2003, 17:45:07  
Job time : 15.0786 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model ;  
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Title: US-09-544-664-56  
Perfect score: 143  
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Scoring table: BLOSUM62  
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Searched: 541936 seqs, 145912426 residues

Total number of hits satisfying chosen parameters: 541936

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
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2	135	94.4	204	14	US-10-066-179-3
3	114	79.7	25	15	US-10-059-261-258
4	114	79.7	168	9	US-09-922-378-2
5	114	79.7	168	9	US-09-894-657-1
6	114	79.7	168	9	US-09-894-657-7
7	114	79.7	168	14	US-10-066-179-2
8	71	49.7	15	15	US-10-174-105A-147
9	51	35.7	682	12	US-10-238-075-1077
10	50	35.0	215	15	US-10-156-761-9145
11	47	32.9	35	15	US-10-092-750-1
12	47	32.9	138	15	US-10-092-750-241
13	46	32.2	946	9	US-09-828-423-3
14	44	30.8	272	15	US-10-156-761-11541
15	44	30.8	426	9	US-09-815-242-5704

16	44	30.8	699	14	US-10-008-355-8	Sequence 8, Appli
17	44	30.8	705	9	US-09-815-242-12463	Sequence 12463, A
18	44	30.8	712	14	US-10-008-355-2	Sequence 2, Appli
19	44	30.8	877	12	US-10-369-294-20	Sequence 20, Appli
20	43	30.1	213	9	US-09-843-846-18	Sequence 18, Appli
21	43	30.1	232	10	US-09-881-752A-238	Sequence 238, App
22	43	30.1	270	11	US-09-934-455-162	Sequence 162, App
23	43	30.1	380	9	US-09-149-045-2	Sequence 2, Appli
24	43	30.1	380	15	US-10-166-359-2	Sequence 2, Appli
25	43	30.1	380	15	US-10-166-113-2	Sequence 2, Appli
26	43	30.1	380	15	US-10-166-357-2	Sequence 2, Appli
27	43	30.1	380	15	US-10-166-372-2	Sequence 2, Appli
28	43	30.1	380	15	US-10-184-722-3	Sequence 3, Appli
29	43	30.1	380	15	US-10-251-385-62	Sequence 62, Appli
30	43	30.1	380	15	US-10-251-385-198	Sequence 198, App
31	43	30.1	380	15	US-10-225-567A-233	Sequence 233, App
32	43	30.1	543	15	US-10-156-761-13485	Sequence 13485, A
33	43	30.1	571	9	US-09-815-242-11813	Sequence 11813, A
34	43	30.1	582	10	US-09-331-631A-22	Sequence 22, Appli
35	43	30.1	640	9	US-09-989-722-501	Sequence 501, App
36	43	30.1	640	9	US-09-989-723-501	Sequence 501, App
37	43	30.1	640	9	US-09-989-279-501	Sequence 501, App
38	43	30.1	640	9	US-09-989-727-501	Sequence 501, App
39	43	30.1	640	10	US-09-989-731-501	Sequence 501, App
40	43	30.1	640	10	US-09-989-732-501	Sequence 501, App
41	43	30.1	640	10	US-09-991-073-501	Sequence 501, App
42	43	30.1	640	10	US-09-909-320-292	Sequence 292, App
43	43	30.1	640	10	US-09-990-442-501	Sequence 501, App
44	43	30.1	640	10	US-09-991-163-501	Sequence 501, App
45	43	30.1	640	10	US-09-993-604-501	Sequence 501, App

ALIGNMENTS

RESULT 1  
US-09-922-378-3  
; Sequence 3, Application US/09922378  
; Patent No. US20020037869A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, William A.  
; APPLICANT: Oltersdorf, Tilman  
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC  
; FILE OF INVENTION: ACIDS AND METHODS OF USE  
; FILE REFERENCE: 480140.428D3  
; CURRENT APPLICATION NUMBER: US/09/922.378  
; CURRENT FILING DATE: 2001-08-03  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 204  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-922-378-3

Query Match 94.4%; Score 135; DB 9; Length 204;  
Best local Similarity 96.2%; Pred. No. 5.5e-12;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 NLWAAQRYGRELRLKMSDFEGSKGL 27  
|||||  
DB 140 NLWAAQRYGRELRLKMSDFEGSKGL 165

RESULT 2  
US-10-066-179-3  
; Sequence 3, Application US/10066179  
; Publication No. US20020115631A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, William A.  
; APPLICANT: Oltersdorf, Tilman  
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC  
; FILE OF INVENTION: ACIDS AND METHODS OF USE

```
; FILE REFERENCE: 480140.428C1
; CURRENT APPLICATION NUMBER: US/10/066.179
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-066-179-3

Query Match          94.4%; Score 135; DB 14; Length 204;
Best Local Similarity 96.2%; Pred. No. 5.5e-12;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 NLWAAQRYGRELRRMSDEFGSKGL 27
Db 140 NLWAAQRYGRELRRMTDEFGSKGL 165

RESULT 3
US-10-059-261-258
; Sequence 258, Application US/10059261
; Publication No. US20030077826A1
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: JACOPOT, ETIENNE DANIEL FRANCOIS
; APPLICANT: BRIAND, JEAN-PAUL
; TITLE OF INVENTION: CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET
; TITLE OF INVENTION: SPECIFIC CELLS AND A MODULE REGULATING THE APOPTOGENIC
; TITLE OF INVENTION: FUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX
; TITLE OF INVENTION: (PTPC)
; FILE REFERENCE: 03495.0216
; CURRENT APPLICATION NUMBER: US/10/059.261
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/265,594
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 258
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: TOX peptide
US-10-059-261-258

Query Match          79.7%; Score 114; DB 15; Length 25;
Best Local Similarity 91.7%; Pred. No. 7.4e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NLWAAQRYGRELRRMSDEFGSKF 25
Db 1 NLWAAQRYGRELRRMSDEFVDSFK 24

RESULT 4
US-09-922-378-2
; Sequence 2, Application US/09922378
; Patent No. US20020037869A1
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
; TITLE OF INVENTION: ACIDS AND METHODS OF USE
; FILE REFERENCE: 480140.428D3
; CURRENT APPLICATION NUMBER: US/09/922,378
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 168
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
US-09-922-378-2

Query Match          79.7%; Score 114; DB 9; Length 168;
Best Local Similarity 91.7%; Pred. No. 5.1e-09;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NLWAAQRYGRELRRMSDEFGSKF 25
Db 103 NLWAAQRYGRELRRMSDEFVDSFK 126

RESULT 5
US-09-894-657-1
; Sequence 1, Application US/09894657
; Patent No. US20020098569A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION NUMBER: US/09/894,657
; FILING DATE: 28-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/410,372
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0421 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SYNORAB01
; CLONE: 358673
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-894-657-1

Query Match          79.7%; Score 114; DB 9; Length 168;
Best Local Similarity 91.7%; Pred. No. 5.1e-09;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NLWAAQRYGRELRRMSDEFGSKF 25
Db 103 NLWAAQRYGRELRRMSDEFVDSFK 126

RESULT 6
US-09-894-657-7
```

Sequence 7, Application US/09894657  
 Patent No. US20020098569A1  
 GENERAL INFORMATION:  
 APPLICANT: Hillman, Jennifer L.  
 Yue, Henry  
 Lal, Preeti  
 Shah, Purvi  
 Corley, Neil C.  
 TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL  
 PROLIFERATION  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 STREET: 3174 Porter Dr.  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/894,657  
 FILING DATE: 28-Jun-2001  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/410,372  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Billings, Lucy J.  
 REGISTRATION NUMBER: 36,749  
 REFERENCE/DOCKET NUMBER: PF-0421 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-855-0555  
 TELEFAX: 650-845-4186  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 168 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: GenBank  
 CLONE: 1683637  
 SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
 US-09-894-657-7

Query Match 79.7%; Score 114; DB 9; Length 168;  
 Best Local Similarity 91.7%; Pred. No. 5.1e-09;  
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NLWAAQRYGRELRRMSDEFEGSPK 25  
 |||||  
 Db 103 NLWAAQRYGRELRRMSDEFVDSFK 126

RESULT 7  
 US-10-066-179-2  
 Sequence 2, Application US/10066179  
 Publication No. US20020115631A1  
 GENERAL INFORMATION:  
 APPLICANT: Horne, William A.  
 APPLICANT: Oltersdorf, Tilman  
 TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC  
 ACIDS AND METHODS OF USE  
 FILE REFERENCE: 480140.428C1  
 CURRENT APPLICATION NUMBER: US/10/066,179  
 CURRENT FILING DATE: 2002-02-01  
 NUMBER OF SEQ ID NOS: 15  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 2  
 LENGTH: 168

TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-066-179-2  
 Query Match 79.7%; Score 114; DB 14; Length 168;  
 Best Local Similarity 91.7%; Pred. No. 5.1e-09;  
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 NLWAAQRYGRELRRMSDEFEGSPK 25  
 |||||  
 Db 103 NLWAAQRYGRELRRMSDEFVDSFK 126

RESULT 8  
 US-10-174-105A-147  
 Sequence 147, Application US/10174105A  
 Publication No. US20030068652A1  
 GENERAL INFORMATION:  
 APPLICANT: Cell Signaling Technology, Inc.  
 APPLICANT: ZHANG, Hui  
 APPLICANT: TAN, Yi  
 TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPEC.  
 CONTEXT-INDEPENDENT ANTIBODIES COUPLED WITH DATABASE SEARCH  
 FILE REFERENCE: CST-138 CIP3  
 CURRENT APPLICATION NUMBER: US/10/174,105A  
 CURRENT FILING DATE: 2002-06-18  
 PRIOR APPLICATION NUMBER: US 09/148,712  
 PRIOR FILING DATE: 1998-09-04  
 PRIOR APPLICATION NUMBER: US 09/535,364  
 PRIOR FILING DATE: 2000-03-24  
 NUMBER OF SEQ ID NOS: 193  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 147  
 LENGTH: 15  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Synthetic Peptide  
 NAME/KEY: MOD\_RES  
 LOCATION: (8)..(8)  
 OTHER INFORMATION: PHOSPHORYLATION; serine at position 8 is phosphorylated  
 US-10-174-105A-147

Query Match 49.7%; Score 71; DB 15; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0.0008;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GRELRRMSDEFEGS 23  
 |||||  
 Db 1 GRELRRMSDEFEGS 14

RESULT 9  
 US-10-238-075-1077  
 Sequence 1077, Application US/10238075  
 Publication No. US20030148324A1  
 GENERAL INFORMATION:  
 APPLICANT: I.N.S.E.R.M.  
 TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are iso  
 E.coli, and biological uses of these polynucleotides and of t  
 FILE REFERENCE: BLANDINE  
 CURRENT APPLICATION NUMBER: US/10/238,075  
 CURRENT FILING DATE: 2002-09-10  
 PRIOR APPLICATION NUMBER: 0003145  
 PRIOR FILING DATE: 2000-03-10  
 NUMBER OF SEQ ID NOS: 1576  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 1077  
 LENGTH: 682  
 TYPE: PRT  
 ORGANISM: Escherichia coli

US-10-238-075-1077

Query Match 35.7%; Score 51; DB 12; Length 682;  
Best Local Similarity 40.7%; Pred. No. 32;  
Matches 11; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 KNLWAQRYGRELRRMSDEFGSPKGL 27  
Db 608 KQIWAQRNGAKVPRVRNGFTSMDIGL 634

RESULT 10

US-10-156-761-9145  
; Sequence 9145, Application US/10156761  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI  
; APPLICANT: HATTORI, MASAHIRA  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156,761  
; CURRENT FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: JP 2001-204089  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO 9145  
; LENGTH: 215  
; TYPE: PRT  
; ORGANISM: Streptomyces avermitilis  
US-10-156-761-9145

Query Match 35.0%; Score 50; DB 15; Length 215;  
Best Local Similarity 56.2%; Pred. No. 14;  
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 7 QRYGRELRRMSDEFG 22  
Db 108 ERWGGDLRRMRDEADG 123

RESULT 11

US-10-092-750-1  
; Sequence 1, Application US/10092750  
; Publication No. US20030032157A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammond, Philip W.  
; APPLICANT: Alpin, Julia  
; APPLICANT: Wright, Martin C.  
; TITLE OF INVENTION: Polypeptides Interactive with BCL-XL  
; FILE REFERENCE: 50036/050002  
; CURRENT APPLICATION NUMBER: US/10/092,750  
; CURRENT FILING DATE: 2002-03-07  
; PRIOR APPLICATION NUMBER: US 60/274,526  
; PRIOR FILING DATE: 2001-03-08  
; NUMBER OF SEQ ID NOS: 253  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 35  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-092-750-1

Query Match 32.9%; Score 47; DB 15; Length 35;  
Best Local Similarity 45.5%; Pred. No. 5.9;  
Matches 10; Conservative 3; Mismatches 5; Indels 4; Gaps 1;

QY 3 LWAAQRYGRELRRMSDEFGSF 24  
Db 15 IWIAQ----ELRRIGDEFNAY 32

RESULT 12

US-10-092-750-241  
; Sequence 241, Application US/10092750  
; Publication No. US20030032157A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammond, Philip W.  
; APPLICANT: Alpin, Julia  
; APPLICANT: Wright, Martin C.  
; TITLE OF INVENTION: Polypeptides Interactive with BCL-XL  
; FILE REFERENCE: 50036/050002  
; CURRENT APPLICATION NUMBER: US/10/092,750  
; CURRENT FILING DATE: 2002-03-07  
; PRIOR APPLICATION NUMBER: US 60/274,526  
; PRIOR FILING DATE: 2001-03-08  
; NUMBER OF SEQ ID NOS: 253  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 241  
; LENGTH: 138  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-092-750-241

Query Match 32.9%; Score 47; DB 15; Length 138;  
Best Local Similarity 45.5%; Pred. No. 24;  
Matches 10; Conservative 3; Mismatches 5; Indels 4; Gaps 1;

QY 3 LWAAQRYGRELRRMSDEFGSF 24  
Db 86 IWIAQ----ELRRIGDEFNAY 103

RESULT 13

US-09-828-423-3  
; Sequence 3, Application US/09828423  
; Patent No. US20020099178A1  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; Guegler, Karl J.  
; Patterson, Chandra  
; TITLE OF INVENTION: GROWTH-ASSOCIATED TRYPsin-TYPE  
; INHIBITOR HEAVY CHAIN PRECURSOR  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: Word Perfect 6.1/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/828,423  
; FILING DATE: 05-Apr-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/388,774  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cerrone, Michael C  
; REGISTRATION NUMBER: 39,132  
; REFERENCE/DOCKET NUMBER: PF-0505 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166

J: 3 :

core 46; DB 9; Length 945;  
Pred. No. 2.4e+02;  
5; Mismatches 13; Indels 0; Gaps 0;

QY .SDEFEFGSKGL 27  
: | | | | | :  
Db .LHVPDTFEGHFDGV 237

## RESULT 14

US-10-156-761-115  
; Sequence 11541, Application US/10156761  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI  
; APPLICANT: HATTORI, MASAHIRA  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156.761  
; CURRENT FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: JP 2001-204089  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO 11541  
; LENGTH: 272  
; TYPE: PRT  
; ORGANISM: Streptomyces avermitilis  
US-10-156-761-11541

Query Match 30.8%; Score 44; DB 15; Length 272;  
Best Local Similarity 53.3%; Pred. No. 1.3e+02;  
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 WAAQRYGRELRRMSD 18  
: | | : | | | | : |  
Db 29 WIAAHGAEILRRAD 43

## RESULT 15

US-09-815-242-5704  
; Sequence 5704, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815.242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5704  
; LENGTH: 426  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
US-09-815-242-5704  
Query Match 30.8%; Score 44; DB 9; Length 426;  
Best Local Similarity 36.8%; Pred. No. 2.1e+02;  
Matches 7; Conservative 4; Mismatches 8; Indels 0; Gaps 0;  
QY 9 YGRELRRMSDEFGSKGL 27  
: | | | | : | | | :  
Db 386 FGSRLRQDENFDGKIKAI 404

Search completed: September 15, 2003, 17:47:53  
Job time : 21.4071 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 15, 2003, 17:18:16 : Search time 12.15 Seconds  
(without alignments)  
213.708 Million cell updates/sec

Title: US-09-544-664-56  
Perfect score: 143  
Sequence: 1 KNLWAAQRYGRELRRMSDEFEGSFKGL 27

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_76.\*

1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	138	96.5	204	2 A55671	bad protein - mous
2	54	37.8	946	2 JC5575	inter-alpha-trypsi
3	53	37.1	223	2 D70760	hypothetical prote
4	53	37.1	946	2 S54354	inter-alpha-inhibi
5	52	36.4	370	2 S38185	2-dehydro-3-deoxy-
6	51	35.7	232	2 A42095	floral homeotic pr
7	50	35.0	374	2 C84338	spermidine/putresc
8	50	35.0	516	2 A96753	probable threonine
9	49	34.3	453	2 E83517	conserved hypotnet
10	48.5	33.9	134	2 S40376	Ig kappa chain - h
11	48.5	33.9	314	2 T02975	annexin p35 - maiz
12	48	33.6	206	2 C36365	transforming prote
13	48	33.6	220	2 F72289	oxidoreductase, so
14	48	33.6	526	2 T08545	threonine synthase
15	47.5	33.2	334	2 A39172	Antho-RFamide neur
16	47	32.9	597	2 G82308	oxaloacetate decar
17	47	32.9	967	2 F82668	oxoglutarate dehyd
18	47	32.9	5138	2 B96895	hypothetical prote
19	46.5	32.5	314	2 T02961	annexin p33 - maiz
20	46.5	32.5	435	2 A44308	Artho-RFamide prec
21	46.5	32.5	1140	2 T09486	hypothetical prote
22	46	32.2	165	2 S59899	chlorocruorin chal
23	46	32.2	399	2 T35440	probable polyamine
24	46	32.2	946	1 IYHU2	inter-alpha-trypsi
25	46	32.2	1164	2 T24806	hypothetical prote
26	46	32.2	1378	2 A81393	DNA-directed RNA p
27	45.5	31.8	261	2 G69510	conserved hypotnet
28	45.5	31.8	287	2 S43852	neuropeptide Pol-R
29	45.5	31.8	327	2 AF2859	conserved hypotnet

30 45.5 31.8 327 2 D97636 probable secreted  
31 45.5 31.8 562 2 C71473 hypothetical prote  
32 45.5 31.8 905 2 G83314 NADH dehydrogenase  
33 45 31.5 273 2 S06736 photosystem II oxy  
34 45 31.5 273 2 AG2287 manganese-stabilizi  
35 45 31.5 295 2 F83201 conserved hypotnet  
36 45 31.5 346 2 H95406 conserved hypotnet  
37 45 31.5 591 2 B44465 sodium ion pump ox  
38 45 31.5 591 2 A80509 oxaloacetate decar  
39 45 31.5 591 2 A80909 oxaloacetate decar  
40 45 31.5 596 2 A28088 oxaloacetate decar  
41 45 31.5 715 2 S52675 probable membrane  
42 45 31.5 864 1 VCLJG4 env polyprotein -  
43 45 31.5 915 2 B59433 chromosome 5 GAP-1  
44 45 31.5 1199 2 T23005 hypothetical prote  
45 45 31.5 1217 2 T22672 hypothetical prote

#### ALIGNMENTS

##### RESULT 1

A55671

bad protein - mouse

C:Species: Mus musculus (house mouse)

C:Date: 03-Mar-1995 #sequence\_revision 03-Mar-1995 #text\_change 05-Nov-1999

C:Accession: A55671

R:Yang, B.; Zha, J.; Jockel, J.; Boise, L.H.; Thompson, C.B.; Korsmeyer, S.J.

Cell 80, 285-291, 1995

A:Title: Bad, a heterodimeric partner for Bcl-X-L and Bcl-2, displaces Bax and promot

A:Reference number: A55671; MUID:95136361; PMID:7834748

A:Accession: A55671

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-204 <YAN>

A:Cross-references: GB:L37296; NID:g639778; PIDN:AAA64465.1; PID:g639779

C:Keywords: heterodimer

Query Match 96.5%; Score 138; DB 2; Length 204;

Best Local Similarity 100.0%; Pred. No. 9.3e-13;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NLWAAQRYGRELRRMSDEFEGSFKGL 27

|||||

Db 140 NLWAAQRYGRELRRMSDEFEGSFKGL 165

##### RESULT 2

JC5575

inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster

C:Species: Mesocricetus auratus (golden hamster)

C:Date: 23-Sep-1997 #sequence\_revision 23-Sep-1997 #text\_change 20-Jun-2000

C:Accession: JC5575; PC4485

R:Nakatani, T.; Suzuki, Y.; Yamamoto, T.; Sinochana, H.

J. Biochem. 122, 71-82, 1997

A:Title: Molecular cloning and sequencing of cDNAs encoding three heavy-chain precurs

sin inhibitor heavy chain family.

A:Reference number: JC5574; MUID:97420688; PMID:9276673

A:Accession: JC5575

A:Molecule type: mRNA

A:Residues: 1-946 <NAK>

A:Cross-references: DDBJ:D89286; NID:g1694689; PIDN:BAAL3939.1; PID:g1694690

A:Experimental source: liver

A:Accession: PC4485

A:Molecule type: protein

A:Residues: 55-64;140-146;151-156;424-447;500-528;577-605 <NA2>

C:Comment: In the plasma three inter-alpha-trypsin inhibitor heavy chains 1, 2 and 3

that the complexes play important role for pancreatic cancer.

C:Superfamily: inter-alpha-trypsin inhibitor complex component II

F:261-264,717-916/Disulfide bonds: #status predicted

Query Match 37.8%; Score 54; DB 2; Length 946;

Best Local Similarity 34.6%; Pred. No. 9.9;

A;Title: The complete sequence of a 6794 bp segment located on the right arm of chromosome 10p11.23, containing the human ARO4 gene, encoding the tyrosine aminotransferase (EC 2.6.1.5).  
A;Reference number: S38185; MUID:94078675; PMID:8256522  
A;Accession: S38185  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-370 <DOI>  
A;Cross-references: GB:120296; NID:g311101; PIDN:AAA65607.1; PID:g311102  
R:Aljinovic, G.; Pohl, F.M.; Pohl, T.M.  
submitted to the Protein Sequence Database, August 1994  
A;Reference number: S45906  
A;Accession: S46126  
A;Molecule type: DNA  
A;Residues: 1-370 <ALJ>  
A;Cross-references: EMBL:Z36118; NID:g536664; PIDN:CAA85212.1; PID:g536665; MIPS:YBR2  
R:Aigle, M.; Bailet, M.C.; Barthe, C.; Bitaou, N.; Crouzet, M.; Doignon, F.  
submitted to the Protein Sequence Database, August 1994  
A;Reference number: S45940  
A;Accession: S46130  
A;Molecule type: DNA  
A;Residues: 1-370 <AIG>  
A;Cross-references: EMBL:Z36118; NID:g536664; PIDN:CAA85212.1; PID:g536665; MIPS:YBR2  
R:Kuenzler, M.; Paravicini, G.; Egli, C.M.; Irniger, S.; Braus, G.H.  
Gene 113, 67-74, 1992  
A;Title: Cloning, primary structure and regulation of the ARO4 gene, encoding the tyrosine aminotransferase (EC 2.6.1.5).  
A;Reference number: JN0322; MUID:92225349; PMID:1348717  
A;Accession: JN0322  
A;Molecule type: DNA  
A;Residues: 1-204,208-370 <KUE>  
A;Cross-references: EMBL:X61107  
R:Kuenzler, M.; Balmelli, T.; Egli, C.M.; Paravicini, G.; Braus, G.H.  
J. Bacteriol. 175, 5548-5558, 1993  
A;Title: Cloning, primary structure, and regulation of the HIS7 gene encoding a bifunctional histidinol-phosphatase.  
A;Reference number: A48651; MUID:93374850; PMID:8366040  
A;Accession: B48651  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 352-370 <KU2>  
A;Cross-references: GB:X61107  
C;Comment: This enzyme catalyzes the condensation of phosphoenolpyruvate and D-erythrose 4-phosphate to form 2-keto-3-deoxyheptulon.  
C;Genetics:  
A;Gene: SGD:ARO4  
A;Cross-references: SGD:S0000453; MIPS:YBR249C  
A;Map position: 2R  
C;Function:  
A;Description: aldehyde-lyase; carbon-carbon lyase  
A;Pathway: aromatic amino acid biosynthesis; shikimate pathway  
A;Note: first step in shikimate pathway  
C;Superfamily: phospho-2-dehydro-3-deoxyheptonate aldolase  
C;Keywords: aldehyde-lyase; aromatic amino acid biosynthesis; carbon-carbon lyase; cy

Query Match 36.4%; Score 52; DB 2; Length 370;  
Best Local Similarity 47.6%; Pred. No. 7.5;  
Matches 10; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 2 NLWAAQRYGRELREMSDFEG 22  
: | | | | | : : : : : |  
Db 80 DLEAAQEFYALRLKKLSDELKG 100

RESULT 6  
A42095  
floral homeotic protein APETALA3 (AP3) - Arabidopsis thaliana  
N;Alternate names: homeotic protein APETALA3; MADS-box regulatory protein AP3  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jul-2000  
C;Accession: A42095; S52633; T47593  
R;Jack, T.; Brockman, L.L.; Meyerowitz, E.M.  
Cell 68, 683-697, 1992  
A;Title: The homeotic gene APETALA3 of Arabidopsis thaliana encodes a MADS box and is  
A;Reference number: A42095; MUID:92154682; PMID:1346756  
A;Accession: A42095  
A;Status: preliminary  
A;Molecule type: mRNA

A;Residues: 1-232 <JAC>  
A;Cross-references: GB:M86357; NID:gl66607; PIDN:AAA32740.1; PID:gl66608  
A;Experimental source: petals, stamens  
A;Note: sequence extracted from NCBI backbone (NCBIN:82520, NCBIP:82521)  
R;Okamoto, H.; Yano, A.; Shiraishi, H.; Okada, K.; Shimura, Y.  
Plant Mol. Biol. 26, 465-472, 1994  
A;Title: Genetic complementation of a floral homeotic mutation, apetalaa3, with an Arabid  
A;Reference number: S52633; MUID:95036018; PMID:7948893  
A;Accession: S52633  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-63 <OKA>  
A;Cross-references: GB:D21125  
R;Bloeker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat M.Mewes,  
submitted to the Protein Sequence Database, March 2000  
A;Reference number: Z24469  
A;Accession: T47593  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-232 <BLO>  
A;Cross-references: EMBL:AL132971  
A;Experimental source: cultivar Columbia; BAC clone T12E18  
C;Genetics:  
A;Map position: 3  
A;Introns: 63/2; 85/3; 106/2; 139/3; 153/3; 168/3  
A;Note: T12E18.30  
C;Superfamily: transcription factor squa; serum response factor DNA-binding domain homol  
C;Keywords: DNA binding; nucleus; transcription regulation  
F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>  
Query Match 35.7%; Score 51; DB 2; Length 232;  
Best Local Similarity 44.4%; Pred. No. 6.5;  
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;  
QY 7 QRYG-----RELRMSDEFGSPK 25  
||| :|||: ||| :||  
Db 107 QRLGCELDLDIQELRLDEMENTFK 133  
RESULT 7  
C84338  
A;Title: Complete genome sequence of Halobacterium sp. NRC-1  
C;Species: Halobacterium sp. NRC-1  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C;Accession: C84338  
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S  
; Leichauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo  
Jung, K.H.; Alam, M.; Freitas, T.  
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li  
A;Title: Genome sequence of Halobacterium species NRC-1.  
A;Reference number: A84160; MUID:20504483; PMID:11016950  
A;Accession: C84338  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-374 <STO>  
A;Cross-references: GB:AE004437; NID:gl0581314; PIDN:AAC20071.1; GSPDB:GN00138  
C;Genetics:  
A;Gene: potA2  
Query Match 35.0%; Score 50; DB 2; Length 374;  
Best Local Similarity 76.9%; Pred. No. 15;  
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 12 ELRMSDEFGSF 24  
||||: ||| ||||  
Db 197 ELRLSDAVEGSF 209  
RESULT 8  
A96753  
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.  
C;Species: Arabidopsis thaliana (mouse-ear cross)  
A;Reference number: S40312; MUID:94080891; PMID:8258341  
A;Accession: S40376  
A;Status: preliminary; translation not shown

C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C;Accession: A96753  
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; MUID:21016719; PMID:11130712  
A;Accession: A96753  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-516 <STO>  
A;Cross-references: GB:AE005173; NID:g5903070; PIDN:AA055628.1; GSPDB:GN00141  
C;Genetics:  
A;Gene: F3N23.1  
A;Map position: 1  
Query Match 35.0%; Score 50; DB 2; Length 516;  
Best Local Similarity 35.3%; Pred. No. 21;  
Matches 12; Conservative 7; Mismatches 7; Indels 8; Gaps 1;  
QY 2 NLWAAQRYGRELRRMSD-----EFGESFKGL 27  
||| :|||: ||| :|||  
Db 163 NLFWAERFGKQLQMDLWVKHGIGSHTGSKDL 196  
RESULT 9  
E83517  
A;Title: conserved hypothetical protein PA1031 [imported] - Pseudomonas aeruginosa (strain PAO  
C;Species: Pseudomonas aeruginosa  
C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C;Accession: E83517  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L  
; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pa  
A;Reference number: A82950; MUID:20437337; PMID:10984043  
A;Accession: E83517  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-453 <STO>  
A;Cross-references: GB:AE004535; GB:AE004091; NID:g9946936; PIDN:AAG04420.1; GSPDB:GN  
A;Experimental source: strain PAO1  
C;Genetics:  
A;Gene: PA1031  
Query Match 34.3%; Score 49; DB 2; Length 453;  
Best Local Similarity 55.6%; Pred. No. 25;  
Matches 10; Conservative 4; Mismatches 2; Indels 2; Gaps 1;  
QY 4 WAAQRYGR--ELRRMSDE 19  
||| :||| :||| :||  
Db 65 WASERQGREELRLRIASE 82  
RESULT 10  
S40376  
A;Title: Ig kappa chain - human  
C;Species: Homo sapiens (man)  
C;Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C;Accession: S40376  
R;Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A;Reference number: S40312; MUID:94080891; PMID:8258341  
A;Accession: S40376  
A;Status: preliminary; translation not shown

```

A:Molecule type: mRNA
A:Residues: 1-134 <KLE>
A:Cross-references: EMBL:X72486; NID:g441440; PIDN:CAA51154.1; PID:g441441
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-113/Domain: immunoglobulin homology <IMV>

Query Match      33.9%; Score 48.5; DB 2; Length 134;
Best Local Similarity 38.2%; Pred. No. 8.6;
Matches 13; Conservative 1; Mismatches 9; Indels 11; Gaps 1;

QY 4 WAAQRYGRELRLM-----SDEFEGSKG 26
      | | | | |
Db 58 WFORPGSPRLIYNVSKRDSGVDRFSGSG 91

RESULT 11
T02975
C:Species: Zea mays (maize)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
C:Accession: T02975
R:Battey, N.H.; James, N.C.; Greenland, A.J.
Plant Physiol. 112, 1391-1396, 1996
A:Title: CDNA isolation and gene expression of maize annexins P33 and P35.
A:Reference number: 214796; MUID:97092863; PMID:8938425
A:Accession: T02975
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-314 <BAT>
A:Cross-references: EMBL:X98245; NID:g1370602; PIDN:CAA66901.1; PID:g1370603
A:Experimental source: cultivar clipper; root tip
C:Superfamily: annexin I; annexin repeat homology
F:14-85/Domain: annexin repeat homology <AXR>

Query Match      33.9%; Score 48.5; DB 2; Length 314;
Best Local Similarity 47.6%; Pred. No. 21;
Matches 10; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 6 AORYGRE-LRRMSDFEGSKF 25
      | | | | |
Db 54 AEAYGKELLRALGDEIHGKFE 74

RESULT 12
C36365
Transforming protein homolog MRAS3 - Rhizomucor racemosus
C:Species: Rhizomucor racemosus
C:Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 19-Jan-2001
C:Accession: C36365
R:Casale, W.L.; McConnell, D.G.; Wang, S.Y.; Lee, Y.J.; Linz, J.E.
Mol. Cell. Biol. 10, 6654-6663, 1990
A:Title: Expression of a gene family in the dimorphic fungus Mucor racemosus which exhib
A:Reference number: A36365; MUID:91061774; PMID:1701021
A:Accession: C36365
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-206 <CAS>
A:Cross-references: GB:M55177
C:Superfamily: ras transforming protein; translation elongation factor Tu homology
C:Keywords: GTP binding; nucleotide binding; P-loop
F:11-126/Domain: translation elongation factor Tu homology <ETU>
F:17-24/Region: nucleotide-binding motif A (P-loop)
F:123-126/Region: GTP-binding NKXD motif
F:153-155/Region: GTP-binding SAK/Y motif
F:23,24,42,123,124,126,153/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser) #sta

Query Match      33.6%; Score 48; DB 2; Length 206;
Best Local Similarity 52.5%; Pred. No. 16;
Matches 10; Conservative 2; Mismatches 4; Indels 4; Gaps 0;

QY 11 RELRRMSDFEGSKG 26
      | | | | |

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Db 169 REIRRNKQEGRSKG 184

RESULT 13
F72289
oxidoreductase, sol/devB family - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: F72289
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: F72289
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-220 <ARN>
A:Cross-references: GB:AE001772; GB:AE000512; NID:g4981693; PIDN:AAD36230.1; PID:g498
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM1154
C:Superfamily: yeast SOL3 protein

Query Match      33.6%; Score 48; DB 2; Length 220;
Best Local Similarity 34.8%; Pred. No. 17;
Matches 8; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 5 AAQRYGRELRRMSDFEGSKGL 27
      | : | | | | : | : | : |
Db 111 ACEKYREIRSATDQFDLAILGM 133

RESULT 14
T08545
threonine synthase (EC 4.2.3.1) precursor - Arabidopsis thaliana
N:Alternate names: protein F27B13.80
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 03-Jun-2002
C:Accession: T08545; S71362; S74307
R:Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.;
submitted to the Protein Sequence Database, May 1999
A:Reference number: Z16442
A:Accession: T08545
A:Molecule type: DNA
A:Residues: 1-526 <BEV>
A:Cross-references: EMBL:AL050352; GSPDB:GN00062; ATSP:F27B13.80
A:Experimental source: cultivar Columbia; BAC clone F27B13
R:Curien, G.; Dumas, R.; Ravanel, S.; Douce, R.
FEBS Lett. 390, 85-90, 1996
A:Title: Characterization of an Arabidopsis thaliana cDNA encoding an S-adenosylmethi
A:Reference number: S71362; MUID:96314555; PMID:8706836
A:Accession: S71362
A:Molecule type: mRNA
A:Residues: 1-526 <CUR>
A:Cross-references: EMBL:L41666; NID:g1448916; PIDN:AA04607.1; PID:g1448917
A:Accession: S74307
A:Molecule type: protein
A:Residues: 40-54 <GUI>
C:Genetics:
A:Gene: ATSP:F27B13.80
A:Map position: 4
A:Genome: nuclear
C:Keywords: carbon-oxygen lyase; chloroplast
F:1-39/Domain: transit peptide (chloroplast) #status predicted <NTP>
F:40-526/Product: threonine synthase #status experimental <MAT>

Query Match      33.6%; Score 48; DB 2; Length 526;
Best Local Similarity 35.3%; Pred. No. 42;
Matches 12; Conservative 6; Mismatches 8; Indels 8; Gaps 1;

QY 2 NLWAAQRYGRELRRMSD-----EFEGSKGL 27

```

Db 172 NLFWAERFGKQFLGMNDLWVKHCGISHTGSFKDL 205

RESULT 15

A39172  
 Antho-Ramide neuropeptide 19 repeat precursor - sea anemone (Calliactis parasitica)  
 C:Species: Calliactis parasitica  
 C>Date: 07-Feb-1992 #sequence\_revision 07-Feb-1992 #text\_change 21-Jul-2000  
 C;Accession: A39172  
 R;Darmer, D.; Schmutzler, C.; Diekhoff, D.; Grimmelikhuijzen, C.J.P.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 2555-2559, 1991  
 A;Title: Primary structure of the precursor for the sea anemone neuropeptide Antho-RFam  
 A;Reference number: A39172; MUID:91172845; PMID:1706527  
 A;Accession: A39172  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-334 <DAR>  
 A;Cross-references: GB:M59166; NID:gl56133; PIDN:AAA27878.1; PID:gl56134  
 C;Keywords: neuropeptide

Query Match 33.2%; Score 47.5; DB 2; Length 334;  
 Best Local Similarity 44.0%; Pred. No. 31;  
 Matches 11; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

QY 1 KNLWAAQRYGRELK-RMSDEFEQSF 24

Db 89 KRYVPGRYGREFGREFGREF 113

Search completed: September 15, 2003, 17:27:04  
 Job time : 13.15 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 15, 2003, 17:16:55 ; Search time 6.36429 Seconds  
(without alignments)  
199.507 Million cell updates/sec

Title: US-09-544-664-56  
Perfect score: 143  
Sequence: 1 KNLWAAQRYGRELRRMSDEFEGSKGL 27

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	138	96.5	204	1 BAD_MOUSE	Q61337 mus musculus
2	138	96.5	205	1 BAD_RAT	Q51147 rattus norv
3	114	79.7	168	1 BAD_HUMAN	Q92934 homo sapien
4	54	37.8	946	1 ITH2_MESAU	P97279 mesocricetu
5	53	37.1	946	1 ITH2_MOUSE	Q61703 mus musculus
6	52.5	36.7	506	1 MATK_LEDPA	Q62992 ledum palus
7	52.5	36.7	506	1 MATK_RHOFR	Q62984 rhododendro
8	52.5	36.7	506	1 MATK_RHOTS	Q62991 rhododendro
9	52	36.4	370	1 AROG_YEAST	P32449 saccharomyc
10	51	35.7	232	1 AP3_ARATH	P35632 arabidopsis
11	51	35.7	851	1 CE05_MOUSE	Q8k2h3 mus musculus
12	49	34.3	453	1 RMUC_PSEAE	Q9i4u3 pseudomonas
13	48	33.6	205	1 RAS3_RHIRA	P22280 rhizomucor
14	48	33.6	220	1 PGGL_THEMA	Q9x0n8 thermotoga
15	48	33.6	519	1 THRC_SOLTU	Q9mt28 solanum tub
16	48	33.6	526	1 THRC_ARATH	Q9s7b5 arabidopsis
17	47.5	33.2	334	1 FMRA_CALPA	Q01133 callactis
18	47.5	33.2	507	1 MATK_LOIPR	Q47159 loiseleuria
19	47	32.9	198	1 BIM_HUMAN	Q43521 homo sapien
20	46.5	32.5	429	1 FMR2_ATEL	Q16994 anthopleura
21	46.5	32.5	435	1 FMRL_ATEL	P10419 anthopleura
22	46	32.2	946	1 ITH2_HUMAN	P19823 homo sapien
23	46	32.2	1378	1 RPOB_CAMJE	Q46124 campylobact
24	45.5	31.8	287	1 PREFA_POLPE	P21259 polyorchis
25	45	31.5	273	1 PSBO_ANASP	P13907 anabaena sp
26	45	31.5	328	1 SNF4_KLULA	Q9p869 kluyveromyc
27	45	31.5	590	1 DCOA_SALTY	Q03030 salmonella
28	45	31.5	595	1 DCOA_KLEPN	P13187 klebsiella
29	45	31.5	653	1 HT2A_HUMAN	Q13049 homo sapien
30	45	31.5	865	1 ENV_SIVAT	P05886 simian immu
31	45	31.5	915	1 CE05_HUMAN	Q9nyf5 homo sapien
32	45	31.5	1535	1 LML1_CABEL	Q18823 caenorhabdi
33	44.5	31.1	506	1 MATK_GAUFR	Q959j0 gaultheria

RESULT 1				
BAD_MOUSE				
ID	BAD_MOUSE	STANDARD;	PRT;	204 AA.
AC	Q61337;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component			
DE	6) (Bcl-xL/Bcl-2 associated death promoter).			
GN	BAD OR BBC6.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain, and Thymus;			
RX	MEDLINE=95136361; PubMed=7834748;			
RA	Yang E., Zha J., Jockel J., Boise L.H., Thompson C.B., Korsmeyer S.J.;			
RT	"Bad, a heterodimeric partner for Bcl-XL and Bcl-2, displaces Bax and			
RT	promotes cell death.";			
RL	Cell 80:285-291(1995).			
RN	[2]			
RP	PHOSPHORYLATION, AND MUTAGENESIS OF SER-112 AND SER-136.			
RX	MEDLINE=98022383; PubMed=9381178;			
RA	Del Peso L., Gonzalez-Garcia M., Page C., Herrera R., Nunez G.;			
RT	"Interleukin-3-induced phosphorylation of BAD through the protein			
RT	kinase Akt.";			
RL	Science 278:687-689(1997).			
RN	[3]			
RP	MUTAGENESIS OF SERINE RESIDUES.			
RX	MEDLINE=20403302; PubMed=10949026;			
RA	Datta S.R., Katsov A., Hu L., Petros A., Fesik S.W., Yaffe M.B.,			
RA	Greenberg M.E.;			
RT	"14-3-3 proteins and survival kinases cooperate to inactivate BAD by			
RT	BH3 domain phosphorylation.";			
RL	Mol. Cell 6:41-51(2000).			
CC	-!- FUNCTION: Promotes cell death. Successfully competes for the			
CC	binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level			
CC	of heterodimerization of these proteins with BAX. Can reverse the			
CC	death repressor activity of Bcl-x(L), but not that of Bcl-2.			
CC	Appears to act as a link between growth factor receptor signaling			
CC	and the apoptotic pathways.			
CC	-!- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-			
CC	x(L), Bcl-2 and Bcl-w. Also binds protein S100A10 (By similarity).			
CC	The Ser-112/Ser-136 phosphorylated form binds 14-3-3 proteins.			
CC	-!- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon			
CC	phosphorylation, locates to the cytoplasm.			
CC	-!- DOMAIN: Intact BH3 domain is required by BIK, BID, BAX, BAD AND			
CC	BAX for their pro-apoptotic activity and for their interaction			
CC	with anti-apoptotic members of the Bcl-2 family.			
CC	-!- PTM: Phosphorylated on Ser-112 in response to survival stimuli.			
CC	Subsequent phosphorylation on Ser-136 promotes heterodimerization			
CC	with 14-3-3 proteins. This interaction then facilitates the			
CC	phosphorylation at Ser-155, a site within the BH3 domain, leading			
CC	to the release of Bcl-x(L) and the promotion of cell survival.			

34	44.5	31.1	512	1	MATK_LILTS	Q9gig3 liium tsin
35	44.5	31.1	907	1	NUOG_ECOLI	P33602 escherichia
36	44.5	31.1	907	1	NUOG_SALTY	P33900 salmonella
37	44	30.8	196	1	BIM_MOUSE	O54918 mus musculu
38	44	30.8	196	1	BIM_RAT	O88498 rattus norv
39	44	30.8	262	1	END8_ECO57	Q8x9c6 escherichia
40	44	30.8	262	1	END8_ECOLI	P50465 escherichia
41	44	30.8	262	1	END8_SALTY	O828d2 salmonella
42	44	30.8	262	1	END8_SALTY	Q8zqu6 salmonella
43	44	30.8	629	1	SYN_THEMEA	O33925 thermotoga
44	44	30.8	768	1	ENV_SIVAT	P27757 simian immu
45	44	30.8	877	1	ENV_SIVAG	P27977 simian immu

ALIGNMENTS

CC Ser-136 is the major site of AKT/PKB phosphorylation, Ser-155 the  
CC major site of protein kinase A (CAPK) phosphorylation.  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.  
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
CC -----  
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CC -----  
DR EMBL; L37296; AAA64465.1; -;  
DR PIR; A55671; A55671.  
DR HSSP; Q92934; IG5J.  
DR MGD; MGI:1096330; Bad.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR PROSITE; PS01259; BH3; FALSE\_NEG.  
KW Apoptosis; Phosphorylation.  
FT DOMAIN 147 161 BH3  
FT MOD\_RES 112 112 PHOSPHORYLATION (BY PKA AND PKB).  
FT MOD\_RES 136 136 PHOSPHORYLATION (BY PKA AND PKB).  
FT MOD\_RES 155 155 PHOSPHORYLATION (BY PKA AND PKB).  
FT MUTAGEN 112 112 S->A: NO PHOSPHORYLATION.  
FT MUTAGEN 136 136 S->A: NO PHOSPHORYLATION.  
FT MUTAGEN 155 155 S->A: NO PHOSPHORYLATION; INTERACTS WITH  
FT BCL-X(L).  
SQ SEQUENCE 204 AA; 22080 MW; 6C2BA910205053F7 CRC64;  
  
Query Match 96.5%; Score 138; DB 1; Length 204;  
Best Local Similarity 100.0%; Pred. No. 1.8e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 NLWAAQRYGRELRRMSDFEGSPKGL 27  
Db 140 NLWAAQRYGRELRRMSDFEGSPKGL 165  
|||||  
  
RESULT 2  
BAD\_RAT STANDARD; PRT; 205 AA.  
AC O35147; O70256; Q9JHX1;  
DT 16-OCT-2001 (Rel. 40, Created)  
DI 16-OCT-2001 (Rel. 40, Last sequence update)  
DI 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component  
DE 6) (Bcl-xL/Bcl-2 associated death promoter).  
GN BAD.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF SER-113 AND SER-137.  
RC TISSUE=Ovary;  
RX MEDLINE=98034386; PubMed=9369453;  
RA Hsu S.Y., Kaipia A., Zhu L., Hsueh A.J.W.;  
RT "Interference of BAD (Bcl-xL/Bcl-2-associated death promoter)-induced  
RT apoptosis in mammalian cells by 14-3-3 isoforms and P11.";  
RL Mol. Endocrinol. 11:1858-1867(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=98194755; PubMed=9535132;  
RA D'Agata V., Magro G., Travali S., Musco S., Cavallaro S.;  
RT "Cloning and expression of the programmed cell death regulator BAD in  
RT the rat brain.";  
RL Neurosci. Lett. 243:137-140(1998).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).  
RC TISSUE=Brain;  
RX MEDLINE=21109372; PubMed=11161472;

RA Hamner S., Arumae U., Yu L.-Y., Sun Y.-F., Saarna M., Lindholm D.;  
RT "Functional characterization of two splice variants of rat BAD and  
RT their interaction with Bcl-w in sympathetic neurons.";  
RL Mol. Cell. Neurosci. 17:97-106(2001).  
CC -!- FUNCTION: Promotes cell death. Successfully competes for the  
CC binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level  
CC of heterodimerization of these proteins with BAX. Can reverse the  
CC death repressor activity of Bcl-x(L), but not that of Bcl-2 (By  
CC similarity). Appears to act as a link between growth factor  
CC receptor signaling and the apoptotic pathways.  
CC -!- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-  
CC x(L), Bcl-2 and Bcl-w. Also binds protein S100A10. The Ser-  
CC 113/Ser-137 phosphorylated form binds 14-3-3 proteins.  
CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon  
CC phosphorylation, locates to the cytoplasm (By similarity).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event-Alternative splicing; Named isoforms=2;  
CC Name=Alpha;  
CC IsoId=O35147-1; Sequence=Displayed;  
CC Name=Beta;  
CC IsoId=O35147-2; Sequence=VSP\_000534;  
CC -!- TISSUE SPECIFICITY: Expressed in all tissues tested, including  
CC brain, liver, spleen and heart. In the brain, restricted to  
CC epithelial cells of the choroid plexus. Isoform alpha is the more  
CC abundant form.  
CC -!- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND  
CC BAX for their pro-apoptotic activity and for their interaction  
CC with anti-apoptotic members of the Bcl-2 family.  
CC -!- PTM: Phosphorylated on Ser-113 in response to survival stimuli.  
CC Subsequent phosphorylation on Ser-137 promotes heterodimerization  
CC with 14-3-3 proteins. This interaction then facilitates the  
CC phosphorylation at Ser-156, a site within the BH3 domain, leading  
CC to the release of Bcl-x(L) and the promotion of cell survival.  
CC Ser-137 is the major site of AKT/PKB phosphorylation, Ser-156 the  
CC major site of protein kinase A (CAPK) phosphorylation (By  
CC similarity).  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.  
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
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CC -----  
DR EMBL; AF003523; AAC53374.1; -;  
DR EMBL; AF031227; AAC15100.1; -;  
DR EMBL; AF279910; AAF91427.1; -;  
DR EMBL; AF279911; AAF91428.1; -;  
DR HSSP; Q92934; IG5J.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR PROSITE; PS01259; BH3; FALSE\_NEG.  
KW Apoptosis; Phosphorylation; Alternative splicing.  
FT DOMAIN 148 162 BH3.  
FT MOD\_RES 113 113 PHOSPHORYLATION (BY PKA AND PKB)  
FT MOD\_RES 137 137 (BY SIMILARITY).  
FT MOD\_RES 156 156 PHOSPHORYLATION (BY PKA AND PKB)  
FT MOD\_RES 156 156 (BY SIMILARITY).  
FT MOD\_RES 156 156 PHOSPHORYLATION (BY PKA AND PKB)  
FT MOD\_RES 156 156 (BY SIMILARITY).  
FT VARSPLIC 166 205 LPRPKSAGTATQMQSASWTRIIQSWDRNLKGGSTPSQ  
FT -> BELTYSVEFLPVRAIAMEGWPLLWSFQSPFHTLPPTPEP  
FT /FTId=VSP\_000534.  
FT EVAMPFLRYWTALRLC (in isoform Beta).  
FT S->A: NO EFFECT ON HETERODIMERIZATION  
FT WITH 14-3-3 PROTEINS.  
FT S->A: NO HETERODIMERIZATION WITH 14-3-3  
FT PROTEINS. NO EFFECT ON HETERODIMERIZATION  
FT WITH BCL2 NOR WITH PROTEIN P11.  
FT SDAGGR -> ERGRK (IN REF. 1).  
FT CONFLICT 29 34  
SQ SEQUENCE 205 AA; 22228 MW; 7AFA71DAE9CF4A81 CRC64;

Query Match 96.5%; Score 138; DB 1; Length 205;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-13;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NLWAAQRYGRELRLMSDEFEGSFKGL 27  
 |||||  
 Db 141 NLWAAQRYGRELRLMSDEFEGSFKGL 166

RESULT 3  
 BAD\_HUMAN  
 ID BAD\_HUMAN STANDARD; PRT; 168 AA.  
 AC Q92934; O14803;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component 6) (Bcl-  
 XL/Bcl-2 associated death promoter) (BCL2-like 8 protein).  
 GN BAD OR BBC6 OR BCL2L8.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Yin D.X., Li Z., Huang B., Chen S., Zhou H.;  
 RT "A human protein that interacts with Bcl-2 and have homology to mouse  
 BAD.";  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A., AND PHOSPHORYLATION BY RAF-1.  
 RA MEDLINE=97083574; PubMed=8929532;  
 RA Wang H.-G., Rapp U.R., Reed J.C.;  
 RT "Bcl-2 targets the protein kinase Raf-1 to mitochondria.";  
 RL Cell 87:629-638(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Takayama S., Reed J.C.;  
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A., AND DIMERIZATION.  
 RC TISSUE=Bone marrow;  
 RX MEDLINE=98049554; PubMed=9388232;  
 RA Otilie S., Diaz J.-L., Horne W., Chang J., Wang Y., Wilson G.,  
 RA Chang S., Weeks S., Fritz L.C., Oltersdorf T.;  
 RT "Dimerization properties of human BAD.";  
 RL J. Biol. Chem. 272:30866-30872(1997).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg K.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Villalón D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Green E.D., Dickson M.C.,  
 RA Blakesley R.W., Touchman J.W., Shevchenko Y., Bouffard G.G.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [6]

RP STRUCTURE BY NMR OF 103-127.  
 RX MEDLINE=21073561; PubMed=11206074;  
 RA Petros A.M., Nettlesheim D.G., Wang Y., Olejniczak E.T., Meadows R.P.,  
 RA Mack J., Swift K., Matayoshi E.D., Zhang H., Thompson C.B.,  
 RA Resik S.W.;  
 RT "Rationale for Bcl-xL/Bad peptide complex formation from structure,  
 mutagenesis, and biophysical studies.";  
 RL Protein Sci. 9:2528-2534(2000).  
 CC -!- FUNCTION: Promotes cell death. Successfully competes for the  
 binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level  
 of heterodimerization of these proteins with BAX. Can reverse the  
 death repressor activity of Bcl-x(L), but not that of Bcl-2 (By  
 similarity). Appears to act as a link between growth factor  
 receptor signaling and the apoptotic pathways.  
 CC -!- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-  
 x(L), Bcl-2 and Bcl-w. Also binds protein S100A10 (By similarity).  
 CC The Ser-75/Ser-99 phosphorylated form binds 14-3-3 proteins (By  
 similarity).  
 CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon  
 phosphorylation, locates to the cytoplasm.  
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.  
 CC -!- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND  
 BAX for their pro-apoptotic activity and for their interaction  
 with anti-apoptotic members of the Bcl-2 family.  
 CC -!- PTM: Phosphorylated on Ser-75 in response to survival stimuli.  
 CC Subsequent phosphorylation on Ser-99 promotes heterodimerization  
 with 14-3-3 proteins. This interaction then facilitates the  
 phosphorylation at Ser-118, a site within the BH3 domain, leading  
 to the release of Bcl-x(L) and the promotion of cell survival.  
 CC Ser-99 is the major site of AKT/PKB phosphorylation, Ser-118 the  
 major site of protein kinase A (CAK) phosphorylation (By  
 similarity).  
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.  
 CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -!- CAUTION: Ref.1 sequence differs from that shown due to frameshifts  
 in position 64 and 91.  
 -----  
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 -----  
 DR EMBL; U6879; AAB36516.1; ALT\_FRAME.  
 DR EMBL; AF021792; AAB72092.1; -.  
 DR EMBL; AF031523; AAB88124.1; -.  
 DR EMBL; BC001901; AAB01901.1; -.  
 DR PDB; 1G5J; 07-FEB-01.  
 DR Genew; HGNC:936; BAD.  
 DR MIM; 603167; -.  
 DR GO; GO:0005737; Cytoplasm; NAS.  
 DR GO; GO:0005741; Mitochondrial outer membrane; NAS.  
 DR GO; GO:0005515; Protein binding activity; NAS.  
 DR GO; GO:0008632; P:apoptotic program; TAS.  
 DR GO; GO:0006917; P:induction of apoptosis; NAS.  
 DR InterPro; IPR000712; BCL2\_BH.  
 DR PROSITE; PS01259; BH3; FALSE\_NEG.  
 KW Apoptosis; Phosphorylation; Polymorphism; 3D-structure.  
 FT DOMAIN 110 124 BH3.  
 FT MOD\_RES 75 75  
 FT MOD\_RES 99 99  
 FT MOD\_RES 118 118  
 FT MOD\_RES 107 107  
 FT VARIANT 106 121  
 FT HELIX 106 121  
 FT SEQUENCE 168 AA; 18392 MW; 69FD8D27DDEE3241 CRC64;  
 SQ  
 Query Match 79.7%; Score 114; DB 1; Length 168;

DR EMBL; D89286; BAA13939.1; -;  
DR PIR; JC5575; JC5575.  
DR InterPro; IPR006587; VIT.  
DR InterPro; IPR002035; VWF\_A.  
DR Pfam; PF00092; vwa; 1.  
DR SMART; SM00609; VIT; 1.

cc between

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DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Maturase K (Intron maturase).  
 GN MATK.  
 OS Rhododendron tsusiophyllum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; Ericales; Ericaceae; Rhododeae; Rhododendron.  
 OX NCBI\_TaxID=49629;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,  
 RA Yukawa T.;  
 RT "Investigation of sectional relationships in the genus  
 RT Rhododendron (Ericaceae) based on matk sequences."  
 RL Shokubutsu Kenkyu Zasshi 73:143-154(1998).  
 CC -!- FUNCTION: Probably assists in splicing chloroplast group II  
 CC introns (BY similarity).  
 CC -!- SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK  
 CC SUBFAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; AB012750; BAA25871.1; -  
 DR InterPro; IPR000442; Intron\_maturase2.  
 DR InterPro; IPR002866; MatK\_N.  
 DR Pfam; PF01348; Intron\_maturase2; 1.  
 DR Pfam; PF01824; MatK\_N; 1.  
 DR mRNA processing; Chloroplast.  
 KW SEQUENCE 506 AA; 60569 MW; AEEL2FF8809C223E CRC64;  
 SQ SEQUENCE 506 AA; 60569 MW; AEEL2FF8809C223E CRC64;  
 Query Match 36.7%; Score 52.5; DB 1; Length 506;  
 Best Local Similarity 37.5%; Pred. No. 3.1;  
 Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;  
 QY 1 KNLWAA-----QRYGRELRLMSDEFESFK 25  
 Db 391 KPWWAALSDSDIIERFGRIYRLNLSHYSGSLK 422  
 RESULT 9  
 AROG\_YEAST STANDARD; PRT; 370 AA.  
 ID AROG\_YEAST  
 AC P32449;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited  
 DE (EC 4.1.2.15) (Phospho-2-keto-3-deoxyheptonate aldolase) (DHP  
 DE synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase).  
 GN ARO4 OR YBR249C OR YBR1701.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9225349; PubMed=1348717;  
 RA Kuenzler M., Paravicini G., Egli C., Irniger S., Braus G.H.;  
 RT "Cloning, primary structure and regulation of the ARO4 gene, encoding  
 RT the tyrosine-inhibited 3-deoxy-D-arabino-heptulosonate-7-phosphate  
 RT synthase from Saccharomyces cerevisiae."  
 RL Gene 113:67-74(1992).  
 RN [2]  
 RP REVISIONS TO 205-207.

RA Kuenzler M.;  
 RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=S288C;  
 RX MEDLINE=94078675; PubMed=8256522;  
 RA Doignon F., Biteau N., Aigle M., Crouzet M.;  
 RT "The complete sequence of a 6794 bp segment located on the right arm  
 RT of chromosome II of Saccharomyces cerevisiae. Finding of a putative  
 RT dUTPase in a yeast."  
 RL Yeast 9:1131-1137(1993).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=S288C;  
 RA Aljinovic G., Pohl F.M., Pohl T.M.;  
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: STEREOSPECIFIC CONDENSATION OF PHOSPHOENOLPYRUVATE (PEP)  
 CC AND D-ERYTHROSE-4-PHOSPHATE (E4P) GIVING RISE TO 3-DEOXY-D-  
 CC ARABINO-HEPTULOSONATE-7-PHOSPHATE (DAHP).  
 CC -!- CATALYTIC ACTIVITY: 2-dehydro-3-deoxy-D-arabino-heptonate 7-  
 CC phosphate + phosphate = phosphoenolpyruvate + D-erythrose 4-  
 CC phosphate + H(2)O.  
 CC -!- ENZYME REGULATION: INHIBITED BY TYROSINE.  
 CC -!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;  
 CC first step.  
 CC -!- INDUCTION: By amino acid starvation.  
 CC -!- SIMILARITY: BELONGS TO CLASS-I DAHP SYNTHETASE FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; X61107; CAA43419.1; -  
 DR EMBL; L20296; AAG65607.1; -  
 DR EMBL; Z36118; CAA85212.1; -  
 DR PIR; S38185; S38185.  
 DR HSP; P00886; IQR7.  
 DR SGD; S0000453; ARO4.  
 DR GO; GO:0003849; F:2-dehydro-3-deoxyphosphoheptonate aldolase . . . ; IDA.  
 DR InterPro; IPR006219; AROFGH.  
 DR InterPro; IPR006218; DAHP1/KDSA.  
 DR Pfam; PF00793; DAHP\_synth\_1; 1.  
 DR ProDom; PD005060; AROFGH; 1.  
 DR TIGRFAMs; TIGR00034; aroFGH; 1.  
 KW Aromatic amino acid biosynthesis; Lyase; Multigene family.  
 SQ SEQUENCE 370 AA; 39749 MW; 594ED48F24175979 CRC64;  
 Query Match 36.4%; Score 52; DB 1; Length 370;  
 Best Local Similarity 47.6%; Pred. No. 2.7;  
 Matches 10; Conservative 5; Mismatches 6; Indels 0; Gaps 0;  
 QY 2 NLWAAQRYGRELRLMSDEFEG 22  
 Db 80 DLAAQAYALRLKLKLSDELKG 100  
 RESULT 10  
 AP3\_ARATH STANDARD; PRT; 232 AA.  
 ID AP3\_ARATH  
 AC P35632; Q39003; Q8LB79; Q9S703; Q9SQ14; Q9SQ15; Q9SQ16; Q9SQ17;  
 AC Q9SQ18; Q9SQ19; Q9SQ20; Q9SQ21; Q9SQ22; Q9SX13;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Floral homeotic protein APETALA3.  
 GN AP3 OR AT3G54340 OR T12E18\_30.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Petal;  
RX MEDLINE=92154682; PubMed=1346756;  
RA Jack T., Brockman L.L., Meyerowitz E.M.;  
RT "The homeotic gene APETALA3 of Arabidopsis thaliana encodes a MADS  
RT box and is expressed in petals and stamens.";  
RL Cell 68:683-697(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Landsberg erecta;  
RX MEDLINE=95036018; PubMed=7948893;  
RA Okamoto H., Yano A., Shiraisi H., Okada K., Shimura Y.;  
RT "Genetic complementation of a floral homeotic mutation, apetal3,  
RT with an Arabidopsis thaliana gene homologous to DEFICIENS of  
RT Antirrhinum majus.";  
RL Plant Mol. Biol. 26:465-472(1994).  
RN [3]  
RP SEQUENCE FROM N.A., AND VARIANTS.  
RC STRAIN=cv. Bla-1, cv. Bretagny, cv. Bs-1, cv. Bu-0, cv. Bu-2,  
RC cv. Chi-1, cv. Co-1, cv. Columbia, cv. Corsacalla-1, cv. Cvi-0,  
RC cv. Gr-3, cv. J1-1, cv. Kas-1, cv. Kent, cv. Landsberg erecta,  
RC cv. Li-3, cv. Li-8, and cv. Lisse;  
RX MEDLINE=99126449; PubMed=9927474;  
RA Purugganan M.D., Suddith J.I.;  
RT "Molecular population genetics of floral homeotic loci: departures  
RT from the equilibrium-neutral model at the APETALA3 and PISTILLATA  
RT genes of Arabidopsis thaliana.";  
RL Genetics 151:839-848(1999).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RX MEDLINE=21016720; PubMed=11130713;  
RA Salanoubat M., Lemcke K., Rieger M., Ansong W., Unseld M.,  
RA Fartmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,  
RA Delserny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,  
RA De Simone V., Choisme N., Artiguenave F., Robert C., Brottier P.,  
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,  
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Beres V.,  
RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,  
RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,  
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,  
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordsiek G.,  
RA Reichelt J., Scharfe M., Schoen O., Barques M., Terol J., Climent J.,  
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,  
RA Cooke R., Laudie M., Berger-Liauro C., Purnelle B., Masuy D.,  
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,  
RA Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,  
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mexes H.-W.,  
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,  
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,  
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,  
RA Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,  
RA Preuss D., Lin X., Nierman W.C., Salzberg S.B., White O., Venter J.C.,  
RA Fraser C.M., Kaneo T., Nakamura Y., Sato S., Kato T., Asamizu E.,  
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,  
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,  
RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,  
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;  
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis  
RT thaliana.";  
RL Nature 408:820-822(2000).  
RN [5]  
RP SEQUENCE FROM N.A.  
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,  
RA Feldmann K.;  
RT "Full-length cDNA from Arabidopsis thaliana.";  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;  
RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the  
RT SSP consortium (Salk/Stanford/PGEC).";  
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE OF 36-128 FROM N.A.  
RC STRAIN=cv. Columbia;  
RX MEDLINE=99311297; PubMed=10382288;  
RA Brunel D., Froger N., Pelletier G.;  
RT "Development of amplified consensus genetic markers (ACGM) in Brassica  
RT napus from Arabidopsis thaliana sequences of known biological  
RT function.";  
RL Genome 42:387-402(1999).  
RN [8]  
RP FUNCTION.  
RX PubMed=8565821;  
RA Krizek B.A., Meyerowitz E.M.;  
RT "The Arabidopsis homeotic genes APETALA3 and PISTILLATA are sufficient  
RT to provide the B class organ identity function.";  
RL Development 122:11-22(1996).  
RN [9]  
RP CHARACTERIZATION.  
RX PubMed=8643482;  
RA Riechmann J.L., Krizek B.A., Meyerowitz E.M.;  
RT "Dimerization specificity of Arabidopsis MADS domain homeotic proteins  
RT APETALA1, APETALA3, PISTILLATA, and AGAMOUS.";  
RL Proc. Natl. Acad. Sci. U.S.A. 93:4793-4798(1996).  
RN [10]  
RP GENETIC REGULATION.  
RX PubMed=11283333;  
RA Ng M., Yanofsky M.F.;  
RT "Activation of the Arabidopsis B class homeotic genes by APETALA1.";  
RL Plant Cell 13:739-753(2001).  
RN [11]  
RP CHARACTERIZATION.  
RX PubMed=11205550;  
RA Honma T., Goto K.;  
RT "Complexes of MADS-box proteins are sufficient to convert leaves into  
RT floral organs.";  
RL Nature 409:525-529(2001).  
CC -!- FUNCTION: Probable transcription factor involved in the genetic  
CC control of flower development. Is required for normal development  
CC of petals and stamens in the wild-type flower. Forms an  
CC heterodimer with PISTILLATA that is required for autoregulation of  
CC both AP3 and PI genes. AP3/PI heterodimer interacts with APETALA1  
CC or SEPALLATA3 to form a ternary complex that could be responsible  
CC for the regulation of the genes involved in the flower  
CC development.  
CC -!- SUBUNIT: Forms an heterodimer with PISTILLATA, capable of binding  
CC to CARG-box sequences. AP3/PI heterodimer binds API or SEP3 to  
CC form complexes.  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- TISSUE SPECIFICITY: Expressed in petals and stamens.  
CC -!- INDUCTION: Positively regulated by the meristem identity proteins  
CC APETALA1 and LEAFY with the cooperation of UFO.  
CC -!- MISCELLANEOUS: Mutations in AP3 cause transformation of petals  
CC into sepals and stamens into carpels.  
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION  
CC FACTORS.  
CC -!- SIMILARITY: Contains 1 K-box dimerization domain.  
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CC -----  
DR EMBL; M86357; AAA32740.1; -.  
DR EMBL; D21125; BAA04665.1; -.  
DR EMBL; AF115798; AAD51887.1; -.  
DR EMBL; AF115799; AAD51888.1; -.

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DR EMBL; AF115800; AAD51889.1; -
DR EMBL; AF115801; AAD51890.1; -
DR EMBL; AF115802; AAD51891.1; -
DR EMBL; AF115803; AAD51892.1; -
DR EMBL; AF115804; AAD51893.1; -
DR EMBL; AF115805; AAD51894.1; -
DR EMBL; AF115806; AAD51895.1; -
DR EMBL; AF115807; AAD51896.1; -
DR EMBL; AF115808; AAD51897.1; -
DR EMBL; AF115809; AAD51898.1; -
DR EMBL; AF115810; AAD51899.1; -
DR EMBL; AF115811; AAD51900.1; -
DR EMBL; AF115812; AAD51901.1; -
DR EMBL; AF115813; AAD51902.1; -
DR EMBL; AF115814; AAD51903.1; -
DR EMBL; AL132971; CAB81799.1; -
DR EMBL; AY087369; AAM64919.1; -
DR EMBL; AY070397; AAL49893.1; -
DR EMBL; AY142590; AAN13159.1; -
DR EMBL; AF056541; AAD41557.1; -
DR PIR; A42095; A42095.
DR HSP; P11746; LMNN.
DR TRANSFAC; T01776; -.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_WADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS00666; MADS_BOX_2; 1.
KW Flowering: Transcription regulation; Activator; Developmental protein;
KW Nuclear protein; DNA-binding; Coiled coil; Polymorphism.
FT DOMAIN 3 57 MADS.
FT DOMAIN 93 165 K-BOX.
FT DOMAIN 75 164 COILED COIL (POTENTIAL).
FT VARIANT 31 31 K -> R (in strain cv. Lisse).
FT VARIANT 47 47 M -> T (in strain cv. Bretagne).
FT VARIANT 61 61 N -> D (in strain cv. Corsacalla-1).
FT VARIANT 73 73 T -> S (in strain cv. Li-8).
FT VARIANT 109 109 L -> V (in strain cv. Kas-1).
FT VARIANT 115 115 E -> K (in strains cv. Chi-1 and cv. Gr-3).

Query Match 35.7%; Score 51; DB 1; Length 232;
Best Local Similarity 44.4%; Pred. No. 2.3;
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;

QY 7 QRYG-----RELRRMSDEFEGSF 25
||| :|||: |||: |||
Db 107 QRLGCLDELDTQLRLRLEDEMENTFK 133

RESULT 11
CE05_MOUSE
ID CE05_MOUSE STANDARD; PRT; 851 AA.
AC Q8K2H3;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein C5orf5 homolog.
GN C5ORF5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10900;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schein C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SIMILARITY: Belongs to the FAM13 family.
CC -!- SIMILARITY: Contains 1 Rho-GAP domain.
-----
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DR EMBL; BC031465; AAH31465.1; -.
DR InterPro; IPR000198; RhoGAP.
DR Pfam; PF00620; RhoGAP; 1.
DR SMART; SM00324; RhoGAP; 1.
DR PROSITE; PS02338; RHO-GAP; 1.
KW GTPase activation.
FT DOMAIN 23 212 RHO-GAP.
FT DOMAIN 189 256 GTP-RICH.
SQ SEQUENCE 851 AA; 97054 MW; C2E26669FB6DB2CE CRC64;

Query Match 35.7%; Score 51; DB 1; Length 851;
Best Local Similarity 41.7%; Pred. No. 9.3;
Matches 10; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 KNLWAQRYGRELRRMSDEFEGSF 24
: ||| : |||: |||: |||
Db 782 EQLWKARAEEKKLKRLREFEF 805

RESULT 12
RMUC_PSEAE
ID RMUC_PSEAE STANDARD; PRT; 453 AA.
AC Q914U3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA recombination protein rmuc homolog.
GN RMUC OR PA1031.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.D., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
opportunistic pathogen.";
RL Nature 406:959-964(2000).

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CC -!- FUNCTION: Involved in DNA recombination (By similarity).
CC -!- SIMILARITY: BELONGS TO THE RMUC FAMILY.
CC -----
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CC -----
DR EMBL; AE004535; AAG04420.1; -.
DR F01; E83517; E83517.
DR InterPro; IPR003798; DUF195.
DR Pfam; PF02646; Rmuc; 1.
KW DNA recombination; Coiled coil; Complete proteome.
FT DOMAIN 16 201 COILED COIL (POTENTIAL).
SQ SEQUENCE 453 AA; 51539 MW; 1E7EA97E82EC5E4B CRC64;

Query Match 34.3%; Score 49; DB 1; Length 453;
Best Local Similarity 55.6%; Pred. No. 9.3;
Matches 10; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

QY 4 WAAQRYGR--ELRRMSDE 19
Db 65 WASERQGREELRLASE 82

RESULT 13
RAS3_RHIRA
ID RAS3_RHIRA STANDARD; PRT; 205 AA.
AC P22280;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ras-like protein 3.
GN RAS3.
OS Rhizomucor racemosus (Mucor circinelloides f. lusitanicus).
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
OC Mucor.
ON NCBI_TaxID=4841;
RX MEDLINE=9106174; PubMed=1701021;
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 1216B;
RA Casale W.L., McConnell D.G., Wang S.-Y., Lee Y.-J., Linz J.E.;
RT "Expression of a gene family in the dimorphic fungus Mucor racemosus
RL Mol. Cell. Biol. 10:6654-6663(1990).
CC -!- ENZYME REGULATION: ALTERNATE BETWEEN AN INACTIVE FORM BOUND TO GDP
CC AND AN ACTIVE FORM BOUND TO GTP. ACTIVATED BY A GUANINE
CC NUCLEOTIDE-EXCHANGE FACTOR (GEF) AND INACTIVATED BY A GTPASE-
CC ACTIVATING PROTEIN (GAP).
CC -!- SUBCELLULAR LOCATION: Plasma membrane.
CC -!- DEVELOPMENTAL STAGE: IN SPORULATING MYCELIUM AND MUCH LESS IN
CC GERMING AND YEAST.
CC -!- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RAS FAMILY.
CC -----
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CC -----
DR EMBL; M55177; AAA83379.1; -.
DR F01; C36365; C36365.
DR HSP; P01112; 1PLL.
DR InterPro; IPR003577; GTPase_Ras.
DR InterPro; IPR001806; Ras_trnsfmg.
DR InterPro; IPR005225; Small_GTP.
DR Pfam; PF00071; ras; 1.

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DR PRINTS; PR00449; RASTRNSFRMNG.
DR SMART; SM00173; RAS; 1.
DR TIGRFAMS; TIGR00231; small_gtp; 1.
KW GTP-binding; Prenylation; Lipoprotein.
FT NP_BIND 16 23 GTP (BY SIMILARITY).
FT NP_BIND 63 67 GTP (BY SIMILARITY).
FT NP_BIND 122 125 GTP (BY SIMILARITY).
FT DOMAIN 38 46 EFFECTOR REGION (PROBABLE).
FT LIPID 202 202 FARNESYL (BY SIMILARITY).
SQ SEQUENCE 205 AA; 23408 MW; DBF086466F09F50 CRC64;

Query Match 33.6%; Score 48; DB 1; Length 205;
Best Local Similarity 62.5%; Pred. No. 5.6;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 11 RELRRMSDEFEGSKG 26
Db 168 REIRRNKEQGRSKG 183

RESULT 14
6PGL_THEMEA
ID 6PGL_THEMEA STANDARD; PRT; 220 AA.
AC Q9X0N8;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 6-phosphogluconolactonase (EC 3.1.1.31) (6PGL).
GN PGL OR DEVB OR TM1154.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RX MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RL Nature 399:323-329(1999).
CC -!- FUNCTION: HYDROLYSIS OF 6-PHOSPHOGLUCONOLACTONE TO 6-
CC PHOSPHOGLUCONATE.
CC -!- CATALYTIC ACTIVITY: 6-phospho-D-glucono-1,5-lactone + H(2)O = 6-
CC phospho-D-gluconate.
CC -!- PATHWAY: Pentose phosphate pathway; second step.
CC -!- SIMILARITY: BELONGS TO THE GLUCOSAMINE/GALACTOSAMINE-6-PHOSPHATE
CC ISOMERASE FAMILY. 6-PHOSPHOGLUCONOLACTONASE SUBFAMILY.
CC -----
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CC -----
DR EMBL; AE001772; AAD36230.1; -.
DR F01; F72289; F72289.
DR TIGR; TM1154; -.
DR InterPro; IPR006143; Gluc_gal_isom.
DR InterPro; IPR005900; Phosphogluconac.
DR Pfam; PF01182; Glucosamine_iso; 1.
DR TIGRFAMS; TIGR01199; pgl; 1.
KW Hydrolase; Complete proteome.
SQ SEQUENCE 220 AA; 25325 MW; 9B0FD07EE01E60C3 CRC64;

Query Match 33.6%; Score 48; DB 1; Length 220;
Best Local Similarity 34.8%; Pred. No. 6;

```

Matches 8; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 5 AAQRYGRELRLMSDEFEFGSKGL 27  
| :| | | | :| | :| |  
DB 111 ACEKYEREIRSATDQFDLAILGM 133

## RESULT 15

THRC\_SOLTU  
ID THRC\_SOLTU STANDARD; PRT; 519 AA.  
AC Q9MT28;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Threonine synthase, chloroplast precursor (EC 4.2.3.1) (TS).  
OS Solanum tuberosum (Potato).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; lamids; Solanales; Solanaceae; Solanum.  
OX NCBI\_TaxID=4113;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Leaf;  
RX PubMed=10940468;  
RA Casazza A.P., Pasner A., Hoefgen R., Hesse H.;  
RT "Expression of threonine synthase from Solanum tuberosum L. is not  
metabolically regulated by photosynthesis-related signals or by  
nitrogenous compounds.";  
RL Plant Sci. 157:43-50(2000).  
CC -!- CATALYTIC ACTIVITY: O-phospho-L-homoserine + H(2)O = L-threonine +  
phosphate.  
CC -!- COFACTOR: Pyridoxal phosphate (By similarity).  
CC -!- ENZYME REGULATION: Allosterically activated by S-adenosyl-  
methionine (SAM) (By similarity).  
CC -!- PATHWAY: Threonine biosynthesis; last step.  
CC -!- SUBUNIT: Homodimer (By similarity).  
CC -!- SUBCELLULAR LOCATION: Chloroplast (By similarity).  
CC -!- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.  
-----  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
CC EMBL; AF082894; AAF74984.1; -  
DR HSSP; Q9S7B5; 1E5X.  
DR InterPro; IPR001926; B6\_enzyme\_beta.  
DR InterPro; IPR000634; S/T\_dehydratse.  
DR InterPro; IPR004450; Thr\_synthase.  
DR Pfam; PF00291; PALP; 1.  
DR TIGRFAMs; TIGR00260; thrC; 1.  
DR PROSITE; PS00165; DEHYDRATASE\_SER\_THR; 1.  
KW Threonine biosynthesis; Lyase; Pyridoxal phosphate; Allosteric enzyme;  
KW Chloroplast; Transit peptide.  
FT TRANSIT 1 40 CHLOROPLAST (BY SIMILARITY).  
FT CHAIN 41 519 THREONINE SYNTHASE.  
FT BINDING 196 196 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
SQ SEQUENCE 519 AA; 57412 MW; 114C0979CD231464 CRC64;

Query Match 33.6%; Score 48; DB 1; Length 519;  
Best Local Similarity 35.3%; Pred. No. 15;  
Matches 12; Conservative 6; Mismatches 8; Indels 8; Gaps 1;  
QY 2 NLWAAQRYGRELRLMSD-----EFGSGSKGL 27  
| :| | | | :| | :| |  
DB 165 NLFWAERFGKPLGMDTLWVKHCGISHTGSKDL 198

Search completed: September 15, 2003, 17:23:01  
Job time : 6.36429 secs

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model  
Run on: September 15, 2003, 17:17:31 ; Search time 29.3143 Seconds  
(without alignments)  
237.680 Million cell updates/sec

Title: US-09-544-664-56  
Perfect score: 143  
Sequence: 1 KNLWAAQRYGRELRRMSDEFEQSFKGL 27

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : SPTREMBL23:\*
- 1: sp\_archaea:\*
  - 2: sp\_bacteria:\*
  - 3: sp\_fungi:\*
  - 4: sp\_human:\*
  - 5: sp\_invertebrate:\*
  - 6: sp\_mammal:\*
  - 7: sp\_mhc:\*
  - 8: sp\_organelle:\*
  - 9: sp\_phage:\*
  - 10: sp\_plant:\*
  - 11: sp\_rodent:\*
  - 12: sp\_virus:\*
  - 13: sp\_vertebrate:\*
  - 14: sp\_unclassified:\*
  - 15: sp\_irvirus:\*
  - 16: sp\_bacteriap:\*
  - 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			ID	Description
		Match	Length	DB		
1	87	60.8	146	13	Q9I9N2	Q9I9N2 brachydanio
2	53	37.1	196	16	Q8VJS3	Q8VJS3 mycobacter
3	53	37.1	223	16	Q10843	Q10843 mycobacter
4	53	37.1	946	11	Q8K016	Q8K016 mus muscul
5	52.5	36.7	505	8	Q47148	Q47148 menziesia c
6	52.5	36.7	506	8	Q47149	Q47149 rhododendro
7	52.5	36.7	506	8	Q47171	Q47171 rhododendro
8	52.5	36.7	506	8	Q63960	Q63960 rhododendro
9	52.5	36.7	506	8	Q62982	Q62982 rhododendro
10	52.5	36.7	506	8	Q62975	Q62975 rhododendro
11	52.5	36.7	506	8	Q62972	Q62972 rhododendro
12	52.5	36.7	506	8	Q62989	Q62989 rhododendro
13	52.5	36.7	506	8	Q62978	Q62978 rhododendro
14	52.5	36.7	506	8	Q47155	Q47155 rhododendro
15	52.5	36.7	506	8	Q47152	Q47152 rhododendro
16	52.5	36.7	506	8	Q47173	Q47173 rhododendro

17	52.5	36.7	506	8	Q62990	Q62990 rhododendro
18	52.5	36.7	506	8	Q62974	Q62974 rhododendro
19	52.5	36.7	506	8	Q62993	Q62993 menziesia m
20	52.5	36.7	506	8	Q47170	Q47170 rhododendro
21	52.5	36.7	506	8	Q47174	Q47174 rhododendro
22	52.5	36.7	506	8	Q62983	Q62983 rhododendro
23	52.5	36.7	506	8	Q62980	Q62980 rhododendro
24	52.5	36.7	506	8	Q62981	Q62981 rhododendro
25	52.5	36.7	506	8	Q62977	Q62977 rhododendro
26	52.5	36.7	506	8	Q47168	Q47168 menziesia p
27	52.5	36.7	506	8	Q62988	Q62988 rhododendro
28	52.5	36.7	506	8	Q62973	Q62973 rhododendro
29	52.5	36.7	506	8	Q62992	Q62992 ledum palus
30	52.5	36.7	506	8	Q47175	Q47175 rhododendro
31	52.5	36.7	506	8	Q8HSP1	Q8HSP1 rhododendro
32	52.5	36.7	506	8	Q8HSP0	Q8HSP0 rhododendro
33	52.5	36.7	506	8	Q8HSN9	Q8HSN9 rhododendro
34	52.5	36.7	506	8	Q8HSN8	Q8HSN8 rhododendro
35	52.5	36.7	506	8	Q8HSN7	Q8HSN7 rhododendro
36	52.5	36.7	506	8	Q8HSN6	Q8HSN6 rhododendro
37	52.5	36.7	506	8	Q8HSN5	Q8HSN5 rhododendro
38	52.5	36.7	506	8	Q8HSN4	Q8HSN4 rhododendro
39	52.5	36.7	507	8	Q62985	Q62985 rhododendro
40	52.5	36.7	507	8	Q62986	Q62986 rhododendro
41	52.5	36.7	508	8	Q62979	Q62979 rhododendro
42	52	36.4	471	17	Q8ZY71	Q8ZY71 pyrobaculum
43	51.5	36.0	506	8	Q47153	Q47153 rhododendro
44	51.5	36.0	506	8	Q47160	Q47160 rhododendro
45	51.5	36.0	506	8	Q8HSP4	Q8HSP4 rhododendro

ALIGNMENTS

RESULT 1:

Q9I9N2 PRELIMINARY; PRT; 146 AA.  
AC Q9I9N2;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
DE Bad.  
GN BAD.  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20373792; PubMed=10917738;  
RA Inohara N., Nunez G.;  
RT "Genes with homology to mammalian apoptosis regulators identified in zebrafish."  
RL Cell Death Differ. 7:509-510(2000).  
DR EMBL; AF231017; AAF66962.2; -;  
DR HSP; Q92934; 1G5J.  
DR ZFIN; ZDB-GENE-000616-1; bad.  
SQ SEQUENCE 146 AA; 16546 MW; 28A5650BB5107ECB CRC64;  
Query Match 60.8%; Score 87; DB 13; Length 146;  
Best Local Similarity 65.2%; Pred. No. 5.9e-05;  
Matches 15; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
QY 3 LWAAQRYGRELRRMSDEFEQSFK 25  
||||:||||:||||:|  
DB 89 LWAAKYGQQLRRMSDEFDXGK 111  
RESULT 2  
Q8VJS3 PRELIMINARY; PRT; 196 AA.  
ID Q8VJS3  
AC Q8VJS3;

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Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 2 NLWAAQRYGRELRRMSD 18
    ||||| ||| : | |
Db 165 NLWAADEYNRAIARGED 181

RESULT 4
Q8K016 PRELIMINARY; PRT; 946 AA.
ID Q8K016
AC Q8K016;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Inter-alpha trypsin inhibitor, heavy chain 2.
GN ITIH2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RP SEQUENCE-LIVER;
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC034341; AAH34341.1; -.
DR MGD; MGI:96619; Itih2.
DR InterPro; IPR006587; VIT.
DR InterPro; IPR002035; VWF_A.
DR SMART; SM00609; VIT; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS00327; VWA; 1.
DR PROSITE; PS0234; VWFA; 1.
SQ SEQUENCE 946 AA; 105945 MW; 8B17DBA71B85BC5C CRC64;

Query Match 37.1%; Score 53; DB 11; Length 946;
Best Local Similarity 34.6%; Pred. No. 48;
Matches 9; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 2 NLWAAQRYGRELRRMSDEFSGFKGL 27
    | : | : | ||| : | :
Db 212 NVWIMEPQGMRFHLVDPDTEFGHFGQV 237

RESULT 5
O47148 PRELIMINARY; PRT; 505 AA.
ID O47148
AC O47148;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Ribosomal maturase (intron maturase) (Maturase K) (Fragment).
GN MATK.
OS Menziesia ciliicalyx.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Menziesia.
OX NCBI_TaxID=49154;
[1]
RN SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RA Kron K.A.;
RT "Phylogenetics of Rhododendroideae (Ericaceae).";
RL Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
CC INTRONS (BY SIMILARITY).
CC -!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
CC AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
CC MITOCHONDRIAL INTRONS.
DR EMBL; U61331; AAC15245.2; -.
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_maturase2; 1.
DR Pfam; PF01824; MatK_N; 1.

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KW mRNA processing; Chloroplast.
FT NON_FER 1
SQ SEQUENCE 505 AA; 60233 MW; E5F927AD2E57DE5 CRC64;

Query Match 36.7%; Score 52.5; DB 8; Length 505;
Best Local Similarity 37.5%; Pred. No. 28;
Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

QY 1 KNLWAA-----QRYGRELRRMSDEFECSFK 25
   | :||| :||| | :| :|||
Db 390 KPVWAALSDSDIIERFGRIYRNLSHYSGSLK 421

RESULT 6
O47149 ID O47149 PRELIMINARY; PRT; 506 AA.
AC O47149;
DT 01-JUN-1998 (TREMELrel. 06, Created)
DT 01-JUN-1998 (TREMELrel. 06, Last sequence update)
DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
DE Ribosomal maturase (Intron maturase) (Maturase K).
GN MATK.
OS Rhododendron kiusianum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
OX NCBI_TaxID=49167;
RN [1]
RP SEQUENCE FROM N.A.
RA Kron K.A.;
RT "Phylogenetics of Rhododendroideae (Ericaceae).";
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
CC INTRONS (BY SIMILARITY).
CC -!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
CC AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
CC MITOCHONDRIAL INTRONS.
DR EMBL; U61332; AAB93753.1; -.
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_maturase2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW mRNA processing; Chloroplast.
SQ SEQUENCE 506 AA; 60502 MW; 0009EA88CD28549F CRC64;

Query Match 36.7%; Score 52.5; DB 8; Length 506;
Best Local Similarity 37.5%; Pred. No. 28;
Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

QY 1 KNLWAA-----QRYGRELRRMSDEFECSFK 25
   | :||| :||| | :| :|||
Db 391 KPVWAALSDSDIIERFGRIYRNLSHYSGSLK 422

RESULT 7
O47171 ID O47171 PRELIMINARY; PRT; 506 AA.
AC O47171;
DT 01-JUN-1998 (TREMELrel. 06, Created)
DT 01-JUN-1998 (TREMELrel. 06, Last sequence update)
DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
DE Ribosomal maturase (Intron maturase) (Maturase K).
GN MATK.
OS Rhododendron edgeworthii.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
OX NCBI_TaxID=49162;
RN [1]
RP SEQUENCE FROM N.A.
RA Kron K.A.;
RT "Phylogenetics of Rhododendroideae (Ericaceae).";
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
CC INTRONS (BY SIMILARITY).
CC -!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
CC AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
CC MITOCHONDRIAL INTRONS.
DR EMBL; U61332; AAB93753.1; -.
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_maturase2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW mRNA processing; Chloroplast.
SQ SEQUENCE 506 AA; 60502 MW; 0009EA88CD28549F CRC64;

Query Match 36.7%; Score 52.5; DB 8; Length 506;
Best Local Similarity 37.5%; Pred. No. 28;
Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

QY 1 KNLWAA-----QRYGRELRRMSDEFECSFK 25
   | :||| :||| | :| :|||
Db 391 KPVWAALSDSDIIERFGRIYRNLSHYSGSLK 422

RESULT 8
O63960 ID O63960 PRELIMINARY; PRT; 506 AA.
AC O63960;
DT 01-AUG-1998 (TREMELrel. 07, Created)
DT 01-AUG-1998 (TREMELrel. 07, Last sequence update)
DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
DE Ribosomal maturase (Intron maturase) (Maturase K).
GN MATK OR YCF14.
OS Rhododendron tashiroi, and
OS Rhododendron farraerae.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
OX NCBI_TaxID=75582, 75580;
RN [1]
RP SEQUENCE FROM N.A.
RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
RA Yukawa T.;
RL J. Jpn. Bot. 0:0-0(1998).
CC -!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
CC INTRONS (BY SIMILARITY).
CC -!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
CC AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
CC MITOCHONDRIAL INTRONS.
DR EMBL; AB012749; BAA25870.1; -.
DR EMBL; AB012745; BAA25866.1; -.
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_maturase2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW mRNA processing; Chloroplast.
SQ SEQUENCE 506 AA; 60389 MW; DE0C07AEE608B787 CRC64;

Query Match 36.7%; Score 52.5; DB 8; Length 506;
Best Local Similarity 37.5%; Pred. No. 28;
Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

QY 1 KNLWAA-----QRYGRELRRMSDEFECSFK 25
   | :||| :||| | :| :|||
Db 391 KPVWAALSDSDIIERFGRIYRNLSHYSGSLK 422

RESULT 9
O62982 ID O62982 PRELIMINARY; PRT; 506 AA.
AC O62982;
DT 01-AUG-1998 (TREMELrel. 07, Created)

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RT "Phylogenetics of Rhododendroideae (Ericaceae).";
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
CC INTRONS (BY SIMILARITY).
CC -!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
CC AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
CC MITOCHONDRIAL INTRONS.
DR EMBL; U61354; AAB93748.1; -.
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_maturase2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW mRNA processing; Chloroplast.
SQ SEQUENCE 506 AA; 60485 MW; 8A6353BFC5F4DC85 CRC64;

Query Match 36.7%; Score 52.5; DB 8; Length 506;
Best Local Similarity 37.5%; Pred. No. 28;
Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

QY 1 KNLWAA-----QRYGRELRRMSDEFECSFK 25
   | :||| :||| | :| :|||
Db 391 KPVWAALSDSDIIERFGRIYRNLSHYSGSLK 422

RESULT 8
O63960 ID O63960 PRELIMINARY; PRT; 506 AA.
AC O63960;
DT 01-AUG-1998 (TREMELrel. 07, Created)
DT 01-AUG-1998 (TREMELrel. 07, Last sequence update)
DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
DE Ribosomal maturase (Intron maturase) (Maturase K).
GN MATK OR YCF14.
OS Rhododendron tashiroi, and
OS Rhododendron farraerae.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
OX NCBI_TaxID=75582, 75580;
RN [1]
RP SEQUENCE FROM N.A.
RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
RA Yukawa T.;
RL J. Jpn. Bot. 0:0-0(1998).
CC -!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
CC INTRONS (BY SIMILARITY).
CC -!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
CC AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
CC MITOCHONDRIAL INTRONS.
DR EMBL; AB012749; BAA25870.1; -.
DR EMBL; AB012745; BAA25866.1; -.
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_maturase2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW mRNA processing; Chloroplast.
SQ SEQUENCE 506 AA; 60389 MW; DE0C07AEE608B787 CRC64;

Query Match 36.7%; Score 52.5; DB 8; Length 506;
Best Local Similarity 37.5%; Pred. No. 28;
Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

QY 1 KNLWAA-----QRYGRELRRMSDEFECSFK 25
   | :||| :||| | :| :|||
Db 391 KPVWAALSDSDIIERFGRIYRNLSHYSGSLK 422

RESULT 9
O62982 ID O62982 PRELIMINARY; PRT; 506 AA.
AC O62982;
DT 01-AUG-1998 (TREMELrel. 07, Created)

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DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
 DE Ribosomal maturase (Intron maturase) (Maturase K).  
 GN MATK.  
 OS Rhododendron nipponicum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.  
 OX NCBI\_TaxID=75577;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,  
 RA Yukawa T.;  
 RT "Investigation of Sectional Relationships in the Genus  
 RT Rhododendron(Ericaceae) based on matk Sequences.";  
 RL J. Jpn. Bot. 0:0-0(1998).  
 CC -!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II  
 CC INTRONS (BY SIMILARITY).  
 CC -!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,  
 CC AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY  
 CC MITOCHONDRIAL INTRONS.  
 DR EMBL; AB012739; BAA25860.1; -.  
 DR InterPro; IPR000442; Intron\_maturase2.  
 DR InterPro; IPR002866; MatK\_N.  
 DR Pfam; PF01348; Intron\_maturas2; 1.  
 DR Pfam; PF01824; MatK\_N; 1.  
 DR mRNA processing; Chloroplast.  
 KW SEQUENCE 506 AA; 60419 MW; 1F95132CCF4F6B40 CRC64;  
 SQ SEQUENCE 506 AA; 60419 MW; 1F95132CCF4F6B40 CRC64;  
 Query Match 36.7%; Score 52.5; DB 8; Length 506;  
 Best Local Similarity 37.5%; Pred. No. 28;  
 Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;  
 QY 1 KNLWAA-----QRYGRELRRMSDEFGSK 25  
 Db 391 KPWWAALSDSDIIERFGRIYRNLSHYSGSLK 422

RESULT 10  
 O62975 PRELIMINARY; PRT; 506 AA.  
 AC O62975;  
 DT 01-AUG-1998 (TREMBLrel. 07, Created)  
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
 DE Ribosomal maturase (Intron maturase) (Maturase K).  
 GN MATK.  
 OS Rhododendron ponticum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.  
 OX NCBI\_TaxID=49628;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,  
 RA Yukawa T.;  
 RT "Investigation of Sectional Relationships in the Genus  
 RT Rhododendron(Ericaceae) based on matk Sequences.";  
 RL J. Jpn. Bot. 0:0-0(1998).  
 CC -!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II  
 CC INTRONS (BY SIMILARITY).  
 CC -!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,  
 CC AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY  
 CC MITOCHONDRIAL INTRONS.  
 DR EMBL; AB012732; BAA25853.1; -.  
 DR InterPro; IPR000442; Intron\_maturase2.  
 DR InterPro; IPR002866; MatK\_N.  
 DR Pfam; PF01348; Intron\_maturas2; 1.  
 DR Pfam; PF01824; MatK\_N; 1.  
 DR mRNA processing; Chloroplast.  
 KW SEQUENCE 506 AA; 60449 MW; 21DF700B071B5B8 CRC64;  
 SQ SEQUENCE 506 AA; 60449 MW; 21DF700B071B5B8 CRC64;

Query Match 36.7%; Score 52.5; DB 8; Length 506;  
 Best Local Similarity 37.5%; Pred. No. 28;  
 Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;  
 QY 1 KNLWAA-----QRYGRELRRMSDEFGSK 25  
 Db 391 KPWWAALSDSDIIERFGRIYRNLSHYSGSLK 422

RESULT 11  
 O62972 PRELIMINARY; PRT; 506 AA.  
 AC O62972;  
 DT 01-AUG-1998 (TREMBLrel. 07, Created)  
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
 DE Ribosomal maturase (Intron maturase) (Maturase K).  
 GN MATK.  
 OS Rhododendron ovatum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.  
 OX NCBI\_TaxID=49169;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,  
 RA Yukawa T.;  
 RT "Investigation of Sectional Relationships in the Genus  
 RT Rhododendron(Ericaceae) based on matk Sequences.";  
 RL J. Jpn. Bot. 0:0-0(1998).  
 CC -!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II  
 CC INTRONS (BY SIMILARITY).  
 CC -!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,  
 CC AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY  
 CC MITOCHONDRIAL INTRONS.  
 DR EMBL; AB012729; BAA25850.1; -.  
 DR InterPro; IPR000442; Intron\_maturase2.  
 DR InterPro; IPR002866; MatK\_N.  
 DR Pfam; PF01348; Intron\_maturas2; 1.  
 DR Pfam; PF01824; MatK\_N; 1.  
 DR mRNA processing; Chloroplast.  
 KW SEQUENCE 506 AA; 60493 MW; D230E54B8C20FEF0 CRC64;  
 SQ SEQUENCE 506 AA; 60493 MW; D230E54B8C20FEF0 CRC64;  
 Query Match 36.7%; Score 52.5; DB 8; Length 506;  
 Best Local Similarity 37.5%; Pred. No. 28;  
 Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;  
 QY 1 KNLWAA-----QRYGRELRRMSDEFGSK 25  
 Db 391 KPWWAALSDSDIIERFGRIYRNLSHYSGSLK 422

RESULT 12  
 O62989 PRELIMINARY; PRT; 506 AA.  
 AC O62989;  
 DT 01-AUG-1998 (TREMBLrel. 07, Created)  
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
 DE Ribosomal maturase (Intron maturase) (Maturase K).  
 GN MATK.  
 OS Rhododendron indicum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.  
 OX NCBI\_TaxID=75581;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,  
 RA Yukawa T.;

```

RT "Investigation of Sectional Relationships in the Genus
RL Rhododendron(Ericaceae) based on matk Sequences.";
RL J. Jpn. Bot. 0:0-0(1998).
CC -!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
CC INTRONS (BY SIMILARITY).
CC -!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
CC AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
CC MITOCHONDRIAL INTRONS.
DR EMBL; AB012747; BAA25868.1; -.
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_maturas2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW mRNA processing; Chloroplast.
SQ SEQUENCE 506 AA; 60489 MW; 6D38A1D4D6FEC9BF CRC64;

Query Match 36.7%; Score 52.5; DB 8; Length 506;
Best Local Similarity 37.5%; Pred. No. 28;
Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

QY 1 KNLWAA-----ORYGRELRRMSDEFECSFK 25
   | :||| :||| | :||| :|||
Db 391 KPVAALSDSDIIERFGRIYRNLSHYSGSLK 422

RESULT 13
O62978 PRELIMINARY; PRT; 506 AA.
AC O62978;
DT 01-AUG-1998 (Tremblrel. 07, Created)
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Ribosomal maturase (Intron maturase) (Maturase X).
GN MATK.
OS Rhododendron canadense.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
OX NCBI_TaxID=49465;
RN [1]
RP SEQUENCE FROM N.A.
RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
RA Yukawa T.;
RT "Investigation of Sectional Relationships in the Genus
RT Rhododendron(Ericaceae) based on matk Sequences.";
RL J. Jpn. Bot. 0:0-0(1998).
CC -!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
CC INTRONS (BY SIMILARITY).
CC -!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
CC AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
CC MITOCHONDRIAL INTRONS.
DR EMBL; AB012735; BAA25836.1; -.
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_maturas2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW mRNA processing; Chloroplast.
SQ SEQUENCE 506 AA; 60350 MW; 5E832589ED64EA25 CRC64;

Query Match 36.7%; Score 52.5; DB 8; Length 506;
Best Local Similarity 37.5%; Pred. No. 28;
Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

QY 1 KNLWAA-----ORYGRELRRMSDEFECSFK 25
   | :||| :||| | :||| :|||
Db 391 KPVAALSDSDIIERFGRIYRNLSHYSGSLK 422

RESULT 14
O47155 PRELIMINARY; PRT; 506 AA.
AC O47155;

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DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Ribosomal maturase (Intron maturase) (Maturase K).
GN MATK.
OS Rhododendron hongkongense.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
OX NCBI_TaxID=49165;
RN [1]
RP SEQUENCE FROM N.A.
RA Kron K.A.;
RT "Phylogenetics of Rhododendroideae (Ericaceae).";
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
CC INTRONS (BY SIMILARITY).
CC -!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
CC AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
CC MITOCHONDRIAL INTRONS.
DR EMBL; U61338; AAB93751.1; -.
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_maturas2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW mRNA processing; Chloroplast.
SQ SEQUENCE 506 AA; 60406 MW; 4B5C675CE32218D8 CRC64;

Query Match 36.7%; Score 52.5; DB 8; Length 506;
Best Local Similarity 37.5%; Pred. No. 28;
Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

QY 1 KNLWAA-----ORYGRELRRMSDEFECSFK 25
   | :||| :||| | :||| :|||
Db 391 KPVAALSDSDIIERFGRIYRNLSHYSGSLK 422

RESULT 15
O47152 PRELIMINARY; PRT; 506 AA.
AC O47152;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Ribosomal maturase (Intron maturase) (Maturase K).
GN MATK.
OS Rhododendron tomentosum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
OX NCBI_TaxID=49170;
RN [1]
RP SEQUENCE FROM N.A.
RA Kron K.A.;
RT "Phylogenetics of Rhododendroideae (Ericaceae).";
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
CC INTRONS (BY SIMILARITY).
CC -!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
CC AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
CC MITOCHONDRIAL INTRONS.
DR EMBL; U61335; AAB93757.1; -.
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_maturas2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW mRNA processing; Chloroplast.
SQ SEQUENCE 506 AA; 60439 MW; 855FDBDB8A5F800D CRC64;

Query Match 36.7%; Score 52.5; DB 8; Length 506;
Best Local Similarity 37.5%; Pred. No. 28;

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 15, 2003, 17:16:01 ; Search time 22.6286 Seconds  
(without alignments)  
112.231 Million cell updates/sec

Title: US-09-544-664-28

Perfect score: 84

Sequence: 1 QRYGRELRLMSDFEG (16)

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*
- 3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*
- 4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*
- 5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*
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- 9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*
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- 22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*
- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	100.0	16	20	AA1980.DAT
2	84	100.0	16	21	AA1981.DAT
3	84	100.0	23	17	AA1982.DAT
4	84	100.0	26	21	AA1983.DAT
5	84	100.0	26	21	AA1984.DAT
6	84	100.0	27	21	AA1985.DAT
7	84	100.0	27	21	AA1986.DAT
8	84	100.0	28	21	AA1987.DAT
9	84	100.0	162	22	AA1988.DAT

10	84	100.0	204	17	AA1989.DAT
11	84	100.0	204	19	AA1990.DAT
12	84	100.0	204	19	AA1991.DAT
13	84	100.0	204	19	AA1992.DAT
14	84	100.0	204	19	AA1993.DAT
15	84	100.0	204	19	AA1994.DAT
16	84	100.0	204	22	AA1995.DAT
17	84	100.0	204	24	AA1996.DAT
18	84	100.0	567	22	AA1997.DAT
19	73	86.9	16	20	AA1998.DAT
20	73	86.9	16	21	AA1999.DAT
21	73	86.9	18	23	AA2000.DAT
22	73	86.9	18	23	AA2001.DAT
23	73	86.9	20	23	AA2002.DAT
24	73	86.9	20	23	AA2003.DAT
25	73	86.9	21	23	AA2004.DAT
26	73	86.9	21	23	AA2005.DAT
27	73	86.9	21	23	AA2006.DAT
28	73	86.9	22	23	AA2007.DAT
29	73	86.9	23	23	AA2008.DAT
30	73	86.9	24	23	AA2009.DAT
31	73	86.9	24	23	AA2010.DAT
32	73	86.9	24	23	AA2011.DAT
33	73	86.9	25	23	AA2012.DAT
34	73	86.9	25	23	AA2013.DAT
35	73	86.9	25	23	AA2014.DAT
36	73	86.9	25	23	AA2015.DAT
37	73	86.9	25	23	AA2016.DAT
38	73	86.9	25	23	AA2017.DAT
39	73	86.9	25	23	AA2018.DAT
40	73	86.9	25	23	AA2019.DAT
41	73	86.9	25	23	AA2020.DAT
42	73	86.9	25	23	AA2021.DAT
43	73	86.9	25	23	AA2022.DAT
44	73	86.9	25	23	AA2023.DAT
45	73	86.9	25	23	AA2024.DAT

ALIGNMENTS

RESULT 1  
AA1989.DAT  
ID AA1989.DAT standard; peptide; 16 AA.

XX AA1989.DAT

AC AA1989.DAT

DE AA1989.DAT

Mouse BAD BH3 domain.

BH3 domain; cell death agonist; bcl homology domain; BCL-2 family; apoptosis promoter; cancer cell; virus infected cell; inflammation; autophagy promoting cell; cancer; lymphoproliferative condition; arthritis; autoimmune disease; therapy.

OS Mus sp.

XX W0916787-A1.

XX 08-APR-1998

XX 22-SEP-1998; 98WO-US19765.

XX 07-OCT-1997; 97US-0945039.

XX 26-SEP-1997; 97US-0060133.

XX (UNIW ) UNIV WASHINGTON.

XX Korsmeyer SJ;

XX WPI; 1999-255058/21.

XX

PT Bcl homology domain 3 polypeptide  
 PS Example 1; Fig 4; 104pp; English.  
 XX  
 CC This sequence represents the BH3 domain of mouse BAD.  
 CC The invention relates to a bcl homology domain 3 (BH3 domain),  
 CC derived from a proapoptotic member of the BCL-2 family. The  
 CC BH3 polypeptide can be used in a method for promoting apoptosis in a  
 CC target cell, especially where the cell is a cancer cell, a virus infected  
 CC cell or an antibody producing cell. The BH3 polypeptide can be used  
 CC in therapeutic compositions for treating disease including cancer, other  
 CC lymphoproliferative conditions, arthritis, inflammation, and autoimmune  
 CC diseases, which may result from the down regulation of cell death  
 CC regulation.  
 XX  
 CC  
 SQ Sequence 16 AA;  
 Query Match 100.0%; Score 84; DB 20; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QRYGRELRRMSDEFEQ 16  
 Db 1 QRYGRELRRMSDEFEQ 16  
 RESULT 2  
 AAB37028  
 ID AAB37028 standard; peptide; 16 AA.  
 AC AAB37028;  
 XX  
 DT 28-FEB-2001 (first entry)  
 XX  
 DE Bcl2 polypeptide BH3 domain peptide #28.  
 XX  
 KW Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;  
 KW cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;  
 KW apoptosis modulation; B cell lymphoma/Leukemia 2; cancer; prostate;  
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;  
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;  
 KW stroke; myocardial infarction.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200059526-A1.  
 XX  
 PD 12-OCT-2000.  
 XX  
 PF 06-APR-2000; 2000WO-US09352.  
 XX  
 PR 07-APR-1999; 99US-0128202.  
 XX  
 PA (UYJE-) UNIV JEFFERSON THOMAS.  
 XX  
 PI Huang Z, Wang J, Zhang Z, Shan S, Lu Z;  
 XX  
 DR WPI; 2000-679325/66.  
 XX  
 PT New peptide conjugates for modulating apoptosis or for inhibiting B  
 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for  
 PT treating neurodegenerative disorders, stroke, or cancer -  
 XX  
 PS Claim 18; Page 18; 74pp; English.  
 XX  
 CC The invention relates to a peptide conjugate having the formula:  
 CC (R-X)<sub>n</sub>-peptide where n = 1-10; X = C=O, when the R-X group is attached  
 CC to the N-terminus of the peptide, or a side chain of the peptide where  
 CC the functional group of the side chain is NH2 or OH; or X = O or NH,  
 CC when the R-X group is attached to the C-terminus of the peptide, or a  
 CC side chain of the peptide, where the side chain functional group is COOH  
 CC or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one  
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally

CC monosubstituted with a 1-5C straight or branched chain alkyl group,  
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain  
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples  
 CC of the peptide portion of the conjugate. The peptides represent analogues  
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of  
 CC the BH3 domain of the cell death agonist Bad. The peptide conjugate is  
 CC useful for modulating apoptosis in the cells of a subject, or for  
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of  
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2  
 CC function. In particular, the peptide conjugate is useful for treating a  
 CC subject afflicted with a cancer characterized by cancer cells that  
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,  
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or  
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide  
 CC conjugate is also useful for treating disorders characterized by  
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired  
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.  
 XX  
 SQ Sequence 16 AA;  
 Query Match 100.0%; Score 84; DB 21; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QRYGRELRRMSDEFEQ 16  
 Db 1 QRYGRELRRMSDEFEQ 16  
 RESULT 3  
 AAR95166  
 ID AAR95166 standard; peptide; 23 AA.  
 XX  
 AC AAR95166;  
 XX  
 DT 03-JAN-1997 (first entry)  
 XX  
 DE bcl-x(L)/bcl-2 associated death promoter epitope, residues 138-160.  
 XX  
 KW Epitope; murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke;  
 KW polypeptide; bcl-x; cell death; regulate; BH1; BH2; apoptotic cell death;  
 KW cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS;  
 KW neurodegenerative disease; senescence; ischaemia; neoplasia.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO9613614-A1.  
 XX  
 PD 09-MAY-1996.  
 XX  
 PF 31-OCT-1995; 95WO-US14246.  
 XX  
 PR 31-OCT-1994; 94US-0333565.  
 XX  
 PA (UNIW ) UNIV WASHINGTON.  
 XX  
 PI Korsmeyer SJ;  
 XX  
 DR WPI; 1996-251465/25.  
 XX  
 PT Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter -  
 PT useful to treat neoplasia and apoptosis and to identify agents  
 PT inhibiting its binding to bcl-2 or bcl-x(L) to form heteromultimers  
 XX  
 PS Claim 2; Page 103; 130pp; English.  
 XX  
 CC The sequences given in AAR95155-67 represent epitopes derived from the  
 CC murine bcl-x(L)/bcl-2 associated death promoter (Bad) polypeptide (see  
 CC also AAR95168). Bad is a 22.1 kD protein which interacts with bcl-2 and  
 CC bcl-x proteins and regulates cell death. It has homology to the bcl-2-  
 CC related family clustered in the BH1 and BH2 domain. Bad has been found  
 CC to hybridize to bcl-x(L) and bcl-2 in yeast two-hybrid assays and in  
 CC vivo in mammalian cells. Overexpressed Bad counters the death

CC inhibitory activity of bcl-x(L), but is much less effective at countering  
 CC the death inhibitory activity of bcl-2. Bad expression can accelerate  
 CC apoptotic cell death induced by cytokine deprivation in an IL-3 dependent  
 CC cell line expressing bcl-x(L), and its also counters the death repressor  
 CC activity of bcl-x(L). Bad competes with Bax for binding to bcl-x(L).  
 CC Bad may be used to identify agents which inhibit its binding to bcl-2  
 CC or bcl-x(L) to form heterodimers. Such agents may be used to treat  
 CC neurodegenerative diseases, immunodeficiency diseases, e.g. AIDS,  
 CC senescence or ischaemia.

SQ Sequence 23 AA;  
 Query Match 100.0%; Score 84; DB 17; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEFEG 16  
 D6 8 QRYGRELRRMSDEFEG 23

RESULT 4  
 AAB37001  
 ID AAB37001 standard; peptide; 26 AA.

XX AC AAB37001;

DT 28-FEB-2001 (first entry)

XX Bcl2 polypeptide BH3 domain peptide #1.

XX Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;  
 KW cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;  
 KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;  
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;  
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;  
 KW stroke; myocardial infarction.

XX Homo sapiens.

XX WO200059526-A1.

XX 12-OCT-2000.

XX 06-APR-2000; 2000WO-US09352.

XX 07-APR-1999; 99US-0128202.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Huang Z, Wang J, Zhang Z, Shan S, Lu Z;

DR WPI; 2000-679325/66.

XX New peptide conjugates for modulating apoptosis or for inhibiting B  
 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for  
 PT treating neurodegenerative disorders, stroke, or cancer -

XX Claim 18; Page 17; 74pp; English.

XX The invention relates to a peptide conjugate having the formula:

CC (R-X)n-peptide where n = 1-10; X = C=O, when the R-X group is attached  
 CC to the N-terminus of the peptide, or a side chain of the peptide where  
 CC the functional group of the side chain is NH2 or OH; or X = O or NH,  
 CC when the R-X group is attached to the C-terminus of the peptide, or a  
 CC side chain of the peptide, where the side chain functional group is COOH  
 CC or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one  
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally  
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,  
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain  
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples  
 CC of the peptide portion of the conjugate. The peptides represent analogues  
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of

CC the BH3 domain of the cell death agonist Bad. The peptide conjugate is  
 CC useful for modulating apoptosis in the cells of a subject, or for  
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of  
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2  
 CC function. In particular, the peptide conjugate is useful for treating a  
 CC subject afflicted with a cancer characterized by cancer cells that  
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,  
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or  
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide  
 CC conjugate is also useful for treating disorders characterized by  
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired  
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.

SQ Sequence 26 AA;

Query Match 100.0%; Score 84; DB 21; Length 26;

Best Local Similarity 100.0%; Pred. No. 4.2e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEFEG 16

D6 6 QRYGRELRRMSDEFEG 21

RESULT 5

AAB37002

ID AAB37002 standard; peptide; 26 AA.

XX AC AAB37002;

DT 28-FEB-2001 (first entry)

XX Bcl2 polypeptide BH3 domain peptide #2.

XX Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;  
 KW cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;  
 KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;  
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;  
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;  
 KW stroke; myocardial infarction.

XX Homo sapiens.

XX WO200059526-A1.

XX 12-OCT-2000.

XX 06-APR-2000; 2000WO-US09352.

XX 07-APR-1999; 99US-0128202.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Huang Z, Wang J, Zhang Z, Shan S, Lu Z;

DR WPI; 2000-679325/66.

XX New peptide conjugates for modulating apoptosis or for inhibiting B  
 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for  
 PT treating neurodegenerative disorders, stroke, or cancer -

XX Claim 18; Page 17; 74pp; English.

XX The invention relates to a peptide conjugate having the formula:

CC (R-X)n-peptide where n = 1-10; X = C=O, when the R-X group is attached  
 CC to the N-terminus of the peptide, or a side chain of the peptide where  
 CC the functional group of the side chain is NH2 or OH; or X = O or NH,  
 CC when the R-X group is attached to the C-terminus of the peptide, or a  
 CC side chain of the peptide, where the side chain functional group is COOH  
 CC or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one  
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally  
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,  
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain

alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples of the peptide portion of the conjugate. The peptides represent analogues of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of the BH3 domain of the cell death agonist Bad. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting Bcl-2 function. In particular, the peptide conjugate is useful for treating a subject afflicted with a cancer characterized by cancer cells that express Bcl-2. The cancer includes prostate, colorectal, gastric, non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.

SQ Sequence 26 AA;

Query Match 100.0%; Score 84; DB 21; Length 26;

Best Local Similarity 100.0%; Pred. No. 4.2e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEFEG 16

Db 6 QRYGRELRRMSDEFEG 21

#### RESULT 6

AAB37003

ID AAB37003 standard; peptide; 27 AA.

XX

AC AAB37003;

XX

DT 28-FEB-2001 (first entry)

XX

DE Bcl2 polypeptide BH3 domain peptide #3.

XX

KW Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction.

XX

OS Homo sapiens.

XX

PN WO200059526-A1.

XX

PD 12-OCT-2000.

XX

PF 06-APR-2000; 2000WO-US09352.

XX

PR 07-APR-1999; 99US-0128202.

XX

PA (UYJE-) UNIV JEFFERSON THOMAS.

XX

PI Huang Z, Wang J, Zhang Z, Shan S, Lu Z;

XX

DR WPI; 2000-679325/66.

XX

PT New peptide conjugates for modulating apoptosis or for inhibiting B cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer

XX

PS Claim 18; Page 17; 74pp; English.

XX

CC The invention relates to a peptide conjugate having the formula:

(R-X)n-peptide where n = 1-10; X = C=O, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH2 or OH; or X = O or NH, when the R-X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COOH or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one

or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, phenyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples of the peptide portion of the conjugate. The peptides represent analogues of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of the BH3 domain of the cell death agonist Bad. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting Bcl-2 function. In particular, the peptide conjugate is useful for treating a subject afflicted with a cancer characterized by cancer cells that express Bcl-2. The cancer includes prostate, colorectal, gastric, non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.

SQ Sequence 27 AA;

Query Match 100.0%; Score 84; DB 21; Length 27;

Best Local Similarity 100.0%; Pred. No. 4.4e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEFEG 16

Db 6 QRYGRELRRMSDEFEG 21

#### RESULT 7

AAB37056

ID AAB37056 standard; peptide; 27 AA.

XX

AC AAB37056;

XX

DT 28-FEB-2001 (first entry)

XX

DE Bcl2 polypeptide BH3 domain peptide #56.

XX

KW Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction.

XX

OS Homo sapiens.

XX

PN WO200059526-A1.

XX

PD 12-OCT-2000.

XX

PF 06-APR-2000; 2000WO-US09352.

XX

PR 07-APR-1999; 99US-0128202.

XX

PA (UYJE-) UNIV JEFFERSON THOMAS.

XX

PI Huang Z, Wang J, Zhang Z, Shan S, Lu Z;

XX

DR WPI; 2000-679325/66.

XX

PT New peptide conjugates for modulating apoptosis or for inhibiting B cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer

XX

PS Claim 18; Page 19; 74pp; English.

XX

CC The invention relates to a peptide conjugate having the formula:

(R-X)n-peptide where n = 1-10; X = C=O, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH2 or OH; or X = O or NH, when the functional group of the side chain is NH2 or OH; or X = O or NH,

CC when the R-X group is attached to the C-terminus of the peptide, or a  
 CC side chain of the peptide, where the side chain functional group is COOH  
 CC or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl optionally  
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally  
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,  
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain  
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples  
 CC of the peptide portion of the conjugate. The peptides represent analogues  
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of  
 CC the BH3 domain of the cell death agonist Bad. The peptide conjugate is  
 CC useful for modulating apoptosis in the cells of a subject, or for  
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of  
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2  
 CC function. In particular, the peptide conjugate is useful for treating a  
 CC subject afflicted with a cancer characterized by cancer cells that  
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,  
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or  
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide  
 CC conjugate is also useful for treating disorders characterized by  
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired  
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.

XX Sequence 27 AA;

Query Match 100.0%; Score 84; DB 21; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEFEG 16  
 |||||  
 Db 7 QRYGRELRRMSDEFEG 22

RESULT 8  
 AAB37055

ID AAB37055 standard; peptide; 28 AA.

XX AAB37055;

DT 28-FEB-2001 (first entry)

XX Bcl2 polypeptide BH3 domain peptide #55.

XX Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;  
 KW cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;  
 KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;  
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;  
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;  
 KW stroke; myocardial infarction.

XX Homo sapiens.

XX WO200059526-A1.

XX 12-OCT-2000.

XX 06-APR-2000; 2000WO-US09352.

XX 07-APR-1999; 99US-0128202.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Huang Z, Wang J, Zhang Z, Shan S, Lu Z;

XX WPI; 2000-679325/66.

XX New peptide conjugates for modulating apoptosis or for inhibiting B  
 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for  
 PT treating neurodegenerative disorders, stroke, or cancer -

XX Claim 18; Page 19; 74pp; English.

XX The invention relates to a peptide conjugate having the formula:

CC (R-X)n-peptide where n = 1-10; X = C=O, when the R-X group is attached  
 CC to the N-terminus of the peptide, or a side chain of the peptide where  
 CC the functional group of the side chain is NH2 or OH; or X = O or NH,  
 CC when the R-X group is attached to the C-terminus of the peptide, or a  
 CC side chain of the peptide, where the side chain functional group is COOH  
 CC or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl optionally  
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally  
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,  
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain  
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples  
 CC of the peptide portion of the conjugate. The peptides represent analogues  
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of  
 CC the BH3 domain of the cell death agonist Bad. The peptide conjugate is  
 CC useful for modulating apoptosis in the cells of a subject, or for  
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of  
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2  
 CC function. In particular, the peptide conjugate is useful for treating a  
 CC subject afflicted with a cancer characterized by cancer cells that  
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,  
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or  
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide  
 CC conjugate is also useful for treating disorders characterized by  
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired  
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.

XX Sequence 28 AA;

Query Match 100.0%; Score 84; DB 21; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEFEG 16  
 |||||  
 Db 7 QRYGRELRRMSDEFEG 22

RESULT 9

AAB70370

ID AAB70370 standard; protein; 162 AA.

XX AAB70370;

XX 02-MAY-2001 (first entry)

XX Shorter murine BAD mutant amino acid sequence SEQ ID NO:3.

XX Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;  
 KW immunostimulant; neuroprotective; nootropic; antischismic; vulnary;  
 KW cytosstatic; antiviral; antiarthritic; antiinflammatory; wound healing;  
 KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;  
 KW immunodeficiency disease; neurodegenerative disease; viral infection;  
 KW ischaemic cell death; reperfusion cell death; arthritis; infertility;  
 KW lymphoproliferative condition; inflammation; autoimmune disease.

XX Mus musculus.

XX Synthetic.

XX WO200110888-A1.

XX 15-FEB-2001.

XX 30-MAY-2000; 2000WO-US11864.

XX 28-MAY-1999; 99US-0136783.

XX (APOP-) APOPTOSIS TECHNOLOGY INC.

XX Zhou X;

XX WPI; 2001-138734/14.

XX New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,  
 PT useful for screening for candidate compounds which induce or inhibit

PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or  
 PT Ser113 -  
 XX  
 PS Claim 7; Page 148-149; 157pp; English.  
 XX  
 CC The present invention describes an isolated or synthetic polypeptide  
 CC (I) comprising a less than full length amino acid sequence of a mutant  
 CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its  
 CC fragment, which contains amino acid substitutions at Ser118 of a human  
 CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine  
 CC BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,  
 CC neurotropic, antiischaemic, vulnerary, cytostatic, antiviral,  
 CC antiarthritic, antiinflammatory and immunosuppressive activities, and  
 CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and  
 CC polynucleotides can be used for screening candidate compounds and drugs  
 CC for activity that promote cell survival or apoptosis. Other uses include  
 CC inducing or inhibiting apoptosis in a cell. Candidate compounds  
 CC identified and (mutant) BAD polypeptides are useful in treating  
 CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell  
 CC death, reperfusion cell death, wound healing, cancer, viral infections,  
 CC lymphoproliferative conditions, arthritis, infertility, inflammation and  
 CC autoimmune diseases. The present sequence represents a specifically  
 CC claimed shorter murine BAD mutant amino acid sequence from the present  
 CC invention.  
 XX  
 SQ Sequence 162 AA;  
 Query Match 100.0%; Score 84; DB 22; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QRYGRELRLMSDEFEQ 16  
 Db 103 QRYGRELRLMSDEFEQ 118  
 |||||  
 RESULT 10  
 AAR95168  
 ID AAR95168 standard; Protein: 204 AA.  
 XX  
 AC AAR95168;  
 DT 06-JAN-1997 (first entry)  
 XX  
 DE bcl-x(L)/bcl-2 associated death promoter protein.  
 XX  
 KW Epitope; murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke;  
 KW polypeptide; bcl-x; cell death; regulate; BH1; BH2; apoptotic cell death;  
 KW cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS;  
 KW neurodegenerative disease; senescence; ischaemia; neoplasia.  
 XX  
 OS Mus musculus.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 147..149  
 FT /note= "BH1 conserved amino acids"  
 FT Region 191..192  
 FT /note= "BH2 conserved amino acids"  
 FT Domain 38..61  
 FT /note= "PEST sequence"  
 FT Domain 111..130  
 FT /note= "PEST sequence"  
 XX  
 XX WO9613614-A1.  
 PN 09-MAY-1996.  
 XX  
 PD 31-OCT-1995; 95WO-US14246.  
 XX  
 PF 31-OCT-1994; 94US-0333565.  
 PR  
 XX (UNIW ) UNIV WASHINGTON.  
 PA  
 XX

PI Korsmeyer SJ;  
 XX  
 DR WPI; 1996-251465/25.  
 DR N-PSDB; AAT29479.  
 XX  
 PT Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter -  
 PT useful to treat neoplasia and apoptosis and to identify agents  
 PT inhibiting its binding to bcl-2 or bcl-x(L) to form heteromultimers  
 XX  
 PS Claim 3; Fig 1; 130pp; English.  
 XX  
 CC This sequence represents the murine bcl-x(L)/bcl-2 associated death  
 CC promoter (Bad) gene. Bad is a 22.1 kD protein which interacts with  
 CC bcl-2 and bcl-x proteins and regulates cell death. It has homology  
 CC to the bcl-2-related family clustered in the BH1 and BH2 domain. Bad  
 CC has been found to hybridise to bcl-x(L) and bcl-2 in yeast two-hybrid  
 CC assays and in vivo in mammalian cells. Overexpressed Bad counters the  
 CC death inhibitory activity of bcl-x(L), but is much less effective at  
 CC countering the death inhibitory activity of bcl-2. Bad expression can  
 CC accelerate apoptotic cell death induced by cytokine deprivation in an  
 CC IL-3 dependent cell line expressing bcl-x(L), and its also counters the  
 CC death repressor activity of bcl-x(L). Bad competes with Bax for binding  
 CC to bcl-x(L). Bad may be used to identify agents which inhibit its  
 CC binding to bcl-2 or bcl-x(L) to form heterodimers. Such agents may be  
 CC used to treat neurodegenerative diseases, immunodeficiency diseases,  
 CC e.g. AIDS, senescence or ischaemia.  
 XX  
 SQ Sequence 204 AA;  
 Query Match 100.0%; Score 84; DB 17; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QRYGRELRLMSDEFEQ 16  
 Db 145 QRYGRELRLMSDEFEQ 160  
 |||||  
 RESULT 11  
 AAW61315  
 ID AAW61315 standard; Protein: 204 AA.  
 XX  
 AC AAW61315;  
 DT 07-OCT-1998 (first entry)  
 XX  
 DE Murine BCL-XL/BCL-2 associated cell death regulator.  
 XX  
 KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;  
 KW serine substituted mutant; apoptosis; cancer; viral infection.  
 XX  
 OS Mus sp.  
 XX  
 PN WO9817682-A1.  
 XX  
 PD 30-APR-1998.  
 XX  
 PF 17-OCT-1997; 97WO-US19175.  
 XX  
 PR 18-OCT-1996; 96US-0733505.  
 XX  
 PA (UNIW ) UNIV WASHINGTON.  
 XX  
 PI Korsmeyer SJ;  
 XX  
 DR WPI; 1998-261422/23.  
 DR N-PSDB; AAV27833.  
 XX  
 PT New mutant BAD polypeptide with phosphorylatable serine replaced -  
 PT useful for, e.g. treating reduced apoptosis such as in cancer or  
 PT viral infection  
 XX  
 PS Claim 1; Fig 10; 95pp; English.

XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell  
 CC death regulator) proteins, having an amino acid other than Ser at  
 CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The  
 CC present sequence is the murine BAD protein. Also described are: (1)  
 CC fragments of mutant BAD protein able to decrease cell viability; (2)  
 CC fusion proteins of mutant BAD with a heterologous polypeptide that  
 CC increases intracellular delivery. Mutant BAD proteins are used to treat  
 CC or prevent diseases associated with reduced apoptosis, e.g. cancer,  
 CC viral infection, lymphoproliferation, arthritis, infertility,  
 CC inflammation and autoimmune disease. Polynucleotide sequences encoding  
 CC mutant BAD proteins can be used similarly by gene therapy or to produce  
 CC transgenic animals for use as disease models or in drug screening. BAD  
 CC proteins phosphorylated at specified Ser are used to screen for enhancers  
 CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful  
 CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,  
 CC aging or ischaemic cell death. The apoptotic status of cells is  
 CC determined by measuring relative amounts of phosphorylated and non-  
 CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have  
 CC greater death-promoting activity than wild-type BAD which can become  
 CC phosphorylated on the specified Ser, forming a product that does not  
 CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family  
 CC proteins in the cytosol, thus promoting cell survival. The mutants with  
 CC Ser substituted cannot bind 14-3-3.  
 XX

SQ Sequence 204 AA;

Query Match 100.0%; Score 84; DB 19; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEFEG 16  
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 Db 145 QRYGRELRRMSDEFEG 160

RESULT 12

AAW61316  
 ID AAW61316 standard; Protein; 204 AA.  
 XX  
 AC AAW61316;  
 XX  
 DT 07-OCT-1998 (first entry)  
 XX  
 DE Mutant BCL-XL/BCL-2 associated cell death regulator #1.  
 XX  
 KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;  
 KW serine substituted mutant; apoptosis; cancer; viral infection.  
 XX  
 OS Mus sp.  
 OS Synthetic.  
 XX  
 PN WO9817682-A1.  
 XX  
 PD 30-APR-1998.  
 XX  
 PF 17-OCT-1997; 97WO-US19175.  
 XX  
 PR 18-OCT-1996; 96US-0733505.  
 XX  
 PA (UNIW ) UNIV WASHINGTON.  
 XX  
 PI Korsmeyer SJ;  
 XX  
 DR WPI; 1998-261422/23.  
 DR N-PSDB; AAV27834.  
 XX  
 XX New mutant BAD polypeptide with phosphorylatable serine replaced -  
 PT useful for, e.g. treating reduced apoptosis such as in cancer or  
 PT viral infection  
 XX  
 PS Claim 7; Page 59; 95pp; English.  
 XX  
 XX

CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell  
 CC death regulator) proteins, having an amino acid other than Ser at  
 CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The  
 CC present sequence represents a mutant BAD protein. Also described are: (1)  
 CC fragments of mutant BAD protein able to decrease cell viability; (2)  
 CC fusion proteins of mutant BAD with a heterologous polypeptide that  
 CC increases intracellular delivery. Mutant BAD proteins are used to treat  
 CC or prevent diseases associated with reduced apoptosis, e.g. cancer,  
 CC viral infection, lymphoproliferation, arthritis, infertility,  
 CC inflammation and autoimmune disease. Polynucleotide sequences encoding  
 CC mutant BAD proteins can be used similarly by gene therapy or to produce  
 CC transgenic animals for use as disease models or in drug screening. BAD  
 CC proteins phosphorylated at specified Ser are used to screen for enhancers  
 CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful  
 CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,  
 CC aging or ischaemic cell death. The apoptotic status of cells is  
 CC determined by measuring relative amounts of phosphorylated and non-  
 CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have  
 CC greater death-promoting activity than wild-type BAD which can become  
 CC phosphorylated on the specified Ser, forming a product that does not  
 CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family  
 CC proteins in the cytosol, thus promoting cell survival. The mutants with  
 CC Ser substituted cannot bind 14-3-3.  
 XX

SQ Sequence 204 AA;

Query Match 100.0%; Score 84; DB 19; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEFEG 16  
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 Db 145 QRYGRELRRMSDEFEG 160

RESULT 13

AAW61317  
 ID AAW61317 standard; Protein; 204 AA.  
 XX  
 AC AAW61317;  
 XX  
 DT 07-OCT-1998 (first entry)  
 XX  
 DE Mutant BCL-XL/BCL-2 associated cell death regulator #2.  
 XX  
 KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;  
 KW serine substituted mutant; apoptosis; cancer; viral infection.  
 XX  
 OS Mus sp.  
 OS Synthetic.  
 XX  
 PN WO9817682-A1.  
 XX  
 PD 30-APR-1998.  
 XX  
 PF 17-OCT-1997; 97WO-US19175.  
 XX  
 PR 18-OCT-1996; 96US-0733505.  
 XX  
 PA (UNIW ) UNIV WASHINGTON.  
 XX  
 PI Korsmeyer SJ;  
 XX  
 DR WPI; 1998-261422/23.  
 DR N-PSDB; AAV27835.  
 XX  
 XX New mutant BAD polypeptide with phosphorylatable serine replaced -  
 PT useful for, e.g. treating reduced apoptosis such as in cancer or  
 PT viral infection  
 XX  
 PS Claim 7; Page 60; 95pp; English.  
 XX  
 XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell

CC death regulator) proteins, having an amino acid other than Ser at  
 CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The  
 CC present sequence represents a mutant BAD protein. Also described are: (1)  
 CC fragments of mutant BAD protein able to decrease cell viability; (2)  
 CC fusion proteins of mutant BAD with a heterologous polypeptide that  
 CC increases intracellular delivery. Mutant BAD proteins are used to treat  
 CC or prevent diseases associated with reduced apoptosis, e.g. cancer,  
 CC viral infection, lymphoproliferation, arthritis, infertility,  
 CC inflammation and autoimmune disease. Polynucleotide sequences encoding  
 CC mutant BAD proteins can be used similarly by gene therapy or to produce  
 CC transgenic animals for use as disease models or in drug screening. BAD  
 CC proteins phosphorylated at specified Ser are used to screen for enhancers  
 CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful  
 CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,  
 CC aging or ischaemic cell death. The apoptotic status of cells is  
 CC determined by measuring relative amounts of phosphorylated and non-  
 CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have  
 CC greater death-promoting activity than wild-type BAD which can become  
 CC phosphorylated on the specified Ser, forming a product that does not  
 CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family  
 CC proteins in the cytosol, thus promoting cell survival. The mutants with  
 CC Ser substituted cannot bind 14-3-3.  
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Query Match 100.0%; Score 84; DB 19; Length 204;  
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 Db 145 QRYGRELRMSDEFEQ 160

RESULT 14  
 AAW61318  
 ID AAW61318 standard; Protein; 204 AA.  
 XX  
 AC AAW61318;  
 XX  
 DT 07-OCT-1998 (first entry)  
 XX  
 DE Mutant BCL-XL/BCL-2 associated cell death regulator #3.  
 XX  
 KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;  
 KW serine substituted mutant; apoptosis; cancer; viral infection.  
 XX  
 OS Mus sp.  
 OS Synthetic.  
 XX  
 PN WO9817682-A1.  
 XX  
 PD 30-APR-1998.  
 XX  
 PF 17-OCT-1997; 97WO-US19175.  
 XX  
 PR 18-OCT-1996; 96US-0733505.  
 XX  
 PA (UNIW ) UNIV WASHINGTON.  
 XX  
 PI Korsmeyer SJ;  
 XX  
 DR WPI; 1998-261422/23.  
 DR N-PSDB; AAV27836.  
 XX  
 PT New mutant BAD polypeptide with phosphorylatable serine replaced -  
 PT useful for, e.g. treating reduced apoptosis such as in cancer or  
 PT viral infection  
 XX  
 PS Claim 7; Page 60-61; 95pp; English.  
 XX  
 CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell  
 CC death regulator) proteins, having an amino acid other than Ser at

CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The  
 CC present sequence represents a mutant BAD protein. Also described are: (1)  
 CC fragments of mutant BAD protein able to decrease cell viability; (2)  
 CC fusion proteins of mutant BAD with a heterologous polypeptide that  
 CC increases intracellular delivery. Mutant BAD proteins are used to treat  
 CC or prevent diseases associated with reduced apoptosis, e.g. cancer,  
 CC viral infection, lymphoproliferation, arthritis, infertility,  
 CC inflammation and autoimmune disease. Polynucleotide sequences encoding  
 CC mutant BAD proteins can be used similarly by gene therapy or to produce  
 CC transgenic animals for use as disease models or in drug screening. BAD  
 CC proteins phosphorylated at specified Ser are used to screen for enhancers  
 CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful  
 CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,  
 CC aging or ischaemic cell death. The apoptotic status of cells is  
 CC determined by measuring relative amounts of phosphorylated and non-  
 CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have  
 CC greater death-promoting activity than wild-type BAD which can become  
 CC phosphorylated on the specified Ser, forming a product that does not  
 CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family  
 CC proteins in the cytosol, thus promoting cell survival. The mutants with  
 CC Ser substituted cannot bind 14-3-3.  
 XX  
 SQ Sequence 204 AA;

Query Match 100.0%; Score 84; DB 19; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRELRMSDEFEQ 16  
 |||||  
 Db 145 QRYGRELRMSDEFEQ 160

RESULT 15  
 AAW58832  
 ID AAW58832 standard; protein; 204 AA.  
 XX  
 AC AAW58832;  
 XX  
 DT 23-JUL-1998 (first entry)  
 XX  
 DE Murine BAD protein.  
 XX  
 KW BAD protein; BCL-XL/BCL-2 associated cell death regulator; 14-3-3;  
 KW serine phosphorylation; post-translational modification; apoptosis;  
 KW signal transduction regulator; phosphoserine phosphatase; senescence;  
 KW immunodeficiency disease; neurodegenerative disease; infertility;  
 KW cancer; viral infection; lymphoproliferative condition; arthritis;  
 KW inflammation; autoimmune diseases.  
 XX  
 OS Mus sp.  
 XX  
 PN WO9809643-A1.  
 XX  
 PD 12-MAR-1998.  
 XX  
 PF 09-SEP-1997; 97WO-US15871.  
 XX  
 PR 09-SEP-1996; 96US-0707868.  
 XX  
 PA (UNIW ) UNIV WASHINGTON.  
 XX  
 PI Korsmeyer SJ;  
 XX  
 DR WPI; 1998-207049/18.  
 XX  
 PT Serine-phosphorylated Bcl-X-L/Bcl-2 Associated cell Death regulator  
 PT polypeptide - useful for modulation of apoptosis associated with,  
 PT e.g. cancer and immunodeficiency diseases  
 XX  
 PS Claim 3; Fig 8; 61pp; English.  
 XX  
 CC This sequence represents a novel serine-phosphorylated protein, BAD

CC (Bcl-XL/Bcl-2 associated cell death regulator). The serine residue is  
CC phosphorylated in a post-translational modification and allows binding  
CC to the 14-3-3 protein which is a signal transduction regulator.  
CC Modulators of phosphorylated BAD, which act through inhibition/activation  
CC of a phosphoserine phosphatase, are useful for preventing/treating  
CC increased/decreased apoptosis in a cell. The increased apoptosis may  
CC result from immunodeficiency diseases, senescence, neurodegenerative  
CC disease, ischaemic cell death, reperfusion cell death, infertility and  
CC wound-healing. Decreased apoptosis may result from cancer, viral  
CC infection, lymphoproliferative conditions, arthritis, infertility,  
CC inflammation and autoimmune diseases. Measuring the amount of  
CC phosphorylated compared to unphosphorylated BAD polypeptide and/or total  
CC BAD in a cell is useful for determining the apoptotic state of a cell.  
XX

SQ Sequence 204 AA;

Query Match 100.0%; Score 84; DB 19; Length 204;  
Best Local Similarity 100.0%; Pred. No. 3.5e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRELRMSDEPEG 16  
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Job time : 22.6286 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 15, 2003, 17:22:21; Search time 8.34286 Seconds  
(without alignments)  
81.144 Million cell updates/sec

Title: US-09-544-664-28

Perfect score: 84

Sequence: 1 QRYGRELRRMSDEFEG 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	84	100.0	23	2	US-08-661-479-10
3	84	100.0	204	1	US-08-333-565-2
4	84	100.0	204	2	US-08-661-479-2
5	84	100.0	204	2	US-08-733-505A-1
6	84	100.0	204	2	US-08-733-505A-12
7	84	100.0	204	2	US-08-733-505A-13
8	84	100.0	204	2	US-08-733-505A-14
9	81	96.4	204	2	US-08-717-123-3
10	81	96.4	204	4	US-09-375-257-3
11	73	86.9	59	2	US-08-733-505A-55
12	73	86.9	59	2	US-08-733-505A-56
13	73	86.9	59	2	US-08-733-505A-57
14	73	86.9	59	2	US-08-733-505A-58
15	73	86.9	166	1	US-08-665-617-2
16	73	86.9	168	2	US-08-717-123-2
17	73	86.9	168	3	US-08-985-335-1
18	73	86.9	168	3	US-08-985-335-7
19	73	86.9	168	3	US-09-410-372-1
20	73	86.9	168	3	US-09-410-372-7
21	73	86.9	168	4	US-09-375-257-2
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23	67	79.8	16	2	US-08-661-479-26
24	43	51.2	213	3	US-08-718-738-18
25	43	51.2	213	3	US-09-221-844-18
26	43	51.2	591	4	US-09-252-991A-27090
27	42	50.0	11	2	US-08-733-505A-34

28	42	50.0	11	2	US-08-706-741B-69	Sequence 69, Appl
29	42	50.0	11	2	US-08-924-695A-69	Sequence 69, Appl
30	41	48.8	322	4	US-09-359-161-7	Sequence 7, Appl
31	40.5	48.2	904	4	US-09-328-352-4656	Sequence 4656, Ap
32	40	47.6	505	4	US-09-252-991A-21995	Sequence 21995, A
33	39	46.4	66	2	US-08-867-087B-40	Sequence 40, Appl
34	39	46.4	333	4	US-09-252-991A-28443	Sequence 28443, A
35	39	46.4	1125	4	US-09-252-991A-18729	Sequence 18729, A
36	38.5	45.8	1112	4	US-09-252-991A-27256	Sequence 27256, A
37	38	45.2	376	4	US-09-252-991A-26270	Sequence 26270, A
38	38	45.2	574	4	US-09-252-991A-29351	Sequence 29351, A
39	38	45.2	670	4	US-09-252-991A-26867	Sequence 26867, A
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45	37	44.0	309	4	US-09-252-991A-32234	Sequence 32234, A

ALIGNMENTS

RESULT 1  
US-08-333-565-10  
; Sequence 10, Application US/08333565  
; Patent No. 5622852  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, Stanley J.  
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Townsend and Townsend Kourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/333,565  
; FILING DATE: 31-OCT-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 15726A-000700  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 23 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-333-565-10

Query Match 100.0%; Score 84; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 5.4e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEFEG 16

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Db 8 QRYGRELRRMSDEFEG 23

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RESULT 3
US-08-333-565-2
; Sequence 2, Application US/08333565
; Patent No. 5622852
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
; TITLE OF INVENTION: REGULATOR
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/333,565
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000700
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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; NAME/KEY: Protein
; LOCATION: 1..204
; OTHER INFORMATION: /note= "Pduced amino acid sequence
; OTHER INFORMATION: of mouse BAD."
US-08-333-565-2

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Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels

QY 1 QRYGRELRRMSDEFEQ 16
Db 145 QRYGRELRRMSDEFEQ 160

RESULT 4
US-08-661-479-2
; Sequence 2, Application US/08661479
; Patent No. 5834209
; GENERAL INFORMATION:
; APPLICANT: KORMSEYER, Stanley J.
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
; TITLE OF INVENTION: REGULATOR
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/661,479
; FILING DATE: 11-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/333,565
; FILING DATE: 31-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000700
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids

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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..204
; OTHER INFORMATION: /note= "Deduced amino acid sequence
; OTHER INFORMATION: of mouse BAD."
US-08-661-479-2

Query Match 100.0%; Score 84; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEFEG 16
Db 145 QRYGRELRRMSDEFEG 160

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US-08-733-505A-1
; Sequence 1, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,505A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,505A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-733-505A-1

Query Match 100.0%; Score 84; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEFEG 16
Db 145 QRYGRELRRMSDEFEG 160

RESULT 6
US-08-733-505A-12
; Sequence 12, Application US/08733505A
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; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,505A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-733-505A-12

Query Match 100.0%; Score 84; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEFEG 16
Db 145 QRYGRELRRMSDEFEG 160

RESULT 7
US-08-733-505A-13
; Sequence 13, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,505A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
```

NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 965458  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 204 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-733-505A-13

Query Match 100.0%; Score 84; DB 2; Length 204;  
Best Local Similarity 100.0%; Pred. No. 5.5e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRELRMSDEFEQ 16  
|||||  
Db 145 QRYGRELRMSDEFEQ 160

## RESULT 8

US-08-733-505A-14  
Sequence 14, Application US/08733505A  
Patent No. 5856445  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, STANLEY J.  
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOWELL & HAFFERKAMP, L.C.  
STREET: 7733 FORSYTH BLVD., SUITE 1400  
CITY: ST. LOUIS  
STATE: MISSOURI  
COUNTRY: USA  
ZIP: 63105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/733,505A  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 965458  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 204 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-733-505A-14

Query Match 100.0%; Score 84; DB 2; Length 204;  
Best Local Similarity 100.0%; Pred. No. 5.5e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRELRMSDEFEQ 16  
|||||  
Db 145 QRYGRELRMSDEFEQ 160

RESULT 9  
US-08-717-123-3  
Sequence 3, Application US/08717123  
Patent No. 5965703  
GENERAL INFORMATION:  
APPLICANT: Horne, William A.  
APPLICANT: Oltersdorf, Tilman  
TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic  
TITLE OF INVENTION: Acids and Methods of Use  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/717,123  
FILING DATE: 20-SEP-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-ID 1929  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 204 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-717-123-3

Query Match 96.4%; Score 81; DB 2; Length 204;  
Best Local Similarity 93.8%; Pred. No. 1.8e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRELRMSDEFEQ 16  
|||||  
Db 145 QRYGRELRMSDEFEQ 160

## RESULT 10

US-09-375-257-3  
Sequence 3, Application US/09375257  
Patent No. 6504022  
GENERAL INFORMATION:  
APPLICANT: Horne, William A.  
APPLICANT: Oltersdorf, Tilman  
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC  
TITLE OF INVENTION: ACIDS AND METHODS OF USE  
FILE REFERENCE: 480140.428D1  
CURRENT APPLICATION NUMBER: US/09/375,257  
CURRENT FILING DATE: 1999-08-16  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 204  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-375-257-3

Query Match 96.4%; Score 81; DB 4; Length 204;  
Best Local Similarity 93.8%; Pred. No. 1.8e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;



Query Match 86.9%; Score 73; DB 2; Length 59;  
Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEF 14  
Db 46 QRYGRELRRMSDEF 59

## RESULT 14

US-08-733-505A-58  
; Sequence 58, Application US/08733505A  
; Patent No. 5856445  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, STANLEY J.  
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF  
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BLVD., SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: USA  
; ZIP: 63105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/733,505A  
; FILING DATE:

CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 965458  
TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 59 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-733-505A-58

Query Match 86.9%; Score 73; DB 2; Length 59;  
Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEF 14  
Db 46 QRYGRELRRMSDEF 59

RESULT 15  
US-08-665-617-2  
; Sequence 2, Application US/08665617  
; Patent No. 5663316  
; GENERAL INFORMATION:  
; APPLICANT: Xudong, Yin  
; TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida

COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/665,617  
FILING DATE:

CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Saliwanchik, David R.  
REGISTRATION NUMBER: 31,794  
REFERENCE/DOCKET NUMBER: CL-8  
TELEPHONE: (352) 375-8100  
TELEFAX: (352) 372-5800  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 166 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-665-617-2

Query Match 86.9%; Score 73; DB 1; Length 166;  
Best Local Similarity 100.0%; Pred. No. 3.4e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEF 14  
Db 106 QRYGRELRRMSDEF 119

Search completed: September 15, 2003, 17:45:06  
Job time : 9.34286 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 15, 2003, 17:25:56 ; Search time 12.6857 Seconds  
(without alignments)  
184.034 Million cell updates/sec

Title: US-09-544-664-28

Perfect score: 84

Sequence: 1 QRYGRELRRMSDEFEQ 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 541936 seqs, 145912426 residues

Total number of hits satisfying chosen parameters: 541936

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
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7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	96.4	204	US-09-922-378-3	Sequence 3, Appli
2	81	96.4	204	US-10-066-179-3	Sequence 3, Appli
3	73	86.9	25	US-10-059-261-258	Sequence 258, App
4	73	86.9	168	US-09-922-378-2	Sequence 2, Appli
5	73	86.9	168	US-09-894-657-1	Sequence 1, Appli
6	73	86.9	168	US-09-894-657-7	Sequence 7, Appli
7	73	86.9	168	US-10-066-179-2	Sequence 2, Appli
8	67	79.8	15	US-10-174-105A-147	Sequence 147, App
9	50	59.5	215	US-10-156-761-9145	Sequence 9145, Ap
10	43	51.2	213	US-09-843-846-18	Sequence 18, Appli
11	41	48.8	282	US-09-331-631A-22	Sequence 22, Appli
12	40	47.6	380	US-10-156-761-13594	Sequence 13594, A
13	40	47.6	2871	US-10-146-473-41	Sequence 41, Appli
14	38.5	45.8	764	US-10-166-087-16	Sequence 16, Appli
15	38	45.2	35	US-10-092-750-1	Sequence 1, Appli

16	38	45.2	50	10	US-09-971-980-64	Sequence 64, Appli
17	38	45.2	64	10	US-09-971-980-62	Sequence 62, Appli
18	38	45.2	138	15	US-10-092-750-241	Sequence 241, App
19	38	45.2	327	15	US-10-102-806-570	Sequence 570, App
20	38	45.2	385	15	US-10-146-772-122	Sequence 122, App
21	38	45.2	571	9	US-09-815-242-11813	Sequence 11813, A
22	38	45.2	1053	9	US-09-841-132-583	Sequence 583, App
23	38	45.2	1053	14	US-10-007-693-97	Sequence 97, Appli
24	38	45.2	4840	15	US-10-156-761-10435	Sequence 10435, A
25	37.5	44.6	1265	15	US-10-198-070-69	Sequence 69, Appli
26	37	44.0	146	15	US-10-121-757B-12	Sequence 12, Appli
27	37	44.0	198	10	US-09-738-626-4812	Sequence 4812, Ap
28	37	44.0	334	10	US-09-794-715A-8	Sequence 8, Appli
29	37	44.0	334	12	US-10-286-581-8	Sequence 8, Appli
30	37	44.0	334	15	US-10-046-924-8	Sequence 8, Appli
31	37	44.0	426	9	US-09-815-242-5704	Sequence 5704, Ap
32	37	44.0	485	14	US-10-047-412A-4	Sequence 4, Appli
33	37	44.0	495	15	US-10-156-761-10045	Sequence 10045, A
34	37	44.0	515	15	US-10-106-698-4658	Sequence 4658, Ap
35	37	44.0	556	12	US-09-949-029-36	Sequence 36, Appli
36	37	44.0	575	9	US-09-839-136-2	Sequence 2, Appli
37	37	44.0	575	9	US-09-839-136-10	Sequence 10, Appli
38	37	44.0	705	9	US-09-815-242-12463	Sequence 12463, A
39	36.5	43.5	817	10	US-09-922-481-4	Sequence 4, Appli
40	36	42.9	61	9	US-09-925-301-1577	Sequence 1577, Ap
41	36	42.9	78	15	US-10-083-357-1237	Sequence 1237, Ap
42	36	42.9	80	15	US-10-106-698-5539	Sequence 5539, Ap
43	36	42.9	87	9	US-09-923-301-1433	Sequence 1433, Ap
44	36	42.9	95	10	US-09-925-300-1788	Sequence 1788, Ap
45	36	42.9	113	10	US-09-925-300-1789	Sequence 1789, Ap

#### ALIGNMENTS

#### RESULT 1

US-09-922-378-3  
; Sequence 3, Application US/09922378  
; Patent No. US20020037869A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, William A.  
; APPLICANT: Oltersdorf, Tilman  
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC  
; TITLE OF INVENTION: ACIDS AND METHODS OF USE  
; FILE REFERENCE: 480140.428D3  
; CURRENT APPLICATION NUMBER: US/09/922,378  
; CURRENT FILING DATE: 2001-08-03  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 204  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-922-378-3

Query Match 96.4%; Score 81; DB 9; Length 204;  
Best Local Similarity 93.8%; Pred. No. 1.4e-05;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEFEQ 16

Db 145 QRYGRELRRMTDEFEQ 160

#### RESULT 2

US-10-066-179-3  
; Sequence 3, Application US/10066179  
; Publication No. US20020115631A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, William A.  
; APPLICANT: Oltersdorf, Tilman  
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC  
; TITLE OF INVENTION: ACIDS AND METHODS OF USE

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; ORGANISM: Homo sapiens
US-09-922-378-2

Query Match      86.9%; Score 73; DB 9; Length 168;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QRYGRELRRMSDEF 14
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Db      108 QRYGRELRRMSDEF 121

RESULT 5
US-09-894-657-1
; Sequence 1, Application US/09894657
; Patent No. US20020098569A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; Yue, Henry
; Lal, Preeti
; Shah, Purvi
; Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; PROLIFERATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/894,657
; FILING DATE: 28-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/410,372
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0421 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SYNORAB01
; CLONE: 358673
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-894-657-1

Query Match      86.9%; Score 73; DB 9; Length 168;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QRYGRELRRMSDEF 14
      |||||
Db      108 QRYGRELRRMSDEF 121

RESULT 6
US-09-894-657-7

```

```
; Sequence 7, Application US/09894657
; Patent No. US20020098569A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
;       Yue, Henry
;       Lal, Preeti
;       Shah, Purvi
;       Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
;                   PROLIFERATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/894,657
; FILING DATE: 28-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/410,372
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0421 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 7:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 168 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1683637
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-894-657-7

Query Match      86.9%; Score 73; DB 9; Length 168;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QRYGRELRRMSDEF 14
      |||||
Db      108 QRYGRELRRMSDEF 121

RESULT 7
US-10-066-179-2
; Sequence 2, Application US/10066179
; Publication No. US20020115631A1
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
; FILE REFERENCE: 480140.428C1
; CURRENT APPLICATION NUMBER: US/10/066,179
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 168

Query Match      86.9%; Score 73; DB 9; Length 168;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QRYGRELRRMSDEF 14
      |||||
Db      108 QRYGRELRRMSDEF 121

RESULT 7
US-10-066-179-2
; Sequence 2, Application US/10066179
; Publication No. US20020115631A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697

Query Match      79.8%; Score 67; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GRELRMSDEFEQ 16
      |||||
Db      1 GRELRMSDEFEQ 13

RESULT 9
US-10-156-761-9145
; Sequence 9145, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697

Query Match      79.8%; Score 67; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GRELRMSDEFEQ 16
      |||||
Db      1 GRELRMSDEFEQ 13

RESULT 9
US-10-156-761-9145
; Sequence 9145, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697

Query Match      86.9%; Score 73; DB 14; Length 168;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QRYGRELRRMSDEF 14
      |||||
Db      108 QRYGRELRRMSDEF 121

RESULT 8
US-10-174-105A-147
; Sequence 147, Application US/10174105A
; Publication No. US20030068652A1
; GENERAL INFORMATION:
; APPLICANT: Cell Signaling Technology, Inc.
; APPLICANT: ZHANG, Hui
; APPLICANT: COMB, Michael J.
; APPLICANT: TAN, Yi
; TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPECIFIC
; FILE REFERENCE: CST-138 CIP3
; CURRENT APPLICATION NUMBER: US/10/174,105A
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 09/148,712
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 09/535,364
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 147
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; NAME/KEY: MOD_RES
; LOCATION: (8)..(8)
; OTHER INFORMATION: PHOSPHORYLATION; serine at position 8 is phosphorylated
US-10-174-105A-147

Query Match      79.8%; Score 67; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GRELRMSDEFEQ 16
      |||||
Db      1 GRELRMSDEFEQ 13

RESULT 9
US-10-156-761-9145
; Sequence 9145, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
```

; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO 9145  
; LENGTH: 215  
; TYPE: PRT  
; ORGANISM: Streptomyces avermitilis  
US-10-156-761-9145

Query Match  
Best Local Similarity 59.5%; Score 50; DB 15; Length 215;  
; Sequence 18, Application US/09843846  
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEFG 16  
Db 108 ERWGGDLRRMRDEADG 123

RESULT 10  
US-09-843-846-18  
; Sequence 18, Application US/09843846  
; Patent No. US20020042362A1  
; GENERAL INFORMATION:  
; APPLICANT: KUNSCHE, CHARLES A  
; APPLICANT: CHOPRA, ARVIND  
; APPLICANT: ROSEN, CRAIG A  
; TITLE OF INVENTION: HUMAN B-CELL TRANSLOCATION GENES-2 AND 3  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/843,846  
; FILING DATE: 30-Apr-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 09/221,844  
; FILING DATE: 29-DEC-1998  
; APPLICATION NUMBER: US 08/718,738  
; FILING DATE: 18-SEP-1996  
; APPLICATION NUMBER: US 08/463,382  
; FILING DATE: 05-JUN-1995  
; APPLICATION NUMBER: US 08/460,104  
; FILING DATE: 02-JUN-1995  
; APPLICATION NUMBER: PCT/US95/03323  
; FILING DATE: 17-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEFFE, ERIC K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.0730005/EKS/PSC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 213 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Query Match 51.2%; Score 43; DB 9; Length 213;

Best Local Similarity 43.8%; Pred. No. 21;  
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;  
QY 1 QRYGRELRRMSDEFG 16  
Db 22 RREGELERLKKVEG 37

RESULT 11  
US-09-331-631A-22  
; Sequence 22, Application US/09331631A  
; Patent No. US20020168392A1  
; GENERAL INFORMATION:  
; APPLICANT: Manners, John M.  
; APPLICANT: Marcus, John Paul  
; APPLICANT: Goulter, Kenneth C.  
; APPLICANT: Green, Jodie L.  
; TITLE OF INVENTION: ANTIMICROBIAL PROTEINS  
; FILE REFERENCE: CULLN23.001APC  
; CURRENT APPLICATION NUMBER: US/09/331,631A  
; CURRENT FILING DATE: 1999-06-21  
; PRIOR APPLICATION NUMBER: PCT/AU97/00874  
; PRIOR FILING DATE: 1997-12-22  
; PRIOR APPLICATION NUMBER: AU PO 4275  
; PRIOR FILING DATE: 1996-12-20  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 22  
; LENGTH: 582  
; TYPE: PRT  
; ORGANISM: Maize  
US-09-331-631A-22

Query Match 48.8%; Score 41; DB 10; Length 582;  
Best Local Similarity 50.0%; Pred. No. 1.3e+02;  
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEFG 16  
Db 533 ERHGREEREKEEREG 548

RESULT 12  
US-10-156-761-13594  
; Sequence 13594, Application US/10156761  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI  
; APPLICANT: HATTORI, MASAHIRA  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156,761  
; CURRENT FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: JP 2001-204089  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO 13594  
; LENGTH: 380  
; TYPE: PRT  
; ORGANISM: Streptomyces avermitilis  
US-10-156-761-13594

Query Match 47.6%; Score 40; DB 15; Length 380;  
Best Local Similarity 53.6%; Pred. No. 1.2e+02;  
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```
QY      3 YGRELRLMSDE 13
      | :||||:|
Db      241 YEKELRLADE 251

RESULT 13
US-10-146-473-41
; Sequence 41, Application US/10146473
; Publication No. US20030108888A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Gout, Ivan
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Gure, Ali
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd
; TITLE OF INVENTION: Breast Cancer Antigens
; FILE REFERENCE: L00461/70130(JRV)
; CURRENT APPLICATION NUMBER: US/10/146,473
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/291,150
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 2871
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-473-41

Query Match      47.6%; Score 40; DB 15; Length 2871;
Best Local Similarity 60.0%; Pred. No. 9.7e+02;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      1 QRYGRELRLMSDEFE 15
      || ||||:|
Db      1648 QRTQELRLSSEVE 1662

RESULT 14
US-10-166-087-16
; Sequence 16, Application US/10166087
; Publication No. US2003007767A1
; GENERAL INFORMATION:
; APPLICANT: Ecopia Biosciences Inc.
; APPLICANT: Farnet, Chris
; APPLICANT: Staiffa, Alfredo
; APPLICANT: Zazopoulos, Emmanuel
; TITLE OF INVENTION: Genes and proteins for the biosynthesis of anthramycin
; FILE REFERENCE: 3014-2US
; CURRENT APPLICATION NUMBER: US/10/166,087
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Streptomyces refuineus subspecies thermotolerans
US-10-166-087-16

Query Match      45.8%; Score 38.5; DB 15; Length 764;
Best Local Similarity 62.5%; Pred. No. 4.3e+02;
Matches 10; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY      1 QRYGRELRLMSDEFE 16
      || |||| |:|
Db      220 QRPGRREL-TYSNEYEG 234

RESULT 15
US-10-092-750-1
; Sequence 1, Application US/10092750
; Publication No. US20030032157A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Hammond, Philip W.
; APPLICANT: Alpin, Julia
; APPLICANT: Wright, Martin C.
; TITLE OF INVENTION: Polypeptides Interactive with BCL-XL
; FILE REFERENCE: 50036/050002
; CURRENT APPLICATION NUMBER: US/10/092,750
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 60/274,526
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-750-1
```

```
Query Match      45.2%; Score 38; DB 15; Length 35;
Best Local Similarity 70.0%; Pred. No. 21;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

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QY      5 RELRLMSDEF 14
      :|||:|
Db      19 QELRRIGDEF 28
```

Search completed: September 15, 2003, 17:47:52  
Job time : 12.6857 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2003, 17:18.16 : Search time 7.2 Seconds  
(without alignments)  
213.708 Million cell updates/sec

Title: US-09-544-664-28  
Perfect score: 84  
Sequence: 1 QRYGRLRRMSDFEG 16  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues  
Total number of hits satisfying chosen parameters: 283308  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	84	100.0	204	2 A55671	bad protein - mous
2	44	52.4	564	2 H75403	glycosyl hydrolase
3	43	51.2	463	2 H83036	probable two-compo
4	42.5	50.6	1014	2 T36031	exonuclease ABC c
5	42	50.0	370	2 S38185	2-dehydro-3-deoxy-
6	42	50.0	445	2 G97123	probable Fe-S oxid
7	41	48.8	84	2 F84388	hypothetical prote
8	41	48.8	113	2 J01128	gas-vesicle operon
9	41	48.8	113	2 T08234	gas-vesicle operon
10	41	48.8	220	2 F72289	oxidoreductase, so
11	41	48.8	271	2 A31762	phosphate ABC tran
12	41	48.8	271	2 A31386	phosphate ABC tran
13	41	48.8	322	1 R6BYC3	regulatory protein
14	41	48.8	398	2 G69496	ATP-dependent 26S
15	41	48.8	582	2 B33234	vicillin-like stora
16	40.5	48.2	334	2 A39172	Antho-Ramide neur
17	40.5	48.2	435	2 A44308	Antho-Ramide prec
18	40	47.6	206	2 C36365	transforming prote
19	40	47.6	219	2 T15466	hypothetical prote
20	40	47.6	374	2 C84338	spermidine/puisc
21	40	47.6	411	2 F87644	transcription regu
22	40	47.6	887	2 T38885	probable ATP-depen
23	40	47.6	967	2 F82668	oxoglutarate dehyd
24	40	47.6	2677	2 A38194	desmoplakin I - hu
25	40	47.6	5138	2 B96695	hypothetical prote
26	39.5	47.0	310	2 D86675	mevalonate kinase
27	39.5	47.0	910	2 G91024	NADH dehydrogenase
28	39.5	47.0	910	2 H58868	NADH dehydrogenase
29	39.5	47.0	910	2 A65000	NADH2 dehydrogenas

30 39.5 47.0 910 2 A10796 NADH2 dehydrogenas  
31 39.5 47.0 914 2 AD0311 NADH2 dehydrogenas  
32 39 46.4 73 2 AC3365 hypothetical prote  
33 39 46.4 87 2 A82928 hypothetical prote  
34 39 46.4 91 2 T26996 ribosomal protein  
35 39 46.4 105 2 B84184 hypothetical prote  
36 39 46.4 232 2 A42095 floral homeotic pr  
37 39 46.4 275 2 C69808 transporter homolo  
38 39 46.4 315 2 T39444 hypothetical prote  
39 39 46.4 331 2 E90121 DNA repair protein  
40 39 46.4 365 2 S42107 RAD51 protein homo  
41 39 46.4 380 2 T32163 hypothetical prote  
42 39 46.4 501 2 H84727 probable inositol  
43 39 46.4 574 2 T48113 inositol-1,4,5-tri  
44 39 46.4 1016 2 H75356 excinuclease ABC c  
45 39 46.4 1248 2 G83278 cobalamin biosynth

ALIGNMENTS

RESULT 1  
A55671  
Bad protein - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 03-Mar-1995 #sequence\_revision 03-Mar-1995 #text\_change 05-Nov-1999  
C:Accession: A55671  
Cell 80, 285-291, 1995  
R:Yang, E.; Zha, J.; Jockel, J.; Boise, L.H.; Thompson, C.B.; Korsmeyer, S.J.  
A:Title: Bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promot  
A:Reference number: A55671; MUID:95136361; PMID:7834748  
A:Accession: A55671  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-204 <YAN>  
A:Cross-references: GB:L37296; NID:g639778; PIDN:AAA64465.1; PID:g639779  
C:Keywords: heterodimer

Query Match 100.0%; Score 84; DB 2; Length 204;  
Best Local Similarity 100.0%; Pred. No. 1.9e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRLRRMSDFEG 16  
|||||  
DB 145 QRYGRLRRMSDFEG 160

RESULT 2  
H75403  
glycosyl hydrolase, family 13 - Deinococcus radiodurans (strain R1)  
C:Species: Deinococcus radiodurans  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 17-Mar-2000  
C:Accession: H75403  
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J  
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;  
Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999  
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A:Reference number: A75250; MUID:20036896; PMID:10567266  
A:Accession: H75403  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-564 <WHT>  
A:Cross-references: GB:AE001983; NID:g6459123; PIDN:AAF10944.1; PID:g645  
A:Experimental source: strain R1  
C:Genetics:  
A:Gene: DRL375  
A:Map position: 1  
C:Superfamily: alpha-glucosidase; alpha-amylase core homology

Query Match 52.4%; Score 44; DB 2; Length 564;  
Best Local Similarity 61.5%; Pred. No. 23;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 YGRELRRMSDEFE 15  
| | | | | | | | | |  
Db 283 YVREMRVVIDEFD 295

RESULT 3  
H83036  
probable two-component sensor PA4886 [imported] - Pseudomonas aeruginosa (strain PA01)  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 14-Sep-2001  
C:Accession: H83036  
R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Miziochuchi, S.D.; Warrenner, P.; Hickey, M.J.; Boman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen  
A:Reference number: A82950; MUID:20437337; PMID:10984043  
A:Accession: H83036  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-463 <STO>  
A:Cross-references: GB:AE004901; GB:AE004091; NID:g9951147; PIDN:AAQ08271.1; GSPDB:GN001  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA4886  
C:Superfamily: hypothetical protein H11707; sensor histidine kinase homology

Query Match 51.2%; Score 43; DB 2; Length 463;  
Best Local Similarity 61.5%; Pred. No. 28;  
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 GRELRMSDEFE 16  
| | | | | | | | | |  
Db 321 GEELRQAEYFE 333

RESULT 4  
T36031  
excinuclease ABC chain A SCC54.18c [similarity] - Streptomyces coelicolor  
N:Contains: excision endonuclease ABC (EC 3.1.-.-) chain A  
C:Species: Streptomyces coelicolor  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 02-Feb-2001  
C:Accession: T36031  
R:Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, March 1999  
A:Reference number: Z1581  
A:Accession: T36031  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1014 <SEE>  
A:Cross-references: EMBL:AL035591; PIDN:CAB38148.1; GSPDB:GN00070; SCOEDB:SCC54.18c  
A:Experimental source: strain A3(2)  
C:Genetics:  
A:Gene: uvrA; SCOEDB:SCC54.18c  
C:Superfamily: excinuclease ABC chain A; ATP-binding cassette homology  
C:Keywords: ATP; DNA binding; DNA repair; hydrolase; nucleotide binding; P-loop  
F;32-39/Region: nucleotide-binding motif A (P-loop)  
F;645-652/Region: nucleotide-binding motif A (P-loop)

Query Match 50.6%; Score 42.5; DB 2; Length 1014;  
Best Local Similarity 66.7%; Pred. No. 75;  
Matches 10; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 2 FYGRELRRMSDEFE 16  
| | | | | | | | | |  
Db 368 FYGRELRRYTTAFEG 381

RESULT 5  
S38185  
2-dehydro-3-deoxy-phosphoheptonate aldolase (EC 4.1.2.15) ARO4 - yeast (Saccharomyces cerevisiae)  
N:Alternate names: 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase; DAP synthase;

C:Species: Saccharomyces cerevisiae  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 03-Jun-2002  
C:Accession: S38185; S46126; S46130; JN0322; B48651  
R:Doignon, F.; Biteau, N.; Aigle, M.; Crouzet, M.  
Yeast 9, 1131-1137, 1993  
A:Title: The complete sequence of a 6794 bp segment located on the right arm of Chromosome 1  
A:Reference number: S38185; MUID:94078675; PMID:8256522  
A:Accession: S38185  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-370 <DOI>  
A:Cross-references: GB:L20296; NID:g311101; PIDN:AAA65607.1; PID:g311102  
R:Aljinovic, G.; Pohl, F.M.; Pohl, T.M.  
submitted to the Protein Sequence Database, August 1994  
A:Reference number: S45906  
A:Accession: S46126  
A:Molecule type: DNA  
A:Residues: 1-370 <ALJ>  
A:Cross-references: EMBL:Z36118; NID:g536664; PIDN:CAA85212.1; PID:g536665; MIPS:YBR2  
R:Aigle, M.; Baclet, M.C.; Barthe, C.; Bateau, N.; Crouzet, M.; Doignon, F.  
submitted to the Protein Sequence Database, August 1994  
A:Reference number: S45940  
A:Accession: S46130  
A:Molecule type: DNA  
A:Residues: 1-370 <AIG>  
A:Cross-references: EMBL:Z36118; NID:g536664; PIDN:CAA85212.1; PID:g536665; MIPS:YBR2  
R:Kuenzler, M.; Paravicini, G.; Egli, C.M.; Paravicini, G.; Braus, G.H.  
Gene 113, 67-74, 1992  
A:Title: Cloning, primary structure and regulation of the ARO4 gene, encoding the tyrosine aminotransferase  
A:Reference number: JN0322; MUID:92225349; PMID:1348717  
A:Accession: JN0322  
A:Molecule type: DNA  
A:Residues: 1-204,208-370 <KUE>  
A:Cross-references: EMBL:X61107  
R:Kuenzler, M.; Balmelli, T.; Egli, C.M.; Paravicini, G.; Braus, G.H.  
J. Bacteriol. 175, 5548-5558, 1993  
A:Title: Cloning, primary structure, and regulation of the HIS7 gene encoding a bifunctional histidinol-phosphatase  
A:Reference number: A48651; MUID:93374850; PMID:8366040  
A:Accession: B48651  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 352-370 <KU2>  
A:Cross-references: GB:X61107  
C:Comment: This enzyme catalyzes the condensation of phosphoenolpyruvate and D-erythrose 4-phosphate to form 2-keto-3-deoxyheptulon and pyruvate  
C:Genetics:  
A:Gene: SGD:ARO4  
A:Cross-references: SGD:S0000453; MIPS:YBR249c  
A:Map position: 2R  
C:Function:  
A:Description: aldehyde-lyase; carbon-carbon lyase  
A:Pathway: aromatic amino acid biosynthesis; shikimate pathway  
A:Note: first step in shikimate pathway  
C:Superfamily: phospho-2-dehydro-3-deoxyheptonate aldolase  
C:Keywords: aldehyde-lyase; aromatic amino acid biosynthesis; carbon-carbon lyase; cy

Query Match 50.0%; Score 42; DB 2; Length 370;  
Best Local Similarity 43.8%; Pred. No. 32;  
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 QYGRELRMSDEFE 16  
| | | | | | | | | |  
Db 85 QYALRLKKLSDELKG 100

RESULT 6  
G97123  
probable Fe-S oxidoreductase CAC1813 [imported] - Clostridium acetobutylicum  
C:Species: Clostridium acetobutylicum  
C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 30-Sep-2001  
C:Accession: G97123  
R:Mölling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeug, Q.; Gibson, R.; Lally, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld  
A;Reference number: A96900; MUID:21359325; PMID:21359325  
A;Accession: G97123  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-445 <KUR>  
A;Cross-references: GB:AE001437; PIDN:AAK79778.1; PID:g15024787; GSPDB:GN00168  
A;Experimental source: Clostridium acetobutylicum ATCC824  
C;Genetics:  
A;Gene: CAC1813  
C;Superfamily: conserved hypothetical protein b0835

Query Match 50.0%; Score 42; DB 2; Length 445;  
Best Local Similarity 46.7%; Pred. No. 39;  
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEFE 15  
:|||||: : : :  
Db 85 QRYGKELKELYPEID 99

RESULT 7  
F84388  
hypothetical protein Vng2379h [imported] - Halobacterium sp. NRC-1  
C;Species: Halobacterium sp. NRC-1  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C;Accession: F84388  
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.  
; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo  
Jung, K.H.; Alam, M.; Freitas, T.  
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li  
A;Title: Genome sequence of Halobacterium species NRC-1.  
A;Reference number: A84160; MUID:20504483; PMID:11016950  
A;Accession: F84388  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-84 <STO>  
A;Cross-references: GB:AE004437; NID:g10581786; PIDN:AAK20474.1; GSPDB:GN00138  
C;Genetics:  
A;Gene: VNG2379H

Query Match 48.8%; Score 41; DB 2; Length 84;  
Best Local Similarity 57.1%; Pred. No. 10;  
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 RYGTASRMDEHD 15  
||| | | | :  
Db 66 RYGTASRMDEHD 79

RESULT 8  
JQ1128  
gas-vesicle operon protein gvpK - Halobacterium salinarum plasmids PHH1 and pNRC100  
C;Species: Halobacterium salinarum  
C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 31-Jan-2000  
C;Accession: JQ1128; S15190  
R;Jones, J.G.; Young, D.C.; Dassarma, S.  
Gene 102, 117-122, 1991  
A;Title: Structure and organization of the gas vesicle gene cluster on the Halobacterium  
A;Reference number: JQ1122; MUID:91323716; PMID:1864501  
A;Accession: JQ1128  
A;Molecule type: DNA  
A;Residues: 1-113 <JON>  
A;Cross-references: GB:M58557; NID:g150406; PID:g455299  
A;Experimental source: strain NRC-1, plasmid pNRC100  
A;Genetics: NRC  
A;Note: the source is designated as Halobacterium halobium  
R;Horne, M.; Englert, C.; Wimmer, C.; Pfeifer, F.  
Mol. Microbiol. 5, 1159-1174, 1991  
A;Title: A DNA region of 9 kbp contains all genes necessary for gas vesicle synthesis in  
A;Reference number: S15183; MUID:92065812; PMID:1956294  
A;Accession: S15190

A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-113 <HOR>  
A;Cross-references: EMBL:X55648; NID:g43516; PID:g43524  
A;Experimental source: plasmid PHH1  
A;Genetics: PHH  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 19;  
A;Note: the source is designated as Halobacterium halobium  
C;Genetics: <NRC>  
A;Gene: gvpK  
A;Genome: plasmid pNRC100  
C;Genetics: <PHH>  
A;Gene: gvpK  
A;Genome: plasmid PHH1

Query Match 48.8%; Score 41; DB 2; Length 113;  
Best Local Similarity 46.7%; Pred. No. 14;  
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEFE 15  
:|||||: : | | |  
Db 50 ERLGRQLQALEDELE 64

RESULT 9  
T08234  
gas-vesicle operon protein gvpK - Halobacterium sp. (strain NRC-1) plasmid pNRC100  
A;Alternate names: hypothetical protein H0228  
C;Species: Halobacterium sp.  
A;Variety: strain NRC-1  
C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 31-Jan-2000  
C;Accession: T08234  
R;Ng, W.V.; Clufo, S.A.; Smith, T.M.; Bumgarner, R.E.; Baskin, D.; Faust, J.; Hall, J.  
Genome Res. 8, 1131-1141, 1998  
A;Title: Snapshot of a large dynamic replicon in a halophilic Archaeon: megaplasmid  
A;Reference number: Z16408; MUID:99063795; PMID:9847077  
A;Accession: T08234  
A;Status: translated from GB/EMBL/DBJ  
A;Residues: 1-113 <NGW>  
A;Cross-references: EMBL:AF016485; NID:g2822278; PID:g2822295; HALOSP:H0228  
A;Experimental source: strain NRC-1  
C;Genetics:  
A;Gene: gvpK; HALOSP:H0228  
A;Genome: plasmid pNRC100

Query Match 48.8%; Score 41; DB 2; Length 113;  
Best Local Similarity 46.7%; Pred. No. 14;  
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEFE 15  
:|||||: : | | |  
Db 50 ERLGRQLQALEDELE 64

RESULT 10  
F72289  
oxidoreductase, sol/dev3 family - Thermotoga maritima (strain MSB8)  
C;Species: Thermotoga maritima  
C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000  
C;Accession: F72289  
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Swinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi  
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,  
C.M.  
Nature 399, 323-329, 1999  
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome  
A;Reference number: A72200; MUID:99287316; PMID:10360571  
A;Accession: F72289  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-220 <ARN>  
A;Cross-references: GB:AE001772; GB:AE000512; NID:g4961693; PIDN:AAK36230.1; PID:g49  
A;Experimental source: strain MSB8

## C:Genetics:

A:Gene: TM1154

C:Superfamily: yeast SOL3 protein

Query Match 48.8%; Score 41; DB 2; Length 220;  
 Best Local Similarity 40.0%; Pred. No. 27;  
 Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 QYGRRLRMSDEFE 15

: : | | | : | : | :  
 113 EKYERIRSATDQFD 127

Db

## RESULT 11

AB1762

phosphate ABC transporter (ATP-binding protein) homolog lin2639 [imported] - Listeria in

C:Species: Listeria innocua

C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 17-May-2002

C:Accession: AB1762

R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker

.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A:Authors: Krefit, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma

ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,

A:Title: Comparative genomics of Listeria species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AB1762

A&gt;Status: preliminary

A:Molecule type: DNA

A:Residues: 1-271 &lt;GLA&gt;

A:Cross-references: GB:AL592022; PIDN:CAC97866.1; PID:gi6415176; GSPDB:GN00178

A:Experimental source: strain Clip11262

## C:Genetics:

A:Gene: lin2639

C:Superfamily: inner membrane protein malk; ATP-binding cassette homology

Query Match 48.8%; Score 41; DB 2; Length 271;  
 Best Local Similarity 57.1%; Pred. No. 34;  
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 YGRRLRMSDEFE 16

: : | | | : | : | :  
 66 YLRALNRNDEIDG 79

Db

## RESULT 12

AH1386

phosphate ABC transporter (ATP-binding protein) homolog lmo2496 [imported] - Listeria m

C:Species: Listeria monocytogenes

C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 17-May-2002

C:Accession: AH1386

R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker

.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A:Authors: Krefit, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma

ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,

A:Title: Comparative genomics of Listeria species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AH1386

A&gt;Status: preliminary

A:Molecule type: DNA

A:Residues: 1-271 &lt;GLA&gt;

A:Cross-references: GB:NC\_003210; PIDN:CAD00574.1; PID:gi6411984; GSPDB:GN00177

A:Experimental source: strain EGD-e

## C:Genetics:

A:Gene: lmo2496

C:Superfamily: inner membrane protein malk; ATP-binding cassette homology

Query Match 48.8%; Score 41; DB 2; Length 271;  
 Best Local Similarity 57.1%; Pred. No. 34;  
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 YGRRLRMSDEFE 16

: : | | | : | : | :  
 66 YLRALNRNDEIDG 79

Db

## RESULT 13

RGBYC3

regulatory protein SNF4 - yeast (Saccharomyces cerevisiae)

N:Alternate names: CAT3 protein; protein G2945; protein YGL115w

C:Species: Saccharomyces cerevisiae

C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 21-Jul-2000

C:Accession: A38906; JT0316; S48508; S64125

R:Calenza, J.L.; Eng, F.J.; Carlson, M.

Mol. Cell. Biol. 9, 5045-5054, 1989

A:Title: Molecular analysis of the SNF4 gene of Saccharomyces cerevisiae: evidence f

A:Reference number: A33480; MUID:90097921; PMID:2481228

A:Accession: A38906

A:Molecule type: DNA

A:Residues: 1-322 &lt;CEL&gt;

A:Cross-references: GB:M30470; NID:gl72635; PIDN:AAA35061.1; PID:gl72636

R:Schueller, H.J.; Entian, K.D.

Gene 67, 247-257, 1988

A:Title: Molecular characterization of yeast regulatory gene CAT3 necessary for gluc

A:Reference number: JT0316; MUID:89006284; PMID:3049255

A:Accession: JT0316

A:Molecule type: DNA

A:Residues: 1-322 &lt;SCH&gt;

A:Cross-references: GB:M21760; NID:gl71164; PIDN:AAA34472.1; PID:gl71165

R:Doi, A.; Doi, K.

submitted to the EMBL Data Library, June 1993

A:Description: Correct end of the ORF for the CDC20 gene of Saccharomyces cerevisiae

A:Reference number: S48507

A:Accession: S48508

A:Molecule type: DNA

A:Residues: 1-21 &lt;DOI&gt;

A:Cross-references: EMBL:D16506; NID:g391938; PIDN:BAA03958.1; PID:g2160324

R:Lauguin, G.

submitted to the Protein Sequence Database, May 1996

A:Reference number: S64122

A:Accession: S64125

A:Molecule type: DNA

A:Residues: 1-322 &lt;LAU&gt;

A:Cross-references: EMBL:Z72637; NID:gl322666; PIDN:CAA96823.1; PID:gl322667; GSPDB:G

A:Experimental source: strain S288C

C:Genetics:

A:Gene: SGD:SNF4; CAT34; MIPS:YGL115w

A:Cross-references: SGD:S0003083; MIPS:YGL115w

A:Map position: 7L

## C:Function:

A:Description: involved in derepression of glucose-repressed genes

C:Superfamily: CAT3 protein

C:Keywords: nucleus; transcription regulation

Query Match 48.8%; Score 41; DB 1; Length 322;  
 Best Local Similarity 61.5%; Pred. No. 41;  
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 GRELRRMSDEFE 16

: : | | | : | : | :  
 258 GEALMRSDDEFE 270

Db

## RESULT 14

G69496

ATP-dependent 26S proteinase regulatory subunit 4 homolog - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus

C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 19-Jan-2001

C:Accession: G69496

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Doc

.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, F

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.  
 Smith, H.O.; Woese, C.R.; Venter, J.C.  
 A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaea  
 A;Reference number: A69250; MUID:98049343; PMID:9389475

A;Accession: G69496  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-398 <KLE>  
 A;Cross-references: GB:AE000967; GB:AE000782; NID:g2689290; PIDN:AAB89280.1; PID:g264856  
 C;Superfamily: ATP-dependent 26S proteinase; FtsH/SEC18/CDC48-type ATP-binding domain ho  
 C;Keywords: ATP; nucleotide binding; P-loop  
 F;155-365/Domain: FtsH/SEC18/CDC48-type ATP-binding domain homology <VATP>  
 F;182-189/Region: nucleotide-binding motif A (P-loop)

Query Match 48.8%; Score 41; DB 2; Length 398;  
 Best Local Similarity 57.1%; Pred. No. 51;  
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 RYGRRLRRMSDEFE 15  
 |||||:  
 Db 43 RYREVRRLRSEVE 56

## RESULT 15

B53234  
 vicilin-like storage protein Glb1-L, embryo - maize  
 N;Alternate names: globulin-1L  
 C;Species: Zea mays (maize)  
 C;Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 24-Nov-1999  
 C;Accession: B53234; S21824  
 R;Belanger, F.C.; Kriz, A.L.  
 Genetics 129, 863-872, 1991  
 A;Title: Molecular basis for allelic polymorphism of the maize Globulin-1 gene.  
 A;Reference number: A53234; MUID:92090707; PMID:1752424  
 A;Accession: B53234  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-582 <BEL>  
 A;Cross-references: EMBL:X59083; NID:g22283; PIDN:CAA41809.1; PID:g22284  
 A;Experimental source: inbred line W64A6  
 A;Note: sequence extracted from NCBI backbone (NCBIP:71285)  
 C;Genetics:  
 A;Gene: Glb1-L  
 A;Introns: 167/1; 225/3; 252/3; 349/3  
 C;Superfamily: glycinin

Query Match 48.8%; Score 41; DB 2; Length 582;  
 Best Local Similarity 50.0%; Pred. No. 75;  
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEFE 16  
 :|:|:|:|:  
 Db 533 ERHGREEREKEERE 548

Search completed: September 15, 2003, 17:27:01  
 Job time : 7.2 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 15, 2003, 17:16:55 ; Search time 3.77143 Seconds  
(without alignments)  
199,507 Million cell updates/sec

Title: US-09-544-664-28  
Perfect score: 84  
Sequence: 1 QRYGRELRRMSDFEG 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84	100.0	204	1 BAD_MOUSE	Q61337 mus musculus
2	84	100.0	205	1 BAD_RAT	O35147 rattus norv
3	73	86.9	168	1 BAD_HUMAN	Q92934 homo sapien
4	42.5	50.6	1014	1 UVR_A_STRCO	Q9Z507 streptomyce
5	42	50.0	196	1 BIM_MOUSE	O54918 mus musculu
6	42	50.0	196	1 BIM_RAT	O88498 rattus norv
7	42	50.0	370	1 AROG_YEAST	P32449 saccharomyc
8	42	50.0	653	1 HT2A_HUMAN	Q13049 homo sapien
9	41	48.8	113	1 GVK1_HA1N1	P24375 halobacteri
10	41	48.8	220	1 6PGL_THEMA	Q9X0n8 thermotoga
11	41	48.8	322	1 SNF4_YEAST	P12904 saccharomyc
12	41	48.8	328	1 SNF4_KLULA	Q9P869 kluyveromyc
13	41	48.8	398	1 PSMP_ARCFU	O28303 archaeoglob
14	40.5	48.2	334	1 FMR_A_CALPA	Q01133 calliactis
15	40.5	48.2	429	1 FMR2_ATEL	Q16994 antiopeura
16	40.5	48.2	435	1 FMR1_ATEL	P10419 antiopeura
17	40	47.6	205	1 RAS3_RHIRA	P22280 rhizomucor
18	40	47.6	887	1 YAV5_SCHPO	Q10213 schizosacch
19	40	47.6	2871	1 DESP_HUMAN	P15924 homo sapien
20	39.5	47.0	907	1 NUOG_ECOLI	P33602 escherichia
21	39.5	47.0	907	1 NUOG_SALTY	P33900 salmonella
22	39	46.4	87	1 Y152_UREPA	Q9Pq22 ureaplasma
23	39	46.4	95	1 R37A_HA1N1	Q9hs98 halobacteri
24	39	46.4	232	1 AP3_ARATH	P35632 arabidopsis
25	39	46.4	365	1 RA51_SCHPO	P36601 schizosacch
26	39	46.4	889	1 SEC3_DROME	Q9vv94 drosophila
27	39	46.4	1016	1 UVR_A_DEIRA	Q46577 deinoococcus
28	39	46.4	1535	1 LML1_CAEEL	Q18823 caenorhabdi
29	39	46.4	8797	1 SNEI_HUMAN	Q8nf91 homo sapien
30	38.5	45.8	323	1 FRG1_CAEEL	O18282 caenorhabdi
31	38.5	45.8	468	1 SELA_PSEAE	Q9hv01 pseudomonas
32	38	45.2	177	1 IF3_CLOPE	Q8xj67 clostridium
33	38	45.2	198	1 BIM_HUMAN	Q43521 homo sapien

## RESULT 1

ID	BAD_MOUSE	STANDARD;	PRT;	204 AA.
AC	Q61337;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component			
DE	6) (Bcl-XL/Bcl-2 associated death promoter).			
GN	BAD OR BHC6.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain, and Thymus;			
RX	MEDLINE=95136361; PubMed=7834746;			
RA	Yang E., Zha J., Jockel J., Boise L.H., Thompson C.B., Korsmeyer S.J.;			
RT	"Bad, a heterodimeric partner for Bcl-XL and Bcl-2, displaces Bax and			
RT	promotes cell death."			
RL	Cell 80:285-291(1995).			
RN	[2]			
RP	PHOSPHORYLATION, AND MUTAGENESIS OF SER-112 AND SER-136.			
RX	MEDLINE=98022383; PubMed=9381178;			
RA	Del Peso L., Gonzalez-Garcia M., Page C., Herrera R., Nunez G.;			
RT	"Interleukin-3-induced phosphorylation of BAD through the protein			
RT	kinase Akt."			
RL	Science 278:687-689(1997).			
RN	[3]			
RP	MUTAGENESIS OF SERINE RESIDUES.			
RX	MEDLINE=20403302; PubMed=10949026;			
RA	Datta S.R., Katsov A., Hu L., Petros A., Fesik S.W., Yaffe M.B.,			
RA	Greenberg M.E.;			
RT	"14-3-3 proteins and survival kinases cooperate to inactivate BAD by			
RT	BH3 domain phosphorylation."			
RL	Mol. Cell 6:41-51(2000).			
CC	-!- FUNCTION: Promotes cell death. Successfully competes for the			
CC	binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level			
CC	of heterodimerization of these proteins with BAX. Can reverse the			
CC	death repressor activity of Bcl-x(L), but not that of Bcl-2.			
CC	Appears to act as a link between growth factor receptor signaling			
CC	and the apoptotic pathways.			
CC	-!- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-			
CC	x(L), Bcl-2 and Bcl-w. Also binds protein S100A10 (By similarity).			
CC	The Ser-112/Ser-136 phosphorylated form binds 14-3-3 proteins.			
CC	-!- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon			
CC	phosphorylation, locates to the cytoplasm.			
CC	-!- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND			
CC	BAX for their pro-apoptotic activity and for their interaction			
CC	with anti-apoptotic members of the Bcl-2 family.			
CC	-!- PTM: Phosphorylated on Ser-112 in response to survival stimuli.			
CC	Subsequent phosphorylation on Ser-136 promotes heterodimerization			
CC	with 14-3-3 proteins. This interaction then facilitates the			
CC	phosphorylation at Ser-155, a site within the BH3 domain, leading			
CC	to the release of Bcl-x(L) and the promotion of cell survival.			

## ALIGNMENTS

34	38	45.2	207	1	THLE_PYRAB	Q9uzq5 pyrococcus
35	38	45.2	370	1	AROG_CANAL	P79023 candida alb
36	38	45.2	570	1	STIM_DROME	P83094 drosophila
37	38	45.2	712	1	PERL_HUMAN	P22079 homo sapien
38	38	45.2	861	1	GCR3_YEAST	P34160 saccharomyc
39	38	45.2	1047	1	RIRL_CHLMU	Q9pl93 chlamydia m
40	38	45.2	1047	1	RIRL_CHLTR	O84834 chlamydia t
41	38	45.2	1268	1	VGLN_HUMAN	Q00341 homo sapien
42	38	45.2	1270	1	VGLN_CHICK	P81021 gallus gall
43	38	45.2	1958	1	UBRL_SCHPO	O60152 schizosacch
44	37.5	44.6	992	1	UVRA_MICLU	P13567 micrococcus
45	37	44.0	126	1	LEU3_BUCUL	Q9aqc8 buchnera ap

CC Ser-136 is the major site of AKT/PKB phosphorylation, Ser-155 the  
 CC major site of protein kinase A (CAPK) phosphorylation.  
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.  
 CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; L37296; AAA64465.1; -;  
 DR PIR; A55671; A55671.  
 DR HSP; Q92934; IG5J.  
 DR MGD; MGI:1096330; Bad.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR PROSITE; PS01259; BH3; FALSE\_NEG.  
 KW Apoptosis; Phosphorylation.  
 FT DOMAIN 147 161  
 FT MOD\_RES 112 112 PHOSPHORYLATION (BY PKA AND PKB).  
 FT MOD\_RES 136 136 PHOSPHORYLATION (BY PKA AND PKB).  
 FT MOD\_RES 155 155 PHOSPHORYLATION (BY PKA AND PKB).  
 FT MUTAGEN 112 112 S->A: NO PHOSPHORYLATION.  
 FT MUTAGEN 136 136 S->A: NO PHOSPHORYLATION.  
 FT MUTAGEN 155 155 S->A: NO PHOSPHORYLATION; INTERACTS WITH  
 FT BCL-X(L).  
 FT SEQUENCE 204 AA; 22080 MW; 6C2BA910205053F7 CRC64;  
 Query Match 100.0%; Score 84; DB 1; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 QRYGRELRRMSDEFEQ 16  
 Db 145 QRYGRELRRMSDEFEQ 160  
 |||||  
 RESULT 2  
 BAD\_RAT STANDARD; PRT; 205 AA.  
 AC Q35147; Q70256; Q9JHX1;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component  
 DE 6) (Bcl-xL/Bcl-2 associated death promoter).  
 GN BAD.  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF SER-113 AND SER-137.  
 RC TISSUE=Ovary;  
 RX MEDLINE=98034386; PubMed=9369453;  
 RA Hsu S.Y., Kaipia A., Zhu L., Hsueh A.J.W.;  
 RT "Interference of BAD (Bcl-xL/Bcl-2-associated death promoter)-induced  
 RT apoptosis in mammalian cells by 14-3-3 isoforms and P11.";  
 RL Mol. Endocrinol. 11:1858-1867(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=98194755; PubMed=9535132;  
 RA D'Agata V., Magro G., Travali S., Musco S., Cavallaro S.;  
 RT "Cloning and expression of the programmed cell death regulator BAD in  
 RT the rat brain.";  
 RL Neurosci. Lett. 243:137-140(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).  
 RC TISSUE=Brain;  
 RX MEDLINE=21109372; PubMed=11161472;

RA Hamner S., Arumae U., Yu L.-Y., Sun Y.-P., Saarna M., Lindholm D.;  
 RT "Functional characterization of two splice variants of rat BAD and  
 RT their interaction with Bcl-w in sympathetic neurons.";  
 RL Mol. Cell. Neurosci. 17:97-106(2001).  
 CC -!- FUNCTION: Promotes cell death. Successfully competes for the  
 CC binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level  
 CC of heterodimerization of these proteins with BAX. Can reverse the  
 CC death repressor activity of Bcl-x(L), but not that of Bcl-2 (By  
 CC similarity). Appears to act as a link between growth factor  
 CC receptor signaling and the apoptotic pathways.  
 CC -!- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-  
 CC x(L), Bcl-2 and Bcl-w. Also binds protein S100A10. The Ser-  
 CC 113/Ser-137 phosphorylated form binds 14-3-3 proteins.  
 CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon  
 CC phosphorylation, locates to the cytoplasm (By similarity).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=2;  
 CC Name=Alpha;  
 CC IsoId=O35147-1; Sequence=Displayed;  
 CC Name=Beta;  
 CC IsoId=O35147-2; Sequence=VSP\_000534;  
 CC -!- TISSUE SPECIFICITY: Expressed in all tissues tested, including  
 CC brain, liver, spleen and heart. In the brain, restricted to  
 CC epithelial cells of the choroid plexus. Isoform alpha is the more  
 CC abundant form.  
 CC -!- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND  
 CC BAX for their pro-apoptotic activity and for their interaction  
 CC with anti-apoptotic members of the Bcl-2 family.  
 CC -!- PTM: Phosphorylated on Ser-113 in response to survival stimuli.  
 CC Subsequent phosphorylation on Ser-137 promotes heterodimerization  
 CC with 14-3-3 proteins. This interaction then facilitates the  
 CC phosphorylation at Ser-156, a site within the BH3 domain, leading  
 CC to the release of Bcl-x(L) and the promotion of cell survival.  
 CC Ser-137 is the major site of AKT/PKB phosphorylation, Ser-156 the  
 CC major site of protein kinase A (CAPK) phosphorylation (By  
 CC similarity).  
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.  
 CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; AF003523; AAC53374.1; -;  
 DR EMBL; AF031227; AAC15100.1; -;  
 DR EMBL; AF279910; AAF91427.1; -;  
 DR EMBL; AF279911; AAF91428.1; -;  
 DR HSP; Q92934; IG5J.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR PROSITE; PS01259; BH3; FALSE\_NEG.  
 KW Apoptosis; Phosphorylation; Alternative splicing.  
 FT DOMAIN 148 162  
 FT MOD\_RES 113 113 PHOSPHORYLATION (BY PKA AND PKB)  
 FT MOD\_RES 137 137 (BY SIMILARITY).  
 FT MOD\_RES 156 156 PHOSPHORYLATION (BY PKA AND PKB)  
 FT MOD\_RES 156 156 (BY SIMILARITY).  
 FT MOD\_RES 156 156 PHOSPHORYLATION (BY PKA AND PKB)  
 FT MOD\_RES 156 156 (BY SIMILARITY).  
 FT VARSPLIC 166 205 LPRPKSAGTATOMRQSASWTRIQSWDRNLKGGSPSQ  
 FT -> BELTYSVEFLPYRAIAMEGWPLLSFOSFHTLPTTP  
 FT EVAMFPLRYWALRLIC (in isoform Beta).  
 FT /FTId=VSP\_000534.  
 FT MUTAGEN 113 113 S->A: NO EFFECT ON HETERODIMERIZATION  
 FT WITH 14-3-3 PROTEINS.  
 FT MUTAGEN 137 137 S->A: NO HETERODIMERIZATION WITH 14-3-3  
 FT PROTEINS. NO EFFECT ON HETERODIMERIZATION  
 FT WITH BCL2 NOR WITH PROTEIN P11.  
 FT CONFLICT 29 34 SDAGGR -> ERRGRK (IN REF. 1).  
 FT SEQUENCE 205 AA; 22228 MW; 7AFA71DAE9CF4A81 CRC64;

Query Match 100.0%; Score 84; DB 1; Length 205;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRLRRMSDFEG 16  
 |||||  
 DB 146 QRYGRLRRMSDFEG 161

RESULT 3  
 BAD\_HUMAN  
 ID BAD\_HUMAN STANDARD; PRT; 168 AA.  
 AC Q92934; O14803;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component 6) (Bcl-2  
 XL/Bcl-2 associated death promoter) (BCL2-like 8 protein).  
 GN BAD OR BOC6 OR BCL2L8.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Yin D.X., Li Z., Huang B., Chen S., Zhou H.;  
 RT "A human protein that interacts with Bcl-2 and have homology to mouse  
 BAD.";  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A., AND PHOSPHORYLATION BY RAF-1.  
 RX MEDLINE=97083574; PubMed=8929532;  
 RA Wang H.-G., Rapp U.R., Reed J.C.;  
 RT "Bcl-2 targets the protein kinase Raf-1 to mitochondria.";  
 RL Cell 87:629-638(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Takayama S., Reed J.C.;  
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A., AND DIMERIZATION.  
 RC TISSUE=Bone marrow;  
 RX MEDLINE=98049554; PubMed=9388232;  
 RA Ottillie S., Diaz J.-L., Horne W., Chang J., Wang Y., Wilson G.,  
 RA Chang S., Weeks S., Fritz L.C., Oltersdorf T.;  
 RT "Dimerization properties of human BAD.";  
 RL J. Biol. Chem. 272:30866-30872(1997).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [6]

RP STRUCTURE BY NMR OF 103-127.  
 RX MEDLINE=21073561; PubMed=11206074;  
 RA Petros A.M., Nettlesheim D.G., Wang Y., Olejniczak E.T., Meadows R.P.,  
 RA Mack J., Swift K., Matayoshi E.D., Zhang H., Thompson C.B.,  
 RA Fesik S.W.;  
 RT "Rationale for Bcl-xL/Bad peptide complex formation from structure,  
 mutagenesis, and biophysical studies.";  
 RL Protein Sci. 9:2528-2534(2000).  
 CC -|- FUNCTION: Promotes cell death. Successfully competes for the  
 CC binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level  
 CC of heterodimerization of these proteins with BAX. Can reverse the  
 CC death repressor activity of Bcl-x(L), but not that of Bcl-2 (By  
 CC similarity). Appears to act as a link between growth factor  
 CC receptor signaling and the apoptotic pathways.  
 CC -|- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-  
 CC x(L), Bcl-2 and Bcl-w. Also binds protein S100A10 (By similarity).  
 CC The Ser-75/Ser-99 phosphorylated form binds 14-3-3 proteins (By  
 CC similarity).  
 CC -|- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon  
 CC phosphorylation, locates to the cytoplasm.  
 CC -|- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.  
 CC -|- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND  
 CC BAX for their pro-apoptotic activity and for their interaction  
 CC with anti-apoptotic members of the Bcl-2 family.  
 CC -|- PTM: Phosphorylated on Ser-75 in response to survival stimuli.  
 CC Subsequent phosphorylation on Ser-99 promotes heterodimerization  
 CC with 14-3-3 proteins. This interaction then facilitates the  
 CC phosphorylation at Ser-118, a site within the BH3 domain, leading  
 CC to the release of Bcl-x(L) and the promotion of cell survival.  
 CC Ser-99 is the major site of AKT/PKB phosphorylation, Ser-118 the  
 CC major site of protein kinase A (CAK) phosphorylation (by  
 CC similarity).  
 CC -|- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.  
 CC -|- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -|- CAUTION: Ref.1 sequence differs from that shown due to frameshifts  
 CC in position 64 and 91.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; U66879; AAB36516.1; ALT\_FRAME.  
 DR EMBL; AF021792; AAB72092.1; -.  
 DR EMBL; AF031523; AAB88124.1; -.  
 DR EMBL; BC001901; AAH01901.1; -.  
 DR PDB; 1G5J; 07-FEB-01.  
 DR Genew; HGNC:936; BAD.  
 DR MIM; 603167; -.  
 DR GO; GO:0005737; C:cytoplasm; NAS.  
 DR GO; GO:0005741; C:mitochondrial outer membrane; NAS.  
 DR GO; GO:0005515; F:protein binding activity; NAS.  
 DR GO; GO:0006632; P:apoptotic program; TAS.  
 DR GO; GO:0006917; P:induction of apoptosis; NAS.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR PROSITE; PS01259; BH3; FALSE\_NEG.  
 KW Apoptosis; Phosphorylation; Polymorphism; 3D-structure.  
 FT DOMAIN 110 124  
 FT MOD\_RES 75 75  
 FT PHOSPHORYLATION (BY PKA AND PKB) (BY  
 FT SIMILARITY).  
 FT MOD\_RES 99 99  
 FT PHOSPHORYLATION (BY PKA AND PKB) (BY  
 FT SIMILARITY).  
 FT MOD\_RES 118 118  
 FT PHOSPHORYLATION (BY PKA AND PKB) (BY  
 FT SIMILARITY).  
 FT VARIANT 107 107  
 FT A -> S (in dbSNP:3729933).  
 FT HELIX 106 121  
 FT SEQUENCE 168 AA; 18392 MW; 69FD8D27DDEE3241 CRC64;  
 SQ

Query Match 86.9%; Score 73; DB 1; Length 168;



```
SQ SEQUENCE 196 AA; 22066 MW; 531C1765F1AC9AA CRC64;

Query Match 50.0%; Score 42; DB 1; Length 196;
Best Local Similarity 61.5%; Pred. No. 8.6;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 RYGRRLRMSDEF 14
Db 145 RIAQLRRIGDEF 157

RESULT 6
BIM_RAT
ID BIM_RAT STANDARD; PRT; 196 AA.
AC 088498; 088497; Q9WU18;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE BCL2-like protein 11 (BCL2 interacting mediator of cell death)
DE (Bcl-2 related ovarian death protein).
GN BCL2L11 OR BIM OR BOD.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, SUBUNIT, AND TISSUE SPECIFICITY
RP (ISOFORMS BOD-L; BOD-M AND BOD-S).
RC TISSUE=Ovary;
RX MEDLINE=98400436; PubMed=9731710;
RA Hsu S.Y., Lin P., Hsueh A.J.W.;
RT "BOD (Bcl-2-related ovarian death gene) is an ovarian BH3 domain-
RT containing proapoptotic Bcl-2 protein capable of dimerization with
RT diverse antiapoptotic Bcl-2 members.";
RL Mol. Endocrinol. 12:1432-1440(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM BIML).
RA Chen D., Simon R.P., Chen J.;
RT "Cloning of rat bimL and bimL, and their differential expression in
RT ischemia and normal rat brain.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INDUCES APOPTOSIS.
CC -!- SUBUNIT: FORMS HETERODIMERS WITH A NUMBER OF ANTIAPOPTOTIC BCL-2
CC PROTEINS INCLUDING MCL-1, BCL-2, BCL-XL, BFL-1, AND BHRF-1. DOES
CC NOT HETERODIMERIZE WITH PROAPOPTOTIC PROTEINS SUCH AS BAD, BOK,
CC BAX OR BAK.
CC -!- SUBCELLULAR LOCATION: ASSOCIATED WITH INTRACYTOSOLIC MEMBRANES
CC (BY SIMILARITY).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=BOD-L;
CC IsoId=088498-1; Sequence=Displayed;
CC Note=Isoform BOD-S is produced by alternative initiation at
CC Met-104 of isoform BOD-L;
CC Name=BimL;
CC IsoId=088498-2; Sequence=VSP_000538;
CC Name=BOD-M;
CC IsoId=088498-3; Sequence=VSP_000539;
CC Event=Alternative initiation;
CC Comment=2 isoforms, BOD-L (shown here) and BOD-S, are produced
CC by alternative initiation at Met-1 and Met-104;
CC -!- TISSUE SPECIFICITY: Widely expressed.
CC -!- DOMAIN: THE BH3 DOMAIN IS REQUIRED FOR BCL-2 BINDING AND
CC CYTOTOXICITY.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC
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CC
DR EMBL; AF065433; AAC23595.1; -
DR EMBL; AF065431; AAC23593.1; -
DR EMBL; AF065432; AAC23594.1; -
DR EMBL; AF136927; AAD26594.1; -
DR InterPro; IPR000712; Bcl2_BH.
DR PROSITE; PS01259; BH3; FALSE_NEG.
KW Apoptosis; Alternative splicing; Membrane; Alternative initiation.
FT CHAIN 1 196 BCL2-LIKE PROTEIN 11, ISOFORM BOD-L.
FT INIT_MET 104 196 BCL2-LIKE PROTEIN 11, ISOFORM BOD-S.
FT DOMAIN 146 160 FOR ISOFORM BOD-S.
FT VARSPLIC 42 97 BH3.
FT Missing (in isoform BimL).
FT /FTID=VSP_000538.
FT VARSPLIC 42 127 Missing (in isoform BOD-M).
FT /FTID=VSP_000539.
FT CONFLICT 136 136 E -> D (IN REF. 1; AAC23594).
SQ SEQUENCE 196 AA; 22055 MW; B4D2146F9C0B37A0 CRC64;

Query Match 50.0%; Score 42; DB 1; Length 196;
Best Local Similarity 61.5%; Pred. No. 8.6;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 RYGRRLRMSDEF 14
Db 145 RIAQLRRIGDEF 157

RESULT 7
AROG_YEAST
ID AROG_YEAST STANDARD; PRT; 370 AA.
AC P32449;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phospho-2-dehydro-3-deoxyheptonsate aldolase, tyrosine-inhibited
DE (EC 4.1.2.13) (Phospho-2-keto-3-deoxyheptonsate aldolase) (DAHP
DE synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase).
GN ARO4 OR YBR249C OR YBR1701.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92225349; PubMed=1348717;
RA Kuenzler M., Paravicini G., Egli C., Irniger S., Braus G.H.;
RT "Cloning, primary structure and regulation of the ARO4 gene, encoding
RT the tyrosine-inhibited 3-deoxy-D-arabino-heptulosonate-7-phosphate
RT synthase from Saccharomyces cerevisiae.";
RL Gene 113:67-74(1992).
RN [2]
RP REVISIONS TO 205-207.
RA Kuenzler M.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=S288c;
RX MEDLINE=94078675; PubMed=8255522;
RA Doignon F., Biteau N., Aigle M., Crouzet M.;
RT "The complete sequence of a 6794 bp segment located on the right arm
RT of chromosome II of Saccharomyces cerevisiae. Finding of a putative
RT dutPase in a yeast.";
RL Yeast 9:1131-1137(1993).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=S288c;
RA Aljinovic G., Pohl F.M., Pohl T.M.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: STEREOSPECIFIC CONDENSATION OF PHOSPHOENOLPYRUVATE (PEP)
CC AND D-ERYTHROSE-4-PHOSPHATE (E4P) GIVING RISE TO 3-DEOXY-D-
CC ARABINO-HEPTULOSONATE-7-PHOSPHATE (DAHP).
CC -!- CATALYTIC ACTIVITY: 2-dehydro-3-deoxy-D-arabino-heptonsate 7-
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CC phosphate + phosphate = phosphoenolpyruvate + D-erythrose 4-
CC phosphate + H2O.
CC -!- ENZYME REGULATION: INHIBITED BY TYROSINE.
CC -!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC first step.
CC -!- INDUCTION: By amino acid starvation.
CC -!- SIMILARITY: BELONGS TO CLASS-I DAHP SYNTHETASE FAMILY.
CC -----
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CC -----
CC EMBL; X61107; CAA43419.1; -.
CC EMBL; L20296; AAA65607.1; -.
CC EMBL; Z36118; CAA85212.1; -.
CC PIR; S38185; S38185.
CC HSSP; P00886; 1QR7.
CC SGD; S0000453; AR04.
CC GO; GO:0003849; F-2-dehydro-3-deoxyphosphoheptonate aldolase . . . ; IDA.
CC InterPro; IPR006219; AROFGH.
CC Pfam; PF00793; DAHP_synth.1; 1.
CC ProDom; PD005060; AROFGH; 1.
CC TIGRFAMs; TIGR00034; aroFGH; 1.
CC Aromatic amino acid biosynthesis; Lyase; Multigene family.
CC SEQUENCE 370 AA; 39749 MW; 594ED48F24175979 CRC64;
CC -----
Query Match 50.0%; Score 42; DB 1; Length 370;
Best Local Similarity 43.8%; Pred. No. 17;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDFEG 16
Db | | |:::| | |
85 QEYALRLKLSDELKG 100

RESULT 8
HT2A_HUMAN
ID HT2A_HUMAN STANDARD; PRT; 653 AA.
AC Q13049; Q9NQPB;
DT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Zinc-finger protein HT2A (72 kDa Tat-interacting protein) (Tripartite
DE motif-containing protein 32).
GN TRIM32 OR HT2A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95297135; PubMed=7778269;
RA Fridell R.A., Harding L.S., Bogerd H.P., Cullen B.R.;
RT "Identification of a novel human zinc finger protein that
RT specifically interacts with the activation domain of lentiviral Tat
RT proteins."
RL Virology 209:347-357(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Sehra H.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: MAY PLAY A SIGNIFICANT ROLE IN MEDIATING THE BIOLOGICAL
CC ACTIVITY OF THE HIV-1 TAT PROTEIN IN VIVO. BINDS SPECIFICALLY TO
CC THE ACTIVATION DOMAIN OF HIV-1 TAT AND CAN ALSO INTERACT WITH THE
CC HIV-2 AND ETAV TAT PROTEINS IN VIVO.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: SPLEEN, THYMUS, PROSTRATE, TESTIS, OVARY,
CC INTESTINE AND COLON.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC -!- SIMILARITY: Contains 1 B box-type zinc finger.
CC -----
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CC -----
CC EMBL; U18543; AAA86474.1; -.
CC EMBL; ALJ33284; CAB92723.1; -.
CC EMBL; BC003154; AAH03154.1; -.
CC HSSP; P29590; 1BOR.
CC Genew; HGNC:16380; TRIM32.
CC MIM; 602290; -.
CC GO; GO:0005634; C:nucleus; TAS.
CC GO; GO:0003713; F:transcription co-activator activity; TAS.
CC InterPro; IPR001258; NHL.
CC InterPro; IPR000315; Znf_Box.
CC InterPro; IPR001841; Znf_ring.
CC Pfam; PF01436; NHL; 5.
CC Pfam; PF00643; zf-B_box; 1.
CC Pfam; PF00097; zf-C3HC4; 1.
CC SMART; SMO0336; BBOX; 1.
CC SMART; SMO0184; RING; 1.
CC PROSITE; PS50119; ZF_BOX; 1.
CC PROSITE; PS00518; ZF_RING_1; 1.
CC PROSITE; PS00089; ZF_RING_2; 1.
CC Zinc-finger; Nuclear protein.
KW DOMAIN 2 6 POLY-ALA.
FT ZN_FING 20 65 RING-TYPE.
FT ZN_FING 103 133 B_BOX-TYPE.
FT CONFLICT 27 27
SQ SEQUENCE 653 AA; 71988 MW; D83B1595CA8378FD CRC64;

Query Match 50.0%; Score 42; DB 1; Length 653;
Best Local Similarity 61.5%; Pred. No. 30;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDE 13
Db | | | | | | | |
186 QEYGEHRRVQDE 198

RESULT 9
GVKL_HALN1
ID GVKL_HALN1 STANDARD; PRT; 113 AA.

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P24375; Q9HI26;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE GvpK protein 1.  
 GN (GVPK11 OR GVPK OR VNG5021G) AND (GVPK12 OR VNG6021G).  
 OS Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081), and  
 OS Halobacterium sp. (strain NRC-817).  
 OG Plasmid pNRC100, Plasmid pNRC200, and Plasmid pH1.  
 OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;  
 OC Halobacteriaceae; Halobacterium.  
 OX NCBI\_TaxID=64091, 148370;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NRC-1; PLASMID=pNRC100;  
 RX MEDLINE=91323716; PubMed=1864501;  
 RA Jones J.G., Young D.C., Dassarma S.;  
 RT "Structure and organization of the gas vesicle gene cluster on the  
 RL Halobacterium halobium plasmid pNRC100.";  
 RL Gene 102:117-122(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NRC-1; PLASMID=pNRC100;  
 RX MEDLINE=99063795; PubMed=9847077;  
 RA Ng W.V., Clufo S.A., Smith T.M., Bumgarner R.E., Baskin D., Faust J.,  
 RA Hall B., Loretz C., Seto J., Slagel J., Hood L., DasSarma S.;  
 RT "Snapshot of a large dynamic replicon in a halophilic archaeon:  
 RT megaplasmid or minichromosome?";  
 RL Genome Res. 8:1131-1141(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NRC-1; PLASMID=pNRC200;  
 RX MEDLINE=20504483; PubMed=11016950;  
 RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,  
 RA Shukla H.D., Lasky S.R., Pallig N.S., Thorsson V., Sroogna J.,  
 RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,  
 RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,  
 RA Madocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,  
 RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,  
 RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,  
 RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;  
 RT "Genome sequence of Halobacterium species NRC-1.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NRC-817; PLASMID=pH1;  
 RX MEDLINE=92065812; PubMed=1956294;  
 RA Horne M., Englert C., Wimmer C., Pfeifer F.;  
 RT "A DNA region of 9 kbp contains all genes necessary for gas vesicle  
 RT synthesis in halophilic archaeobacteria.";  
 RL Mol. Microbiol. 5:1159-1174(1991).  
 CC -!- FUNCTION: MAY PLAY A STRUCTURAL OR REGULATORY ROLE IN GAS  
 CC VESICLE SYNTHESIS.  
 CC -----  
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 CC -----  
 DR EMBL; M58557; AAA98188.1; -.  
 DR EMBL; AF016485; AAC82801.1; -.  
 DR EMBL; AF005141; AAG20718.1; -.  
 DR EMBL; X55648; CAA39178.1; -.  
 DR PIR; T08234; T08234.  
 DR Pfam; PF05121; GvpK; 1.  
 KW Gas vesicle; Plasmid; Complete proteome.  
 SQ SEQUENCE 113 AA; 12695 MW; 97A469D2C1643ABF CRC64;  
 Query Match 48.8%; Score 41; DB 1; Length 113;  
 Best Local Similarity 46.7%; Pred. No. 7;  
 Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 QRYGRELRRMSDEFE 15  
 Db 50 ERLGRLQALEDELE 64  
 RESULT 10  
 6PGL\_THEME  
 ID 6PGL\_THEME STANDARD; PRT; 220 AA.  
 AC Q9X0N8;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE 6-phosphogluconolactonase (EC 3.1.1.31) (6PGL).  
 GN PGL OR DEVB OR TM1154.  
 OS Thermotoga maritima.  
 OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.  
 OX NCBI\_TaxID=2336;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MSB8 / DSM 3109;  
 RX MEDLINE=93287316; PubMed=10360571;  
 RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,  
 RA Hart D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,  
 RA McDonald L., Utterback T.R., Mailek J.A., Linher K.D., Garrett M.M.,  
 RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,  
 RA Heidelberg J., Sutton M.G., Fleischmann R.D., Eisen J.A., White O.,  
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;  
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from  
 RL Nature 393:323-329(1999).  
 CC -!- FUNCTION: HYDROLYSIS OF 6-PHOSPHOGLUCONOLACTONE TO 6-  
 CC PHOSPHOGLUCONATE.  
 CC -!- CATALYTIC ACTIVITY: 6-phospho-D-glucono-1,5-lactone + H(2)O = 6-  
 CC phospho-D-gluconate.  
 CC -!- PATHWAY: Pentose phosphate pathway; second step.  
 CC -!- SIMILARITY: BELONGS TO THE GLUCOSAMINE/GALACTOSAMINE-6-PHOSPHATE  
 CC ISOMERASE FAMILY. 6-PHOSPHOGLUCONOLACTONASE SUBFAMILY.  
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 CC -----  
 DR EMBL; AE001772; AAD36230.1; -.  
 DR PIR; F72289; F72289.  
 DR TIGR; TM1154; -.  
 DR InterPro; IPR006148; Gluc\_gal\_isom.  
 DR InterPro; IPR005900; Phosphogluconlac.  
 DR Pfam; PF01182; Glucosamine\_iso; 1.  
 DR TIGRFams; TIGR01198; pgl; 1.  
 KW Hydrolyase; Complete proteome.  
 SQ SEQUENCE 220 AA; 25325 MW; 9B0FD07EE01E60C3 CRC64;  
 Query Match 48.8%; Score 41; DB 1; Length 220;  
 Best Local Similarity 40.0%; Pred. No. 14;  
 Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEFE 15  
 Db 113 EKYREIRSATDQFD 127  
 RESULT 11  
 SNF4\_YEAST  
 ID SNF4\_YEAST STANDARD; PRT; 322 AA.  
 AC P12904;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Nuclear protein SNF4 (Regulatory protein CAT3).  
GN SNF4 OR CAP3 OR YGL115W.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89006284; PubMed=3049255;  
RA Schueller H.-J., Entian K.-D.;  
RT "Molecular characterization of yeast regulatory gene CAT3 necessary  
for glucose derepression and nuclear localization of its product.";  
RL Gene 67:247-257(1988).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90097921; PubMed=2481228;  
RA Celenza J.L., Eng F.J., Carlson M.;  
RT "Molecular analysis of the SNF4 gene of Saccharomyces cerevisiae:  
evidence for physical association of the SNF4 protein with the SNF1  
protein kinase.";  
RL Mol. Cell. Biol. 9:5045-5054(1989).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX Laquin G.;  
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE OF 1-21 FROM N.A.  
RA Doi A., Doi K.;  
RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE OF 30-34 AND 315-322.  
RX MEDLINE=94131988; PubMed=7905477;  
RA Mitchellhill K.I., Stapleton D., Gao G., House C., Michell B.,  
RA Katsis F., Witters L.A., Kemp B.E.;  
RT "Mammalian AMP-activated protein kinase shares structural and  
functional homology with the catalytic domain of yeast Snf1 protein  
kinase.";  
RL J. Biol. Chem. 269:2361-2364(1994).  
CC -!- FUNCTION: THIS PROTEIN CAUSES EXPRESSION OF GLUCOSE-REPRESSIBLE  
GENES UPON GLUCOSE DEPRIVATION. IT INTERACTS AND HAS FUNCTIONAL  
RELATIONSHIP TO THE PROTEIN-KINASE SNF1.  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA  
SUBUNIT FAMILY.  
CC -!- SIMILARITY: Contains 4 CBS domains.  
CC -----  
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CC -----  
CC EMBL; M21760; AAA34472.1; -  
DR EMBL; M30470; AAA35061.1; -  
DR EMBL; Z72637; CAA96823.1; -  
DR EMBL; D16506; BAA03958.1; -  
DR PIR; A38906; RGYCY3.  
DR SGD; S0003083; SNF4.  
DR GO; GO:0005737; C:cytoplasm; IDA.  
DR GO; GO:0005634; C:nucleus; IDA.  
DR GO; GO:0030295; F:protein kinase activator activity; IGI.  
DR GO; GO:0007031; P:peroxisome organization and biogenesis; IMP.  
DR GO; GO:0006357; P:regulation of transcription from Pol II pro. . .; IGI.  
DR InterPro; IPR000644; CBS\_domain.  
DR Pfam; PF00571; CBS; 4.  
DR SMART; SM00116; CBS; 4.  
KW Carbohydrate metabolism; Transcription regulation; Nuclear protein;  
FT Repeat; CBS domain. 89 CBS 1.  
FT DOMAIN 35 89 CBS 2.  
FT DOMAIN 117 175

FT DOMAIN 192 246 CBS 3.  
FT DOMAIN 259 318 CBS 4.  
SQ SEQUENCE 322 AA; 36401 MW; 51B387E346EE9561 CRC64;  
Query Match 48.8%; Score 41; DB 1; Length 322;  
Best Local Similarity 61.5%; Pred. No. 21;  
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 4 GRELRMSDEFEQ 16  
| | | | | | | | | |  
Db 258 GEALMRRSDDFEG 270  
| | | | | | | | | |  
RESULT 12  
SNF4\_KLULA  
ID SNF4\_KLULA STANDARD; PRT; 328 AA.  
AC Q9P869;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Nuclear protein SNF4.  
GN SNF4.  
OS Kluyveromyces lactis (Yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.  
OX NCBI\_TaxID=28985;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Tomasini L., Ferrero I., Goffrini P.;  
RT "Molecular characterization of KLSNF4 gene";  
Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: THIS PROTEIN CAUSES EXPRESSION OF GLUCOSE-REPRESSIBLE  
GENES UPON GLUCOSE DEPRIVATION. IT INTERACTS AND HAS FUNCTIONAL  
RELATIONSHIP TO THE PROTEIN-KINASE SNF1 (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).  
CC -!- SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA  
SUBUNIT FAMILY.  
CC -!- SIMILARITY: Contains 4 CBS domains.  
CC -----  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; AJ277480; CAB89520.1; -  
DR InterPro; IPR000644; CBS\_domain.  
DR Pfam; PF00571; CBS; 4.  
DR SMART; SM00116; CBS; 4.  
KW Carbohydrate metabolism; Transcription regulation; Nuclear protein;  
KW Repeat; CBS domain. 94 CBS 1.  
FT DOMAIN 40 94 CBS 2.  
FT DOMAIN 122 180 CBS 2.  
FT DOMAIN 198 252 CBS 3.  
FT DOMAIN 271 324 CBS 4.  
SQ SEQUENCE 328 AA; 37163 MW; DC9ED3F85E46BAD3 CRC64;  
Query Match 48.8%; Score 41; DB 1; Length 328;  
Best Local Similarity 61.5%; Pred. No. 21;  
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 4 GRELRMSDEFEQ 16  
| | | | | | | | | |  
Db 264 GEALMRRSDDFEG 276  
| | | | | | | | | |  
RESULT 13  
PSMR\_ARCFU  
ID PSMR\_ARCFU STANDARD; PRT; 398 AA.  
AC O28303;  
DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Proteasome-activating nucleotidase (Proteasome regulatory subunit).  
 GN PAN OR AF1976.  
 OS Archaeoglobus fulgidus.  
 OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;  
 OC Archaeoglobaceae; Archaeoglobus.  
 OX NCBI\_TaxID=2234;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=VC-16 / DSM 4304 / ATCC 49558;  
 RX MEDLINE=98049343; PubMed=9389475;  
 RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,  
 RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,  
 RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,  
 RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,  
 RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,  
 RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,  
 RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,  
 RA Cotton M.D., Spriggs T., Artach P., Kaine B.P., Sykes S.M.,  
 RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,  
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,  
 RA Venter J.C.;  
 RA "The complete genome sequence of the hyperthermophilic, sulphate-  
 RT reducing archaeon Archaeoglobus fulgidus.";  
 RL Nature 390:364-370(1997).  
 CC -!- FUNCTION: Required for the ATP- or CTP-dependent degradation of  
 CC proteins, but not small peptides, by the 20S proteasome (By  
 CC similarity).  
 CC -!- SUBUNIT: Homohexamer (Potential).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -!- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.  
 CC  
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 CC  
 CC EMBL; AF00553; -;  
 CC PIR; G69496; G69496.  
 CC TIGR; AF1976; -;  
 CC HAMAP; MF\_00553; -; 1.  
 CC InterPro; IPR005937; 26S\_p45.  
 CC InterPro; IPR003593; AAA\_ATPase.  
 CC InterPro; IPR003959; AAA\_ATPase\_central.  
 CC InterPro; IPR003960; AAA\_sub.  
 CC Pfam; PF00004; AAA; 1.  
 CC SMART; SM00382; AAA; 1.  
 CC TIGRFAMs; TIGR01242; 26Sp45; 1.  
 CC PROSITE; PS00674; AAA; 1.  
 KW Proteasome; ATP-binding; Complete proteome.  
 FT NP\_BIND 182 189  
 FT ATP (POTENTIAL).  
 SQ SEQUENCE 398 AA; 44964 MW; F3293BB7D6A646B4 CRC64;  
 Query Match 48.8%; Score 41; DB 1; Length 398;  
 Best Local Similarity 57.1%; Pred. No. 26;  
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 2 RYGRRLRMSDEFE 15  
 Db 43 RYERVRRLRGEVE 56  
 RESULT 14  
 FMRA\_CALPA STANDARD; PRT; 334 AA.  
 AC Q01133;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Antho-RFamide neuropeptides precursor.  
 OS Calliactis parasitica (Sea anemone).  
 OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Zoantharia; Actiniaria;  
 OC Nynanthaeae; Hormathiidae; Calliactis.  
 OX NCBI\_TaxID=6114;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91172845; PubMed=1706527;  
 RA Darmer D., Schmutzler C., Diekhoff D., Grimmelikhuijzen C.J.P.;  
 RT "Primary structure of the precursor for the sea anemone neuropeptide  
 RT Antho-RFamide (<Glu-Gly-Arg-Phe-NH2).";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:2555-2559(1991).  
 CC -!- FUNCTION: NOT KNOWN BUT IT COULD ACT AS A TRANSMITTER AT  
 CC NEUROMUSCULAR SYNAPSES.  
 CC -!- TISSUE SPECIFICITY: NEURONS ASSOCIATED WITH SMOOTH MUSCLE FIBERS.  
 CC  
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 CC  
 CC EMBL; M59166; AA227878.1; -;  
 CC PIR; A39172; A39172.  
 CC InterPro; IPR002544; FARP.  
 CC Pfam; PF01581; FARP; 15.  
 KW Neuropeptide; Amidation; Repeat; Signal.  
 FT SIGNAL 1 26  
 FT POTENTIAL.  
 FT PEPTIDE 117 120 ANTHO-RFAMIDE.  
 FT PEPTIDE 126 129 ANTHO-RFAMIDE.  
 FT PEPTIDE 135 138 ANTHO-RFAMIDE.  
 FT PEPTIDE 143 146 ANTHO-RFAMIDE.  
 FT PEPTIDE 152 153 ANTHO-RFAMIDE.  
 FT PEPTIDE 161 164 ANTHO-RFAMIDE.  
 FT PEPTIDE 170 173 ANTHO-RFAMIDE.  
 FT PEPTIDE 179 182 ANTHO-RFAMIDE.  
 FT PEPTIDE 188 191 ANTHO-RFAMIDE.  
 FT PEPTIDE 197 200 ANTHO-RFAMIDE.  
 FT PEPTIDE 206 209 ANTHO-RFAMIDE.  
 FT PEPTIDE 215 218 ANTHO-RFAMIDE.  
 FT PEPTIDE 224 227 ANTHO-RFAMIDE.  
 FT PEPTIDE 234 237 ANTHO-RFAMIDE.  
 FT PEPTIDE 243 246 ANTHO-RFAMIDE.  
 FT PEPTIDE 253 256 ANTHO-RFAMIDE.  
 FT PEPTIDE 263 266 ANTHO-RFAMIDE.  
 FT PEPTIDE 272 275 ANTHO-RFAMIDE.  
 FT PEPTIDE 281 284 ANTHO-RFAMIDE.  
 FT MOD\_RES 120 120 PROVIDE AMIDE GROUP).  
 FT MOD\_RES 129 129 PROVIDE AMIDE GROUP).  
 FT MOD\_RES 138 138 PROVIDE AMIDE GROUP).  
 FT MOD\_RES 146 146 PROVIDE AMIDE GROUP).  
 FT MOD\_RES 155 155 PROVIDE AMIDE GROUP).  
 FT MOD\_RES 164 164 PROVIDE AMIDE GROUP).  
 FT MOD\_RES 173 173 PROVIDE AMIDE GROUP).  
 FT MOD\_RES 182 182 PROVIDE AMIDE GROUP).  
 FT MOD\_RES 191 191 PROVIDE AMIDE GROUP).  
 FT MOD\_RES 200 200 PROVIDE AMIDE GROUP).  
 FT MOD\_RES 209 209 PROVIDE AMIDE GROUP).  
 FT MOD\_RES 218 218 PROVIDE AMIDE GROUP).  
 FT MOD\_RES 227 227 PROVIDE AMIDE GROUP).  
 FT MOD\_RES 237 237 PROVIDE AMIDE GROUP).  
 FT MOD\_RES 246 246 PROVIDE AMIDE GROUP).  
 FT MOD\_RES 256 256 PROVIDE AMIDE GROUP).  
 FT MOD\_RES 266 266 PROVIDE AMIDE GROUP).  
 FT MOD\_RES 275 275 PROVIDE AMIDE GROUP).  
 FT MOD\_RES 284 284 PROVIDE AMIDE GROUP).  
 SQ SEQUENCE 334 AA; 39781 MW; 438E182C736EB583 CRC64;  
 Query Match 48.2%; Score 40.5; DB 1; Length 334;  
 Best Local Similarity 56.2%; Pred. No. 26;  
 Matches 9; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 2 RYGRELR-RMSDEFEQ 16  
| | | | : | | | :  
Db 96 RYGREFQGRFGREFQ 111

RESULT 15  
FMR2\_ANCEL  
ID FMR2\_ANCEL STANDARD; PRT; 429 AA.  
AC Q16994;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Antho-RFamide neuroptides type 2 precursor.  
OS Anthopleura elegantissima (Sea anemone).  
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;  
OX Nynanthae; Actiniidae; Anthopleura.  
OC NCBI\_TaxID=6110;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93054550; PubMed=1429603;  
RA Schmutzler C., Darmer D., Diekhoff D., Grimmelikhuijzen C.J.P.;  
RT "Identification of a novel type of processing sites in the precursor  
for the sea anemone neuroptide Antho-RFamide (<Glu-Gly-Arg-Phe-NH2)  
from Anthopleura elegantissima.";  
RL J. Biol. Chem. 267:22534-22541(1992).  
RN [2]  
RP PARTIAL SEQUENCE (ANTHO-RFAMIDE).  
RX MEDLINE=87092339; PubMed=2879288;  
RA Grimmelikhuijzen C.J.P., Graff D.;  
RT "Isolation of pyroGlu-Gly-Arg-Phe-NH2 (Antho-RFamide), a neuroptide  
from sea anemones.";  
RL Proc. Natl. Acad. Sci. U.S.A. 83:9817-9821(1986).  
CC -!- FUNCTION: NOT KNOWN BUT IT COULD ACT AS A TRANSMITTER AT  
CC NEUROMUSCULAR SYNAPSES.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -----  
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CC -----  
DR EMBL; M99170; AAA27739.1; -  
DR Pfam; PF01581; FARP; 14.  
KW Neuroptide; Amidation; Repeat; Signal.  
FT SIGNAL 1 22  
FT PEPTIDE 234 237 ANTHO-RFAMIDE.  
FT PEPTIDE 242 245 ANTHO-RFAMIDE.  
FT PEPTIDE 250 253 ANTHO-RFAMIDE.  
FT PEPTIDE 258 261 ANTHO-RFAMIDE.  
FT PEPTIDE 266 269 ANTHO-RFAMIDE.  
FT PEPTIDE 274 277 ANTHO-RFAMIDE.  
FT PEPTIDE 290 293 ANTHO-RFAMIDE.  
FT PEPTIDE 298 301 ANTHO-RFAMIDE.  
FT PEPTIDE 306 309 ANTHO-RFAMIDE.  
FT PEPTIDE 322 325 ANTHO-RFAMIDE.  
FT PEPTIDE 330 333 ANTHO-RFAMIDE.  
FT PEPTIDE 343 346 ANTHO-RFAMIDE.  
FT PEPTIDE 356 359 ANTHO-RFAMIDE.  
FT PEPTIDE 369 372 ANTHO-RFAMIDE.  
FT MOD\_RES 237 237 AMIDATION (G-238 PROVIDE AMIDE GROUP).  
FT MOD\_RES 245 245 AMIDATION (G-246 PROVIDE AMIDE GROUP).  
FT MOD\_RES 253 253 AMIDATION (G-254 PROVIDE AMIDE GROUP).  
FT MOD\_RES 261 261 AMIDATION (G-262 PROVIDE AMIDE GROUP).  
FT MOD\_RES 269 269 AMIDATION (G-270 PROVIDE AMIDE GROUP).  
FT MOD\_RES 277 277 AMIDATION (G-278 PROVIDE AMIDE GROUP).  
FT MOD\_RES 293 293 AMIDATION (G-294 PROVIDE AMIDE GROUP).  
FT MOD\_RES 301 301 AMIDATION (G-302 PROVIDE AMIDE GROUP).  
FT MOD\_RES 309 309 AMIDATION (G-310 PROVIDE AMIDE GROUP).  
FT MOD\_RES 325 325 AMIDATION (G-326 PROVIDE AMIDE GROUP).

FT MOD\_RES 333 333 AMIDATION (G-334 PROVIDE AMIDE GROUP).  
FT MOD\_RES 346 346 AMIDATION (G-347 PROVIDE AMIDE GROUP).  
FT MOD\_RES 359 359 AMIDATION (G-360 PROVIDE AMIDE GROUP).  
FT MOD\_RES 372 372 AMIDATION (G-373 PROVIDE AMIDE GROUP).  
SQ SEQUENCE 429 AA; 50564 MW; 7C54F5C606D537F4 CRC64;

Query Match 48.2%; Score 40.5; DB 1; Length 429;  
Best Local Similarity 56.2%; Pred. No. 34;  
Matches 9; Conservative 3; Mismatches 3; Indels 1; Gaps 1;  
QY 2 RYGRELR-RMSDEFEQ 16  
| | | | : | | | :  
Db 212 RYGRELQGRFGREFQ 227

Search completed: September 15, 2003, 17:23:00  
Job time : 4.77143 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 15, 2003, 17:17:31 ; Search time 17.3714 Seconds  
(without alignments)  
237.680 Million cell updates/sec

Title: US-09-544-664-28

Perfect score: 84

Sequence: 1 QRYGRELRLMSDEFE3 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL.23.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	72.6	146	13 Q9T9N2	Q9i9n2 brachydanio
2	47	56.0	216	16 Q9KZC5	Q9kzc5 streptomyce
3	45	53.6	230	16 Q8XXS6	Q8xxs6 ralstonia s
4	45	53.6	567	10 Q9FV20	Q9fv20 oryza sativ
5	45	53.6	1696	10 Q8GTN3	Q8gtn3 oryza sativ
6	45	53.6	1748	16 Q989R4	Q989r4 rhizobium l
7	45	53.6	1798	2 Q8KGY8	Q8kgy8 rhizobium l
8	44	52.4	157	16 Q8ES55	Q8es55 oceanobacil
9	44	52.4	564	16 Q9RUK9	Q9ruk9 deinococcus
10	43.5	51.8	1589	2 Q8KUF5	Q8kuf5 actinosynne
11	43	51.2	463	16 Q9HUS7	Q9hus7 pseudomonas
12	43	51.2	674	10 Q93Y86	Q93y86 oryza sativ
13	43	51.2	5635	5 Q9N9N1	Q9n9n1 leishmania
14	42.5	50.6	904	2 Q9KGW3	Q9kgw3 pseudomonas
15	42.5	50.6	909	16 Q8EI34	Q8ei34 shewanella
16	42	50.0	164	17 Q8ZTI1	Q8zti1 pyrobaculum

17	42	50.0	213	17 Q8TJ31	Q8tj31 methanosarc
18	42	50.0	337	3 Q9P5V2	Q9p5v2 neurospora
19	42	50.0	375	10 Q94H58	Q94h58 oryza sativ
20	42	50.0	425	10 Q8S6J1	Q8s6j1 oryza sativ
21	42	50.0	445	16 Q97I40	Q97i40 clostridium
22	42	50.0	561	10 Q8LM44	Q8lm44 oryza sativ
23	42	50.0	581	16 Q8F646	Q8f646 leptospira
24	42	50.0	606	11 Q8C850	Q8c850 mus musculu
25	42	50.0	606	11 Q8C6N1	Q8c6n1 mus musculu
26	42	50.0	641	10 Q8GTN7	Q8gtn7 oryza sativ
27	42	50.0	677	10 Q9AYG6	Q9ayg6 oryza sativ
28	42	50.0	804	16 Q8EW78	Q8ew78 mycoplasma
29	42	50.0	827	10 Q8GTN2	Q8gtn2 oryza sativ
30	42	50.0	829	10 Q9XEM4	Q9xem4 oryza sativ
31	42	50.0	829	10 Q8GVG4	Q8gv4 oryza sativ
32	42	50.0	1032	10 Q9LGR7	Q9lgr7 oryza sativ
33	42	50.0	1032	10 Q8LHG3	Q8lhg3 oryza sativ
34	42	50.0	1032	10 Q9LGR6	Q9lgr6 oryza sativ
35	42	50.0	1032	10 Q9SSW6	Q9ssw6 oryza sativ
36	42	50.0	1032	10 Q8RYW0	Q8ryw0 oryza sativ
37	42	50.0	1032	10 Q8GTN5	Q8gtn5 oryza sativ
38	42	50.0	1099	10 Q8W3I5	Q8w3i5 oryza sativ
39	42	50.0	1112	10 Q8LSS6	Q8lss6 oryza sativ
40	42	50.0	1126	5 Q9VSM2	Q9vsm2 drosophila
41	42	50.0	1416	10 Q8S609	Q8s609 oryza sativ
42	42	50.0	1429	10 Q94H01	Q94hul oryza sativ
43	42	50.0	1583	10 Q9S7A7	Q9s7a7 oryza sativ
44	42	50.0	1653	5 Q9VSM1	Q9vsm1 drosophila
45	42	50.0	1709	5 Q9VSM0	Q9vsm0 drosophila

ALIGNMENTS

RESULT 1

Q9I9N2	ID	Q9I9N2	PRELIMINARY;	PRT;	146 AA.
AC	Q9I9N2;				
DT	01-OCT-2000	(TREMBLrel. 15, Created)			
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)			
DT	01-OCT-2002	(TREMBLrel. 22, Last annotation update)			
DE	Bad.				
GN	BAD.				
OS	Brachydanio rerio (zebrafish) (Danio rerio).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Actinopterygii; Neopterygii; teleostei; Ostariophysi; Cypriniformes;				
OC	Cyprinidae; Danio.				
OX	NCBI_TaxID=7955;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=20373792; PubMed=10917738;				
RA	Inohara N., Nunez G.;				
RT	"Genes with homology to mammalian apoptosis regulators identified in zebrafish."				
RL	Cell Death Differ. 7:509-510(2000).				
DR	EMBL; AF231017; AAF66962.2; -.				
DR	HSSP; Q92934; 1G5J.				
DR	ZFIN; ZDB-GENE-000616-1; bad.				
SQ	SEQUENCE 146 AA; 16546 MW; 28A5650BB5107ECB CRC64;				

Query Match 72.6%; Score 61; DB 13; Length 146;  
Best Local Similarity 66.7%; Pred. No. 0.028;  
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRYGRELRLMSDEFE 15

:::::|||||

Db 93 KXYGQQLRMSDEFD 107

RESULT 2

Q9KZC5	ID	Q9KZC5	PRELIMINARY;	PRT;	216 AA.
AC	Q9KZC5;				

```

DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein SCO6964.
GN SCO6964 OR SC6F7.17C.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Saunders D.C., Harris D.;
RL Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapante D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL939129; CAB89025.1; -.
DR InterPro; IPR003265; Endo_3c.
DR Pfam; PF00730; HHH-GPD; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 216 AA; 23810 MW; DDD7C717D60F7AA7 CRC64;

Query Match 56.0%; Score 47; DB 16; Length 216;
Best Local Similarity 50.0%; Pred. No. 8.7;
Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 QRYGRELRLMSDEFEG 16
Db 109 ERWGGDLRLRLRDEADG 124

RESULT 3
Q8XXS6 PRELIMINARY; PRT; 230 AA.
AC Q8XXS6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Probable ATP-binding ABC transporter protein.
GN RSC2037 OR RS03602.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Ralstoniaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=GMI1000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Sigulier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL; AL646067; CAD15739.1; -.
DR InterPro; IPR003593; AAA_Atpase.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
KW Complete proteome.
SQ SEQUENCE 230 AA; 25231 MW; 7C3FDA1E7A19A2A4 CRC64;

Query Match 53.6%; Score 45; DB 16; Length 230;
Best Local Similarity 64.3%; Pred. No. 20;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QRYGRELRLMSDEF 14
Db 168 QEIGRTLRLRLVDEF 181

RESULT 4
Q9FV20 PRELIMINARY; PRT; 567 AA.
ID Q9FV20;
AC Q9FV20;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Polypeptide.
OS Oryza sativa (indica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39946;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Zhaiyeging 8; TRANSPOSON=unspecified; TISSUE=Shoot;
RA Yu F., Zhang A., Zhang F., Chen S.;
RL Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF259576; AAG15480.1; -.
DR Gramene; Q9FV20; -.
DR InterPro; IPR002156; RNaseH.
DR InterPro; IPR000477; RVTse.
DR Pfam; PF00075; rnaseH; 1.
DR Pfam; PF00078; rvt; 1.
KW RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 567 AA; 64419 MW; BD4F47AB33A685BE CRC64;

Query Match 53.6%; Score 45; DB 10; Length 567;
Best Local Similarity 50.0%; Pred. No. 52;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 3 YGRELRLMSDEFEG 16
Db 547 YRQEVKXLEDKFEG 560

RESULT 5
Q8GTN3 PRELIMINARY; PRT; 1696 AA.
ID Q8GTN3;
AC Q8GTN3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative GAG-POL precursor.

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GN OSUNBA0041L14.29.  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzeae; Oryza.  
 OX NCBI\_TaxID=39947;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Niponbare;  
 RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,  
 RA Overton II L.L., Tsitin T., Kim M.M., Bera J.J., Jin S.S.,  
 RA Fadrosch D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,  
 RA Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,  
 RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,  
 RA White O., Salzberg S.L., Fraser C.M.;  
 RT "Oryza sativa chromosome 10 BAC OSUNBA0041L14 genomic sequence."  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC099042; AA08247.1;  
 SQ SEQUENCE 1696 AA; 190501 MW; 516B35CFDFA2F068 CRC64;

Query Match 53.6%; Score 45; DB 10; Length 1696;  
 Best Local Similarity 50.0%; Pred. No. 1.7e+02;  
 Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 3 YGRELRRMSDEFEG 16  
 | :|:|:| :|:|:|  
 Db 1341 YRQEVKLEDKFEG 1354

## RESULT 6

Q989R4 ID Q989R4 PRELIMINARY; PRT; 1748 AA.  
 AC Q989R4;  
 DT 01-OCT-2001 (Tremblrel. 18, Created)  
 DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)  
 DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)  
 DE Hypothetical protein mlr6316.  
 GN MLR6316.  
 OS Rhizobium loti (Mesorhizobium loti).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Phyllobacteriaceae; Mesorhizobium.  
 OX NCBI\_TaxID=381;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MAFF303099;  
 RX MEDLINE=21082930; PubMed=11214968;  
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,  
 RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,  
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,  
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,  
 RA Takeuchi C., Yamada M., Tabata S.;  
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti";  
 RL DNA Res. 7:331-338(2000).  
 DR EMBL; AP003008; BAB52630.1;  
 DR InterPro: IPR003653; SUMO\_protease.  
 DR Pfam: PF02902; Peptidase\_C48; 1.  
 DR PROSITE; PS50600; ULP\_PROTEASE; 1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 1748 AA; 190454 MW; 2A9CE7B92C354341 CRC64;

Query Match 53.6%; Score 45; DB 16; Length 1748;  
 Best Local Similarity 69.2%; Pred. No. 1.7e+02;  
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 YGRELRRMSDEFEG 15  
 ||| ||| | :| :|  
 Db 562 YGRLRRFSELE 574

## RESULT 7

Q8KGY8 ID Q8KGY8 PRELIMINARY; PRT; 1798 AA.

AC Q8KGY8;  
 DT 01-OCT-2002 (Tremblrel. 22, Created)  
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 GN MSI059.  
 OS Rhizobium loti (Mesorhizobium loti).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Phyllobacteriaceae; Mesorhizobium.  
 OX NCBI\_TaxID=381;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=R7A;  
 RX MEDLINE=21999272; PubMed=12003951;  
 RA Sullivan J.T., Trzebiatowski J.R., Cruickshank R.W., Gouzy J.,  
 RA Brown S.D., Elliot R.M., Fleetwood D.J., McCallum N.G., Rossbach U.,  
 RA Stuart G.S., Weaver J.E., Webby R.J., de Bruijn F.J., Ronson C.W.;  
 RT "Comparative sequence analysis of the symbiosis island of Mesorhizobium loti strain R7A";  
 RT J. Bacteriol. 184:3086-3095(2002).  
 RL EMBL; AL672112; CAD31464.1;  
 DR InterPro: IPR003653; SUMO\_protease.  
 DR Pfam: PF02902; Peptidase\_C48; 1.  
 DR PROSITE; PS50600; ULP\_PROTEASE; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 1798 AA; 196214 MW; A750A49B8CD581B CRC64;

Query Match 53.6%; Score 45; DB 2; Length 1798;  
 Best Local Similarity 69.2%; Pred. No. 1.8e+02;  
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 YGRELRRMSDEFEG 15  
 ||| ||| | :| :|  
 Db 569 YGRLRRFSELE 581

## RESULT 8

Q8ES55 ID Q8ES55 PRELIMINARY; PRT; 157 AA.  
 AC Q8ES55;  
 DT 01-MAR-2003 (Tremblrel. 23, Created)  
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
 DE Hypothetical conserved protein.  
 GN OB0788.  
 OS Oceanobacillus iheyensis.  
 OC Bacteria; Firmicutes; Bacillales; Oceanobacillus.  
 OX NCBI\_TaxID=182710;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HTE831 / DSM 14371 / JCM 11309;  
 RX MEDLINE=22220767; PubMed=12235376;  
 RA Takami H., Takaki Y., Uchiyama I.;  
 RT Ridge and its unexpected adaptive capabilities to extreme environments";  
 RT Nucleic Acids Res. 30:3927-3935(2002).  
 RL EMBL; AP004595; BAC12744.1;  
 DR EMBL; AP004595; BAC12744.1;  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 157 AA; 17809 MW; 128229251596C18C CRC64;

Query Match 52.4%; Score 44; DB 16; Length 157;  
 Best Local Similarity 50.0%; Pred. No. 19;  
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 YGRELRRMSDEFEG 16  
 : ||| :| :| :|  
 Db 126 FSRELKRIGEFSG 139

## RESULT 9

Q9RUK9 ID Q9RUK9 PRELIMINARY; PRT; 564 AA.

AC Q9RUK9;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Glycosyl hydrolase, family 13.  
 GN DR1375.  
 OS Deinococcus radiodurans.  
 OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;  
 OC Deinococcaceae; Deinococcus.  
 OX NCBI\_TaxID=1299;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=R1;  
 RX MEDLINE=20036896; PubMed=10567266;  
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,  
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,  
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,  
 RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zaleski C.,  
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,  
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,  
 RA Fraser C.M.;  
 RT "Genome sequence of the radioresistant bacterium Deinococcus  
 RT radiodurans R1.";  
 RL Science 286:1571-1577(1999).  
 DR EMBL; AE001983; AAF10944.1; -.  
 DR HSSP; F21332; 1UOK.  
 DR TIGR; DR1375; -.  
 DR InterPro; IPR006047; Alpha\_amyl\_cat.  
 DR InterPro; IPR006589; Alp\_amyl\_cat\_sub.  
 DR Pfam; PF00128; alpha-amylase; 1.  
 DR SMART; SM00642; Amyy; 1.  
 KW Hydrolase; Complete proteome.  
 SQ SEQUENCE 564 AA; 63667 MW; B8F50B9B0DFC8D51 CRC64;

Query Match 52.4%; Score 44; DB 16; Length 564;  
 Best Local Similarity 61.5%; Pred. No. 76;  
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 YGRELRRMSDEFE 15  
 | | | | | | | | | |  
 Db 283 YVEMRRVDEFD 295

RESULT 10  
 Q8KUF5  
 ID Q8KUF5 PRELIMINARY; PRT; 1589 AA.  
 AC Q8KUF5;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Polyketide synthase.  
 GN ASMC.  
 OS Actinosynnema pretiosum (subsp. auranticum).  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Pseudonocardineae; Actinosynnemataceae; Actinosynnema.  
 OX NCBI\_TaxID=42198;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 31565;  
 RX MEDLINE=22056096; PubMed=12060743;  
 RA Yu T.W., Bai L., Clade D., Hoffmann D., Toelzer S., Trinh K.Q., Xu J.,  
 RA Moss S.J., Leistner E., Floss H.G.;  
 RT "The biosynthetic gene cluster of the maytansinoid antitumor agent  
 RT ansanitocin from Actinosynnema pretiosum.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:7968-7973(2002).  
 DR EMBL; AF453501; AAM54077.1; -.  
 DR InterPro; IPR001227; Ac transferase.  
 DR InterPro; IPR000794; Ketoacyl-synt.  
 DR InterPro; IPR006162; Ppantne\_attach.  
 DR InterPro; IPR006163; Pp\_bind.  
 DR Pfam; PF00698; Acyl\_transf; 1.  
 DR Pfam; PF00109; ketoacyl-synt; 1.  
 DR Pfam; PF02801; ketoacyl-synt\_C; 1.

DR Pfam; PF00550; pp-binding; 1.  
 DR PROSITE; PS00075; ACP\_DOMAIN; 1.  
 DR PROSITE; PS00606; B\_KETOACYL\_SYNTHASE; 1.  
 DR PROSITE; PS00012; PHOSPHOPANTHEINE; 1.  
 KW Phosphopantetheine.  
 SQ SEQUENCE 1589 AA; 164712 MW; 5067CF9A772A525F CRC64;

Query Match 51.8%; Score 43.5; DB 2; Length 1589;  
 Best Local Similarity 56.2%; Pred. No. 2.7e+02;  
 Matches 9; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

Qy 1 QRYGRELRRMSDEFE 16  
 | | | | | | | | | |  
 Db 161 QNYGNRRVAEEFE 175

RESULT 11  
 Q9HUS7  
 ID Q9HUS7 PRELIMINARY; PRT; 463 AA.  
 AC Q9HUS7;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Probable two-component sensor.  
 GN PA4886.  
 OS Pseudomonas aeruginosa.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=287;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 15692 / PA01;  
 RX MEDLINE=20437337; PubMed=10984043;  
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,  
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,  
 RA Garber R.L., Goltry L., Tolentino E., Westbrock-wadman S., Yuan Y.,  
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Iarbig K., Lim R.M.,  
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;  
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an  
 RT opportunistic pathogen.";  
 RL Nature 406:959-964(2000).  
 CC -1- SIMILARITY: TO PROKARYOTE SENSORY TRANSDUCTION PROTEINS.  
 DR EMBL; AE004901; AAG08271.1; -.  
 DR HSP; P02933; 1BXD.  
 DR InterPro; IPR003594; ATPbind\_ATPase.  
 DR InterPro; IPR004358; Bact\_sens\_pr\_C.  
 DR InterPro; IPR003660; HAMP.  
 DR InterPro; IPR003661; His\_kinA.  
 DR InterPro; IPR005467; His\_kinase.  
 DR InterPro; IPR000005; HTHArac.  
 DR InterPro; IPR006290; Metal\_his\_kin.  
 DR Pfam; PF00672; HAMP; 1.  
 DR Pfam; PF02518; HATPase\_C; 1.  
 DR Pfam; PF00512; Hiska; 1.  
 DR PRINTS; PR00344; ECTRLSENSOR.  
 DR SMART; SM00304; HAMP; 1.  
 DR SMART; SM00387; HATPase\_C; 1.  
 DR SMART; SM00388; Hiska; 1.  
 DR TIGRFAMs; TIGR01386; czts\_sils\_cops; 1.  
 DR PROSITE; PS0109; HIS\_KIN; 1.  
 DR PROSITE; PS00041; HTH\_ARAC\_FAMILY\_1; 1.  
 KW Kinase; Phosphorylation; Sensory transduction; Transferase;  
 KW Complete proteome.  
 SQ SEQUENCE 463 AA; 50946 MW; 97FF19C2CF38006C CRC64;

Query Match 51.2%; Score 43; DB 16; Length 463;  
 Best Local Similarity 61.5%; Pred. No. 90;  
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GRELRRMSDEFE 16  
 | | | | | | | | | |  
 Db 321 GEELRRQAEYFE 333

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RESULT 12
Q93Y86
ID Q93Y86 PRELIMINARY; PRT; 674 AA.
AC Q93Y86;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Putative gag-pol.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K.,
RA Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsitrin T.,
RA Riggs F., Hsiao J., Zisemann V., Blunt S., Pai G., VanAken S.E.,
RA Utterback T.R., Feldblyum T.V., Quackenbush J., Salzberg S.L.,
RA White O., Fraser C.M.;
RT "Oryza sativa chromosome 3 BAC OSJNBa0026A15 genomic sequence.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC084404; AAK50597.1; -
DR Gramene; Q93Y86; -
DR InterPro; IPR002156; RNaseH.
DR InterPro; IPR001584; Rve.
DR Pfam; PF00075; rnaaseH.1.
DR Pfam; PF00665; rve.1.
SQ SEQUENCE 674 AA; 75473 MW; 9FA929B1426E725E CRC64;

Query Match 51.2%; Score 43; DB 10; Length 674;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEFEG 16
: |||: |||
DB 258 EAYVREVRNRNFDG 273

RESULT 13
Q9N9N1
ID Q9N9N1 PRELIMINARY; PRT; 5635 AA.
AC Q9N9N1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Dynein heavy chain, cytosolic.
GN L3302.02.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Friedlin;
RA Hilbert H., Wedler H., Wedler E., Duesterhoeft A., Ivens A.C.,
RA Quail M., Rajandream M.A., Barrell B.G.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Friedlin;
RX MEDLINE=98146435; PubMed=9477341;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RA Smith D.F.;
RT "A physical map of the Leishmania major Friedlin genome.";
RL Genome Res. 8:135-145(1998).
DR EMBL; AL359781; CAB95305.1; -
DR InterPro; IPR003593; AAA_Atpase.
DR InterPro; IPR004273; Dynein_heavy.
DR InterPro; IPR000169; SHprot_acsite.
DR Pfam; PF03028; Dynein_heavy; 1.

DR SMART; SM00382; AAA; 4.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
KW ATP-binding.
SQ SEQUENCE 5635 AA; 620050 MW; 64A9EE81A9B14641 CRC64;

Query Match 51.2%; Score 43; DB 5; Length 5635;
Best Local Similarity 72.7%; Pred. No. 1.3e+03;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QRYGRELRRMS 11
|||: |||
DB 1535 QRFGRDLRRWS 1545

RESULT 14
Q9KGW3
ID Q9KGW3 PRELIMINARY; PRT; 904 AA.
AC Q9KGW3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE NADH dehydrogenase I subunit G.
GN NUOG.
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=294;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WCS365;
RA Camacho Carvajal M.M., Lugtenberg B.J.J., Bloemberg G.V.;
RT "Characterization of NADH dehydrogenases of Pseudomonas fluorescens
WCS365 and their role in competitive root colonisation.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF281148; AAF97803.1; -
DR InterPro; IPR000283; Complex1_75K.
DR InterPro; IPR001041; Ferredoxin.
DR InterPro; IPR006656; Molybdopterin.
DR InterPro; IPR006963; Molybdop_Fe4S4.
DR Pfam; PF00111; fer2; 1.
DR Pfam; PF00384; molybdopterin; 1.
DR Pfam; PF04879; Molybdop_Fe4S4; 1.
DR PROSITE; PS00641; COMPLEX1_75K_1; 1.
DR PROSITE; PS00642; COMPLEX1_75K_2; 1.
DR PROSITE; PS00643; COMPLEX1_75K_3; 1.
KW Iron; Iron-sulfur.
SQ SEQUENCE 904 AA; 98157 MW; C25B86C6D4DFA457 CRC64;

Query Match 50.6%; Score 42.5; DB 2; Length 904;
Best Local Similarity 56.2%; Pred. No. 2.2e-02;
Matches 9; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 QRYGRELRRMSDEFEG 16
: |||: |||: |||
DB 241 ERYG-ELRRIRNFNG 255

RESULT 15
Q8EI34
ID Q8EI34 PRELIMINARY; PRT; 909 AA.
AC Q8EI34;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE NADH dehydrogenase I, G subunit.
GN NUOG OR S01016.
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Shewanella.
OX NCBI_TaxID=70863;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MR-1;

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RX MEDLINE=22297686; PubMed=12368813;  
RA Heideberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,  
RA Read T.D., Eise J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,  
RA Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,  
RA DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,  
RA Madupu R., Peterson J.D., Unayam L.A., White O., Wolf A.M.,  
RA Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,  
RA Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,  
RA Reiblyum T.V., Smith H.O., Venter J.C., Neelson K.H., Fraser C.M.;  
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium  
RL Shewanella oneidensis";  
RL Nat. Biotechnol. 20:1118-1123(2002).  
DR EMBL; AE015546; AAN54089.1; -.  
DR TIGR; SO1016; -.  
KW Complete proteome.  
SQ SEQUENCE 909 AA; 100079 MW; F71859F385BDCAC8 CRC64;  
  
Query Match 50.6%; Score 42.5; DB 16; Length 909;  
Best Local Similarity 56.2%; Pred. No. 2.2e+02;  
Matches 9; Conservative 3; Mismatches 3; Indels 1; Gaps 1;  
  
QY 1 QRYGRELRRMSDEFEG 16  
:|||||:|:  
Db 241 ERYG-ELRRIRNRFHG 255

Search completed: September 15, 2003, 17:25:48  
Job time : 19.3714 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 15, 2003, 17:16:01 ; Search time 22.6286 Seconds  
(without alignments)  
112.231 Million cell updates/sec

Title: US-09-544-664-29

Perfect score: 83

Sequence: 1 QRYGRLRRMSDEFVD 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	100.0	16	AA05421	Human BAD BH3 doma
2	83	100.0	16	AA337029	Bcl2 polypeptide B
3	83	100.0	20	ABG78499	Mutant Bcl2 compet
4	83	100.0	20	AAU78626	Human Bad peptide
5	83	100.0	21	ABG78500	Mutant Bcl2 compet
6	83	100.0	21	AAU78630	Human Bad peptide
7	83	100.0	22	AAU78629	Human Bad peptide
8	83	100.0	23	AAU78628	Human Bad peptide
9	83	100.0	24	ABG78482	Human Bcl2 fluores

10	83	100.0	24	AAU78605	Human Bad peptide
11	83	100.0	24	AAU78627	Human Bad peptide
12	83	100.0	25	ABP56161	TRPC-interacting T
13	83	100.0	25	ABG78481	Human Bcl2 fluores
14	83	100.0	25	ABG78484	Mutant Bcl2 compet
15	83	100.0	25	ABG78485	Mutant Bcl2 compet
16	83	100.0	25	ABG78486	Mutant Bcl2 compet
17	83	100.0	25	ABG78487	Mutant Bcl2 compet
18	83	100.0	25	ABG78488	Mutant Bcl2 compet
19	83	100.0	25	ABG78489	Mutant Bcl2 compet
20	83	100.0	25	ABG78490	Mutant Bcl2 compet
21	83	100.0	25	ABG78491	Mutant Bcl2 compet
22	83	100.0	25	ABG78492	Mutant Bcl2 compet
23	83	100.0	25	ABG78493	Mutant Bcl2 compet
24	83	100.0	25	ABG78494	Mutant Bcl2 compet
25	83	100.0	25	ABG78495	Mutant Bcl2 compet
26	83	100.0	25	AAU78601	Human Bad peptide
27	83	100.0	25	AAU78610	Human Bad peptide
28	83	100.0	25	AAU78611	Human Bad peptide
29	83	100.0	25	AAU78612	Human Bad peptide
30	83	100.0	25	AAU78613	Human Bad peptide
31	83	100.0	25	AAU78614	Human Bad peptide
32	83	100.0	25	AAU78615	Human Bad peptide
33	83	100.0	25	AAU78616	Human Bad peptide
34	83	100.0	25	AAU78617	Human Bad peptide
35	83	100.0	25	AAU78618	Human Bad peptide
36	83	100.0	25	AAU78619	Human Bad peptide
37	83	100.0	25	AAU78620	Human Bad peptide
38	83	100.0	25	AAU78621	Human Bad peptide
39	83	100.0	25	AAU78622	Human Bad peptide
40	83	100.0	26	AAU96321	Mammalian Bad Bcl-
41	83	100.0	26	AAU70371	BAD BH3 consensus
42	83	100.0	166	AAW32476	BBC6 protein for r
43	83	100.0	168	AAW35779	Human Bcl-xL/Bcl-2
44	83	100.0	168	AAU13512	Human cell prolif
45	83	100.0	168	AAU70368	Human BAD mutant a

ALIGNMENTS

RESULT 1  
AAU05421  
ID AAU05421 standard; peptide; 16 AA.  
AC AAU05421;  
XX  
XX  
DT 02-JUL-1999 (first entry)  
XX  
DE Human BAD BH3 domain.  
XX  
KW BH3 domain; cell death agonist; bcl homology domain; BCL-2 family;  
KW apoptosis promoter; cancer cell; virus infected cell; inflammation;  
KW autoantibody producing cell; cancer; lymphoproliferative condition;  
KW arthritis; autoimmune disease; therapy.  
XX  
OS Homo sapiens.  
XX  
XX WO9916787-A1.  
XX  
PD 08-APR-1999.  
XX  
PF 22-SEP-1998; 98WO-US19765.  
XX  
PR 07-OCT-1997; 97US-0946039.  
XX  
XX 26-SEP-1997; 97US-0060133.  
XX  
XX (UNIW ) UNIV WASHINGTON.  
XX  
XX Korsmeyer SJ;  
XX  
XX WPI; 1999-2550508/21.  
XX

PT Bcl homology domain 3 polypeptide  
 XX Example 1; Fig 4; 104pp; English.  
 XX  
 CC This sequence represents the BH3 domain of human BAD.  
 CC The invention relates to a bcl homology domain 3 (BH3 domain),  
 CC derived from a proapoptotic member of the BCL-2 family. The  
 CC BH3 polypeptide can be used in a method for promoting apoptosis in a  
 CC target cell, especially where the cell is a cancer cell a virus infected  
 CC cell or an autoantibody producing cell. The BH3 polypeptide can be used  
 CC in therapeutic compositions for treating disease including cancer, other  
 CC lymphoproliferative conditions, arthritis, inflammation, and autoimmune  
 CC diseases, which may result from the down regulation of cell death  
 CC regulation.  
 XX  
 SQ Sequence 16 AA;  
 Query Match 100.0%; Score 83; DB 20; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QRYGRELRRMSDEFVD 16  
 Db 1 QRYGRELRRMSDEFVD 16  
 RESULT 2  
 AAB37029  
 ID AAB37029 standard; peptide; 16 AA.  
 XX  
 AC AAB37029;  
 XX  
 DT 28-FEB-2001 (first entry)  
 XX  
 DE Bcl2 polypeptide BH3 domain peptide #29.  
 XX  
 KW Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;  
 KW cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;  
 KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;  
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;  
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;  
 KW stroke; myocardial infarction.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200059526-A1.  
 XX  
 PD 12-OCT-2000.  
 XX  
 PF 06-APR-2000; 2000WO-US09352.  
 XX  
 PR 07-APR-1999; 99US-0128202.  
 XX  
 PA (UYJE-) UNIV JEFFERSON THOMAS.  
 XX  
 PI Huang Z, Wang J, Zhang Z, Shan S, Lu Z;  
 XX  
 DR WPI; 2000-679325/66.  
 XX  
 PT New peptide conjugates for modulating apoptosis or for inhibiting B  
 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for  
 PT treating neurodegenerative disorders, stroke, or cancer -  
 XX  
 PS Claim 18; Page 18; 74pp; English.  
 XX  
 CC The invention relates to a peptide conjugate having the formula:  
 CC (R-X)n-peptide where n = 1-10; X = C=O, when the R-X group is attached  
 CC to the N-terminus of the peptide, or a side chain of the peptide where  
 CC the functional group of the side chain is NH2 or OH; or X = O or NH,  
 CC when the R-X group is attached to the C-terminus of the peptide, or a  
 CC side chain of the peptide, where the side chain functional group is COOH  
 CC or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl containing one  
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally

CC monosubstituted with a 1-5C straight or branched chain alkyl group,  
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain  
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples  
 CC of the peptide portion of the conjugate. The peptides represent analogues  
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of  
 CC the BH3 domain of the cell death agonist Bad. The peptide conjugate is  
 CC useful for modulating apoptosis in the cells of a subject, or for  
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of  
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2  
 CC function. In particular, the peptide conjugate is useful for treating a  
 CC subject afflicted with a cancer characterized by cancer cells that  
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,  
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or  
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide  
 CC conjugate is also useful for treating disorders characterized by  
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired  
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.  
 XX  
 SQ Sequence 16 AA;  
 Query Match 100.0%; Score 83; DB 21; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QRYGRELRRMSDEFVD 16  
 Db 1 QRYGRELRRMSDEFVD 16  
 RESULT 3  
 ABG78499  
 ID ABG78499 standard; Peptide; 20 AA.  
 XX  
 AC ABG78499;  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX  
 DE Mutant Bcl2 competitive binding assay peptide #16.  
 XX  
 KW Human; Bcl2; BclX1; programmed cell death; apoptosis; mutant; mutein.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200240530-A2.  
 XX  
 PD 23-MAY-2002.  
 XX  
 PF 15-NOV-2001; 2001WO-US45693.  
 XX  
 PR 20-NOV-2000; 2000US-0716395.  
 XX  
 PA (ABBO ) ABBOTT LAB.  
 XX  
 PI Fesik SW, Petros AM, Yoon H, Nettesheim DG;  
 XX  
 DR WPI; 2002-490141/52.  
 XX  
 PT New mutant Bcl-2 proteins derived from a wild type human Bcl-2 protein,  
 PT useful in biological assays to identify substances that block the  
 PT ability of Bcl-2 to inhibit programmed cell death or apoptosis -  
 XX  
 PS Example 2; Page 17; 36pp; English.  
 XX  
 CC This invention relates to a novel mutant protein which is derived from  
 CC a wild type human Bcl-2 protein. The mutant is created by replacing a  
 CC sequence of amino acid residues comprising a flexible loop from the wild  
 CC type Bcl-2 protein with an amino acid sequence comprising at least two  
 CC acidic amino acids. The mutant Bcl-2 protein comprises a 166 residue  
 CC shown in the specification. The invention also comprises an assay for  
 CC identifying substances that bind to the Bcl-2 protein. The protein  
 CC sequences of the invention are useful in biological assays to identify  
 CC substances that block the ability of Bcl-2 to inhibit programmed cell

CC death or apoptosis. The present sequence represents a human Bcl2  
 CC peptide of the invention.

XX  
 SQ Sequence 20 AA;

Query Match 100.0%; Score 83; DB 23; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEFVD 16  
 |||||  
 Db 1 QRYGRELRRMSDEFVD 16

RESULT 4  
 AAU78626  
 ID AAU78626 standard; Peptide; 20 AA.

XX AC AAU78626;

XX  
 DT 18-JUN-2002 (first entry)

XX Human Bad peptide #26 which binds to a member of the Bcl-2 family.

DE Human; Bad; Bcl-2; apoptosis; cancer; inducer; degenerative disease;  
 KW ischemic injury; suppressor; BH3 domain.

XX OS Homo sapiens.

XX PN WO200220568-A2.

XX PD 14-MAR-2002.

XX PF 04-SEP-2001; 2001WO-US27410.

XX PR 06-SEP-2000; 2000US-0656399.

XX PA (ABBO ) ABBOTT LAB.

XX PI Fesik SW, Meadows RP, Joseph MK, Olejniczak ET, Petros AM;  
 PI Nettesheim DG, Swift KM, Matayoshi E, Zhang H;

XX DR WPI; 2002-292254/33.

XX New derivatives of Bad peptide, useful for identifying compounds that  
 PT bind to Bcl-2 proteins, potential agents for treating cancer and  
 PT degenerative disease -

XX PS Example 1; Page 14; 31pp; English.

XX The present invention relates to new peptides that are derived from a  
 CC wild-type human Bad peptide and are able to bind to a member of the  
 CC Bcl-2 protein family. The peptides are useful, when labelled, in  
 CC competitive/displacement assays for identifying substances that bind to  
 CC members of the Bcl-2 family and may induce or suppress apoptosis so are  
 CC potentially useful for treating cancer (inducers) or degenerative  
 CC diseases or ischemic injury (suppressors). The peptides of the invention  
 CC have high helix propensity, maintain the contacts of the wild-type Bad  
 CC peptide and, compared with the Bad peptide, may have better physical  
 CC properties, particularly solubility. The present sequence represents one  
 CC of a collection of Bad peptides (AAU78601-AAU78631) that were derived  
 CC from the BH3 domain of the human wild-type Bad peptide.

XX SQ Sequence 20 AA;

Query Match 100.0%; Score 83; DB 23; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEFVD 16  
 |||||  
 Db 1 QRYGRELRRMSDEFVD 16

RESULT 5  
 ABG78500  
 ID ABG78500 standard; Peptide; 21 AA.

XX AC ABG78500;

XX DT 15-NOV-2002 (first entry)

XX DE Mutant Bcl2 competitive binding assay peptide #17.

XX Human; Bcl2; BclXl; programmed cell death; apoptosis; mutant; mutein.

XX OS Homo sapiens.  
 OS Synthetic.

XX PN WO200240530-A2.

XX PD 23-MAY-2002.

XX PF 15-NOV-2001; 2001WO-US45693.

XX PR 20-NOV-2000; 2000US-0716395.

XX PA (ABBO ) ABBOTT LAB.

XX PI Fesik SW, Petros AM, Yoon H, Nettesheim DG;

XX DR WPI; 2002-490141/52.

XX New mutant Bcl-2 proteins derived from a wild type human Bcl-2 protein,  
 PT useful in biological assays to identify substances that block the  
 PT ability of Bcl-2 to inhibit programmed cell death or apoptosis -

XX PS Example 2; Page 17; 36pp; English.

XX This invention relates to a novel mutant protein which is derived from  
 CC a wild type human Bcl-2 protein. The mutant is created by replacing a  
 CC sequence of amino acid residues comprising a flexible loop from the wild  
 CC type Bcl-2 protein with an amino acid sequence comprising at least two  
 CC acidic amino acids. The mutant Bcl-2 protein comprises a 166 residue  
 CC shown in the specification. The invention also comprises an assay for  
 CC identifying substances that bind to the Bcl-2 protein. The protein  
 CC sequences of the invention are useful in biological assays to identify  
 CC substances that block the ability of Bcl-2 to inhibit programmed cell  
 CC death or apoptosis. The present sequence represents a human Bcl2  
 CC peptide of the invention.

XX SQ Sequence 21 AA;

Query Match 100.0%; Score 83; DB 23; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEFVD 16  
 |||||  
 Db 6 QRYGRELRRMSDEFVD 21

RESULT 6

AAU78630

ID AAU78630 standard; Peptide; 21 AA.

XX AC AAU78630;

XX DT 18-JUN-2002 (first entry)

XX Human Bad peptide #30 which binds to a member of the Bcl-2 family.

XX Human; Bad; Bcl-2; apoptosis; cancer; inducer; degenerative disease;  
 KW ischemic injury; suppressor; BH3 domain.

XX OS Homo sapiens.

```

XX PN WO200220568-A2.
XX PD 14-MAR-2002.
XX PF 04-SEP-2001; 2001WO-US27410.
XX PR 06-SEP-2000; 2000US-0656399.
XX PA (ABBO ) ABBOTT LAB.
XX PI Fesik SW, Meadows RP, Joseph MK, Olejniczak ET, Petros AM;
XX PI Nettesheim DG, Swift KM, Matayoshi E, Zhang H;
XX DR WPI; 2002-292254/33.
XX PT New derivatives of Bad peptide, useful for identifying compounds that
XX PT bind to Bcl-2 proteins, potential agents for treating cancer and
XX PT degenerative disease -
XX PS Claim 15; Page 18; 31pp; English.
XX CC The present invention relates to new peptides that are derived from a
XX CC wild-type human Bad peptide and are able to bind to a member of the
XX CC Bcl-2 protein family. The peptides are useful, when labelled, in
XX CC competitive/displacement assays for identifying substances that bind to
XX CC members of the Bcl-2 family and may induce or suppress apoptosis so are
XX CC potentially useful for treating cancer (inducers) or degenerative
XX CC diseases or ischemic injury (suppressors). The peptides of the invention
XX CC have high helix propensity, maintain the contacts of the wild-type Bad
XX CC peptide and, compared with the Bad peptide, may have better physical
XX CC properties, particularly solubility. The present sequence represents one
XX CC of a collection of Bad peptides (AAU78601-AAU78631) that were derived
XX CC from the BH3 domain of the human wild-type Bad peptide.
XX SQ Sequence 21 AA;
XX Query Match 100.0%; Score 83; DB 23; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-07;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QRYGRELRRMSDEFVD 16
Db 6 QRYGRELRRMSDEFVD 21
RESULT 7
AAU78629
ID AAU78629 standard; Peptide; 22 AA.
XX AC AAU78629;
XX DT 18-JUN-2002 (first entry)
XX DE Human Bad peptide #29 which binds to a member of the Bcl-2 family.
XX KW Human; Bad; Bcl-2; apoptosis; cancer; inducer; degenerative disease;
XX KW Ischemic injury; suppressor; BH3 domain.
XX OS Homo sapiens.
XX PN WO200220568-A2.
XX PD 14-MAR-2002.
XX PF 04-SEP-2001; 2001WO-US27410.
XX PR 06-SEP-2000; 2000US-0656399.
XX PA (ABBO ) ABBOTT LAB.
XX PI Fesik SW, Meadows RP, Joseph MK, Olejniczak ET, Petros AM;
XX PI Nettesheim DG, Swift KM, Matayoshi E, Zhang H;
XX DR WPI; 2002-292254/33.
XX PT New derivatives of Bad peptide, useful for identifying compounds that
XX PT bind to Bcl-2 proteins, potential agents for treating cancer and
XX PT degenerative disease -
XX PS Claim 15; Page 18; 31pp; English.
XX CC The present invention relates to new peptides that are derived from a
XX CC wild-type human Bad peptide and are able to bind to a member of the
XX CC Bcl-2 protein family. The peptides are useful, when labelled, in
XX CC competitive/displacement assays for identifying substances that bind to
XX CC members of the Bcl-2 family and may induce or suppress apoptosis so are
XX CC potentially useful for treating cancer (inducers) or degenerative
XX CC diseases or ischemic injury (suppressors). The peptides of the invention
XX CC have high helix propensity, maintain the contacts of the wild-type Bad
XX CC peptide and, compared with the Bad peptide, may have better physical
XX CC properties, particularly solubility. The present sequence represents one
XX CC of a collection of Bad peptides (AAU78601-AAU78631) that were derived
XX CC from the BH3 domain of the human wild-type Bad peptide.
XX SQ Sequence 21 AA;
XX Query Match 100.0%; Score 83; DB 23; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-07;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QRYGRELRRMSDEFVD 16
Db 6 QRYGRELRRMSDEFVD 21
RESULT 7
AAU78629
ID AAU78629 standard; Peptide; 22 AA.
XX AC AAU78629;
XX DT 18-JUN-2002 (first entry)
XX DE Human Bad peptide #29 which binds to a member of the Bcl-2 family.
XX KW Human; Bad; Bcl-2; apoptosis; cancer; inducer; degenerative disease;
XX KW Ischemic injury; suppressor; BH3 domain.
XX OS Homo sapiens.
XX PN WO200220568-A2.
XX PD 14-MAR-2002.
XX PF 04-SEP-2001; 2001WO-US27410.
XX PR 06-SEP-2000; 2000US-0656399.
XX PA (ABBO ) ABBOTT LAB.
XX PI Fesik SW, Meadows RP, Joseph MK, Olejniczak ET, Petros AM;
XX PI Nettesheim DG, Swift KM, Matayoshi E, Zhang H;
XX DR WPI; 2002-292254/33.
XX PT New derivatives of Bad peptide, useful for identifying compounds that
XX PT bind to Bcl-2 proteins, potential agents for treating cancer and
XX PT degenerative disease -
XX PS Claim 15; Page 18; 31pp; English.
XX CC The present invention relates to new peptides that are derived from a
XX CC wild-type human Bad peptide and are able to bind to a member of the
XX CC Bcl-2 protein family. The peptides are useful, when labelled, in
XX CC competitive/displacement assays for identifying substances that bind to
XX CC members of the Bcl-2 family and are able to bind to a member of the
XX CC Bcl-2 protein family. The peptides are useful, when labelled, in
XX CC competitive/displacement assays for identifying substances that bind to
XX CC members of the Bcl-2 family and may induce or suppress apoptosis so are
XX CC potentially useful for treating cancer (inducers) or degenerative
XX CC diseases or ischemic injury (suppressors). The peptides of the invention
XX CC have high helix propensity, maintain the contacts of the wild-type Bad
XX CC peptide and, compared with the Bad peptide, may have better physical
XX CC properties, particularly solubility. The present sequence represents one
XX CC of a collection of Bad peptides (AAU78601-AAU78631) that were derived
XX CC from the BH3 domain of the human wild-type Bad peptide.
XX SQ Sequence 21 AA;
XX Query Match 100.0%; Score 83; DB 23; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-07;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QRYGRELRRMSDEFVD 16
Db 6 QRYGRELRRMSDEFVD 21
RESULT 7
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ID AAU78629 standard; Peptide; 22 AA.
XX AC AAU78629;
XX DT 18-JUN-2002 (first entry)
XX DE Human Bad peptide #28 which binds to a member of the Bcl-2 family.
XX KW Human; Bad; Bcl-2; apoptosis; cancer; inducer; degenerative disease;
XX KW Ischemic injury; suppressor; BH3 domain.
XX OS Homo sapiens.
XX PN WO200220568-A2.
XX PD 14-MAR-2002.
XX PF 04-SEP-2001; 2001WO-US27410.
XX PR 06-SEP-2000; 2000US-0656399.
XX PA (ABBO ) ABBOTT LAB.
XX PI Fesik SW, Meadows RP, Joseph MK, Olejniczak ET, Petros AM;
XX PI Nettesheim DG, Swift KM, Matayoshi E, Zhang H;
XX DR WPI; 2002-292254/33.
XX PT New derivatives of Bad peptide, useful for identifying compounds that
XX PT bind to Bcl-2 proteins, potential agents for treating cancer and
XX PT degenerative disease -
XX PS Claim 15; Page 18; 31pp; English.
XX CC The present invention relates to new peptides that are derived from a
XX CC wild-type human Bad peptide and are able to bind to a member of the
XX CC Bcl-2 protein family. The peptides are useful, when labelled, in
XX CC competitive/displacement assays for identifying substances that bind to
XX CC members of the Bcl-2 family and are able to bind to a member of the
XX CC Bcl-2 protein family. The peptides are useful, when labelled, in
XX CC competitive/displacement assays for identifying substances that bind to
XX CC members of the Bcl-2 family and may induce or suppress apoptosis so are
XX CC potentially useful for treating cancer (inducers) or degenerative
XX CC diseases or ischemic injury (suppressors). The peptides of the invention
XX CC have high helix propensity, maintain the contacts of the wild-type Bad
XX CC peptide and, compared with the Bad peptide, may have better physical
XX CC properties, particularly solubility. The present sequence represents one
XX CC of a collection of Bad peptides (AAU78601-AAU78631) that were derived
XX CC from the BH3 domain of the human wild-type Bad peptide.
XX SQ Sequence 22 AA;
XX Query Match 100.0%; Score 83; DB 23; Length 22;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-07;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QRYGRELRRMSDEFVD 16
Db 6 QRYGRELRRMSDEFVD 21
RESULT 8
AAU78628
ID AAU78628 standard; Peptide; 23 AA.
XX AC AAU78628;
XX DT 18-JUN-2002 (first entry)
XX DE Human Bad peptide #28 which binds to a member of the Bcl-2 family.
XX KW Human; Bad; Bcl-2; apoptosis; cancer; inducer; degenerative disease;
XX KW Ischemic injury; suppressor; BH3 domain.
XX OS Homo sapiens.
XX PN WO200220568-A2.
XX PD 14-MAR-2002.
XX PF 04-SEP-2001; 2001WO-US27410.
XX PR 06-SEP-2000; 2000US-0656399.
XX PA (ABBO ) ABBOTT LAB.
XX PI Fesik SW, Meadows RP, Joseph MK, Olejniczak ET, Petros AM;
XX PI Nettesheim DG, Swift KM, Matayoshi E, Zhang H;
XX DR WPI; 2002-292254/33.
XX PT New derivatives of Bad peptide, useful for identifying compounds that
XX PT bind to Bcl-2 proteins, potential agents for treating cancer and
XX PT degenerative disease -
XX PS Claim 15; Page 18; 31pp; English.
XX CC The present invention relates to new peptides that are derived from a
XX CC wild-type human Bad peptide and are able to bind to a member of the
XX CC Bcl-2 protein family. The peptides are useful, when labelled, in
XX CC competitive/displacement assays for identifying substances that bind to
XX CC members of the Bcl-2 family and are able to bind to a member of the
XX CC Bcl-2 protein family. The peptides are useful, when labelled, in
XX CC competitive/displacement assays for identifying substances that bind to
XX CC members of the Bcl-2 family and may induce or suppress apoptosis so are
XX CC potentially useful for treating cancer (inducers) or degenerative
XX CC diseases or ischemic injury (suppressors). The peptides of the invention
XX CC have high helix propensity, maintain the contacts of the wild-type Bad
XX CC peptide and, compared with the Bad peptide, may have better physical
XX CC properties, particularly solubility. The present sequence represents one
XX CC of a collection of Bad peptides (AAU78601-AAU78631) that were derived
XX CC from the BH3 domain of the human wild-type Bad peptide.
XX SQ Sequence 22 AA;
XX Query Match 100.0%; Score 83; DB 23; Length 22;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-07;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QRYGRELRRMSDEFVD 16
Db 6 QRYGRELRRMSDEFVD 21

```

CC members of the Bcl-2 family and may induce or suppress apoptosis so are  
 CC potentially useful for treating cancer (inducers) or degenerative  
 CC diseases or ischemic injury (suppressors). The peptides of the invention  
 CC have high helix propensity, maintain the contacts of the wild-type Bad  
 CC peptide and, compared with the Bad peptide, may have better physical  
 CC properties, particularly solubility. The present sequence represents one  
 CC of a collection of Bad peptides (AAU78601-AAU78631) that were derived  
 CC from the BH3 domain of the human wild-type Bad peptide.  
 XX  
 CC  
 SQ Sequence 23 AA;

Query Match 100.0%; Score 83; DB 23; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRYGRELRMSDEFVD 16  
 |||||  
 Db 6 QRYGRELRMSDEFVD 21

RESULT 9  
 ABG78482  
 ID ABG78482 standard; Peptide; 24 AA.  
 XX  
 AC ABG78482;  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX  
 DE Human Bcl2 fluorescein labelled peptide #2.  
 XX  
 KW Human; Bcl2; BclXL; programmed cell death; apoptosis; mutant; mutein.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200240530-A2.  
 XX  
 PD 23-MAY-2002.  
 XX  
 PF 15-NOV-2001; 2001WO-US45693.  
 XX  
 PR 20-NOV-2000; 2000US-0716395.  
 XX  
 XX (ABBO ) ABBOTT LAB.  
 XX  
 FI Fesik SW, Petros AM, Yoon H, Nettesheim DG;  
 XX  
 DR WPI; 2002-490141/52.  
 XX

PT New mutant Bcl-2 proteins derived from a wild type human Bcl-2 protein,  
 PT useful in biological assays to identify substances that block the  
 PT ability of Bcl-2 to inhibit programmed cell death or apoptosis -  
 XX  
 XX Example 2; Page 15; 36pp; English.  
 PS  
 XX This invention relates to a novel mutant protein which is derived from  
 CC a wild type human Bcl-2 protein. The mutant is created by replacing a  
 CC sequence of amino acid residues comprising a flexible loop from the wild  
 CC type Bcl-2 protein with an amino acid sequence comprising at least two  
 CC acidic amino acids. The mutant Bcl-2 protein comprises a 166 residue  
 CC shown in the specification. The invention also comprises an assay for  
 CC identifying substances that bind to the Bcl-2 protein. The protein  
 CC sequences of the invention are useful in biological assays to identify  
 CC substances that block the ability of Bcl-2 to inhibit programmed cell  
 CC death or apoptosis. The present sequence represents a human Bcl2  
 CC peptide of the invention.  
 XX  
 SQ Sequence 24 AA;

Query Match 100.0%; Score 83; DB 23; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRYGRELRMSDEFVD 16  
 |||||  
 Db 6 QRYGRELRMSDEFVD 21

RESULT 10  
 AAU78605  
 ID AAU78605 standard; Peptide; 24 AA.  
 XX  
 AC AAU78605;  
 XX  
 DT 18-JUN-2002 (first entry)  
 XX  
 DE Human Bad peptide #5 which binds to a member of the Bcl-2 family.  
 XX  
 KW Human; Bad; Bcl-2; apoptosis; cancer; inducer; degenerative disease;  
 KW ischemic injury; suppressor; BH3 domain.  
 XX  
 OS Homo sapiens.  
 XX  
 PH Key Location/Qualifiers  
 FT Misc-difference 1 /note= "Optionally labelled with 5-FAM,  
 FT (6-carboxy-fluorescein)"  
 XX  
 PN WO200220568-A2.  
 XX  
 PD 14-MAR-2002.  
 XX  
 PE 04-SEP-2001; 2001WO-US27410.  
 XX  
 PR 06-SEP-2000; 2000US-0656399.  
 XX  
 XX (ABBO ) ABBOTT LAB.  
 XX  
 PI Fesik SW, Meadows RP, Joseph MK, Olejniczak ET, Petros AM;  
 PI Nettesheim DG, Swift KM, Matayoshi E, Zhang H;  
 XX  
 DR WPI; 2002-292254/33.  
 XX

PT New derivatives of Bad peptide, useful for identifying compounds that  
 PT bind to Bcl-2 proteins, potential agents for treating cancer and  
 PT degenerative disease -  
 XX  
 PS Claim 4; Page 16; 31pp; English.  
 XX  
 CC The present invention relates to new peptides that are derived from a  
 CC wild-type human Bad peptide and are able to bind to a member of the  
 CC Bcl-2 protein family. The peptides are useful, when labelled, in  
 CC competitive/displacement assays for identifying substances that bind to  
 CC members of the Bcl-2 family and may induce or suppress apoptosis so are  
 CC potentially useful for treating cancer (inducers) or degenerative  
 CC diseases or ischemic injury (suppressors). The peptides of the invention  
 CC have high helix propensity, maintain the contacts of the wild-type Bad  
 CC peptide and, compared with the Bad peptide, may have better physical  
 CC properties, particularly solubility. The present sequence represents one  
 CC of a collection of Bad peptides (AAU78601-AAU78631) that were derived  
 CC from the BH3 domain of the human wild-type Bad peptide.  
 XX  
 SQ Sequence 24 AA;

Query Match 100.0%; Score 83; DB 23; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRYGRELRMSDEFVD 16  
 |||||  
 Db 6 QRYGRELRMSDEFVD 21

RESULT 11  
 AAU78627  
 ID AAU78627 standard; Peptide; 24 AA.

XX AC AAU78627;  
 XX DT 18-JUN-2002 (first entry)  
 XX DE Human Bad peptide #27 which binds to a member of the Bcl-2 family.  
 XX KW Human; Bad; Bcl-2; apoptosis; cancer; inducer; degenerative disease;  
 XX KW ischemic injury; suppressor; BH3 domain.  
 XX OS Homo sapiens.  
 XX PN WO200220568-A2.  
 XX PD 14-MAR-2002.  
 XX PF 04-SEP-2001; 2001WO-US27410.  
 XX PR 06-SEP-2000; 2000US-0656399.  
 XX PA (ABBO ) ABBOTT LAB.  
 XX PI Fesik SW, Meadows RP, Joseph MK, Olejniczak ET, Petros AM;  
 XX PI Nettlesheim DG, Swift KM, Matayoshi E, Zhang H;  
 XX DR WPI; 2002-292254/33.  
 XX PT New derivatives of Bad peptide, useful for identifying compounds that  
 XX PT bind to Bcl-2 proteins, potential agents for treating cancer and  
 XX PT degenerative disease -  
 XX PS Claim 15; Page 18; 31pp; English.  
 XX CC The present invention relates to new peptides that are derived from a  
 XX CC wild-type human Bad peptide and are able to bind to a member of the  
 XX CC Bcl-2 protein family. The peptides are useful, when labelled, in  
 XX CC competitive/displacement assays for identifying substances that bind to  
 XX CC members of the Bcl-2 family and may induce or suppress apoptosis so are  
 XX CC potentially useful for treating cancer (inducers) or degenerative  
 XX CC diseases or ischemic injury (suppressors). The peptides of the invention  
 XX CC have high helix propensity, maintain the contacts of the wild-type Bad  
 XX CC peptide and, compared with the Bad peptide, may have better physical  
 XX CC properties, particularly solubility. The present sequence represents one  
 XX CC of a collection of Bad peptides (AAU78601-AAU78631) that were derived  
 XX CC from the BH3 domain of the human wild-type Bad peptide.  
 XX SQ Sequence 24 AA;  
 Query Match 100.0%; Score 83; DB 23; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QRYGRELRRMSDEFVD 16  
 |||||  
 Db 6 QRYGRELRRMSDEFVD 21  
 RESULT 12  
 ABP56161  
 ID ABP56161 standard; peptide; 25 AA.  
 XX AC ABP56161;  
 XX DT 28-MAR-2003 (first entry)  
 XX DE PTPC-interacting TOX peptide #27.  
 XX KW Mitochondrial membrane permeabilisation; mitochondrion; PTPC;  
 XX KW permeability transition pore complex; virucide; neuroprotective;  
 XX KW vasotropic; cytostatic; infection; cell death regulation; apoptosis;  
 XX KW mitochondrial permeability transition pore complex modulator; cancer;  
 XX KW apoptogenic; ischaemia; neurodegenerative disease; fulminant hepatitis.  
 XX PF 15-NOV-2001; 2001WO-US45693.

OS Synthetic.  
 XX PN WO200261105-A2.  
 XX PD 08-AUG-2002.  
 XX PF 01-FEB-2002; 2002WO-EP01633.  
 XX PR 02-FEB-2001; 2001US-265594P.  
 XX PA (INSP ) INST PASTEUR.  
 XX PA (CNRS ) CENT NAT RECH SCI.  
 XX PI Edelman L, Jacotot E, Briand J;  
 XX DR WPI; 2002-619260/66.  
 XX PT New chimeric bifunctional molecules that target specific cells and  
 XX PT regulate the apoptosis function of the permeability transition pore  
 XX PT complex of the mitochondria, useful for treating or preventing e.g.  
 XX PT cancer or ischemia -  
 XX PS Claim 9; Page 11; 76pp; English.  
 XX CC The present invention describes a chimeric bifunctional molecule (I)  
 XX CC comprising at least a first functional molecule covalently linked to a  
 XX CC second functional molecule, which is able to modulate the activity of  
 XX CC the permeability transition pore complex (PTPC) of the mitochondria.  
 XX CC (I) has the function of specifically targeting and entering a tissue  
 XX CC cell population. The second functional molecule has the function of  
 XX CC specifically targeting, and inducing or preventing the death of the  
 XX CC cells by apoptosis by regulating the opening or the closing of the PTPC  
 XX CC of the mitochondria or its fragment. (I) has virucide, neuroprotective,  
 XX CC vasotropic and cytostatic activities, and can be used as a mitochondrial  
 XX CC permeability transition pore complex (PTPC) modulator. (I) is useful for  
 XX CC treating or preventing a pathological infection or disease. (I) is also  
 XX CC useful for regulating cell death regulatory molecules, specifically the  
 XX CC apoptogenic function of the PTPC, for treating e.g. cancer, ischaemia,  
 XX CC neurodegenerative diseases, fulminant hepatitis or viral infections.  
 XX CC The present sequence represents a PTPC-interacting TOX peptide which is  
 XX CC given in the exemplification of the present invention.  
 XX SQ Sequence 25 AA;  
 Query Match 100.0%; Score 83; DB 23; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QRYGRELRRMSDEFVD 16  
 |||||  
 Db 6 QRYGRELRRMSDEFVD 21  
 RESULT 13  
 ABG78481  
 ID ABG78481 standard; Peptide; 25 AA.  
 XX AC ABG78481;  
 XX DT 15-NOV-2002 (first entry)  
 XX DE Human Bcl2 fluorescein labelled peptide #1.  
 XX KW Human; Bcl2; BclXl; programmed cell death; apoptosis; mutant; mutain.  
 XX OS Homo sapiens.  
 XX OS Synthetic.  
 XX PN WO200240530-A2.  
 XX PD 23-MAY-2002.  
 XX PF 15-NOV-2001; 2001WO-US45693.

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XX 20-NOV-2000; 2000US-0716395.
XX (ABBO ) ABBOTT LAB.
XX Fesik SW, Petros AM, Yoon H, Nettesheim DG;
XX WPI; 2002-490141/52.
XX
XX New mutant Bcl-2 proteins derived from a wild type human Bcl-2 protein,
XX useful in biological assays to identify substances that block the
XX ability of Bcl-2 to inhibit programmed cell death or apoptosis -
XX
XX Example 2; Page 15; 36pp; English.
XX
XX This invention relates to a novel mutant protein which is derived from
XX a wild type human Bcl-2 protein. The mutant is created by replacing a
XX sequence of amino acid residues comprising a flexible loop from the wild
XX type Bcl-2 protein with an amino acid sequence comprising at least two
XX acidic amino acids. The mutant Bcl-2 protein comprises a 166 residue
XX shown in the specification. The invention also comprises an assay for
XX identifying substances that bind to the Bcl-2 protein. The protein
XX sequences of the invention are useful in biological assays to identify
XX substances that block the ability of Bcl-2 to inhibit programmed cell
XX death or apoptosis. The present sequence represents a human Bcl2
XX peptide of the invention.
XX
XX Query Match 100.0%; Score 83; DB 23; Length 25;
XX Best Local Similarity 100.0%; Pred. No. 2.1e-07;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 QRYGRELRMSDEFPD 16
Db |||||
6 QRYGRELRMSDEFPD 21

RESULT 14
ABG78484
ID ABG78484 standard; Peptide; 25 AA.
XX
XX AC ABG78484;
XX
XX DT 15-NOV-2002 (first entry)
XX
XX DE Mutant Bcl2 competitive binding assay peptide #1.
XX
XX KW Human; Bcl2; BclXl; programmed cell death; apoptosis; mutant; mutein.
XX
XX OS Homo sapiens.
XX OS Synthetic.
XX
XX PN WO200240530-A2.
XX
XX PD 23-MAY-2002.
XX
XX PF 15-NOV-2001; 2001WO-US45693.
XX
XX PR 20-NOV-2000; 2000US-0716395.
XX
XX PA (ABBO ) ABBOTT LAB.
XX
XX PI Fesik SW, Petros AM, Yoon H, Nettesheim DG;
XX
XX DR WPI; 2002-490141/52.
XX
XX PT New mutant Bcl-2 proteins derived from a wild type human Bcl-2 protein,
XX useful in biological assays to identify substances that block the
XX ability of Bcl-2 to inhibit programmed cell death or apoptosis -
XX
XX PS Example 2; Page 17; 36pp; English.
XX
XX This invention relates to a novel mutant protein which is derived from
XX a wild type human Bcl-2 protein. The mutant is created by replacing a
XX sequence of amino acid residues comprising a flexible loop from the wild
XX type Bcl-2 protein with an amino acid sequence comprising at least two
XX acidic amino acids. The mutant Bcl-2 protein comprises a 166 residue
XX shown in the specification. The invention also comprises an assay for
XX identifying substances that bind to the Bcl-2 protein. The protein
XX sequences of the invention are useful in biological assays to identify
XX substances that block the ability of Bcl-2 to inhibit programmed cell
XX death or apoptosis. The present sequence represents a human Bcl2
XX peptide of the invention.
XX
XX Query Match 100.0%; Score 83; DB 23; Length 25;
XX Best Local Similarity 100.0%; Pred. No. 2.1e-07;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 QRYGRELRMSDEFPD 16
Db |||||
6 QRYGRELRMSDEFPD 21

RESULT 14
ABG78484
ID ABG78484 standard; Peptide; 25 AA.
XX
XX AC ABG78484;
XX
XX DT 15-NOV-2002 (first entry)
XX
XX DE Mutant Bcl2 competitive binding assay peptide #1.
XX
XX KW Human; Bcl2; BclXl; programmed cell death; apoptosis; mutant; mutein.
XX
XX OS Homo sapiens.
XX OS Synthetic.
XX
XX PN WO200240530-A2.
XX
XX PD 23-MAY-2002.
XX
XX PF 15-NOV-2001; 2001WO-US45693.
XX
XX PR 20-NOV-2000; 2000US-0716395.
XX
XX PA (ABBO ) ABBOTT LAB.
XX
XX PI Fesik SW, Petros AM, Yoon H, Nettesheim DG;
XX
XX DR WPI; 2002-490141/52.
XX
XX PT New mutant Bcl-2 proteins derived from a wild type human Bcl-2 protein,
XX useful in biological assays to identify substances that block the
XX ability of Bcl-2 to inhibit programmed cell death or apoptosis -
XX
XX PS Example 2; Page 17; 36pp; English.
XX
XX This invention relates to a novel mutant protein which is derived from
XX a wild type human Bcl-2 protein. The mutant is created by replacing a
XX sequence of amino acid residues comprising a flexible loop from the wild
XX type Bcl-2 protein with an amino acid sequence comprising at least two
XX acidic amino acids. The mutant Bcl-2 protein comprises a 166 residue
XX shown in the specification. The invention also comprises an assay for
XX identifying substances that bind to the Bcl-2 protein. The protein
XX sequences of the invention are useful in biological assays to identify
XX substances that block the ability of Bcl-2 to inhibit programmed cell
XX death or apoptosis. The present sequence represents a human Bcl2
XX peptide of the invention.
XX
XX Query Match 100.0%; Score 83; DB 23; Length 25;
XX Best Local Similarity 100.0%; Pred. No. 2.1e-07;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 QRYGRELRMSDEFPD 16
Db |||||
6 QRYGRELRMSDEFPD 21

RESULT 15
ABG78485
ID ABG78485 standard; Peptide; 25 AA.
XX
XX AC ABG78485;
XX
XX DT 15-NOV-2002 (first entry)
XX
XX DE Mutant Bcl2 competitive binding assay peptide #2.
XX
XX KW Human; Bcl2; BclXl; programmed cell death; apoptosis; mutant; mutein.
XX
XX OS Homo sapiens.
XX OS Synthetic.
XX
XX PN WO200240530-A2.
XX
XX PD 23-MAY-2002.
XX
XX PF 15-NOV-2001; 2001WO-US45693.
XX
XX PR 20-NOV-2000; 2000US-0716395.
XX
XX PA (ABBO ) ABBOTT LAB.
XX
XX PI Fesik SW, Petros AM, Yoon H, Nettesheim DG;
XX
XX DR WPI; 2002-490141/52.
XX
XX PT New mutant Bcl-2 proteins derived from a wild type human Bcl-2 protein,
XX useful in biological assays to identify substances that block the
XX ability of Bcl-2 to inhibit programmed cell death or apoptosis -
XX
XX PS Example 2; Page 17; 36pp; English.
XX
XX This invention relates to a novel mutant protein which is derived from
XX a wild type human Bcl-2 protein. The mutant is created by replacing a
XX sequence of amino acid residues comprising a flexible loop from the wild
XX type Bcl-2 protein with an amino acid sequence comprising at least two
XX acidic amino acids. The mutant Bcl-2 protein comprises a 166 residue
XX shown in the specification. The invention also comprises an assay for
XX identifying substances that bind to the Bcl-2 protein. The protein
XX sequences of the invention are useful in biological assays to identify
XX substances that block the ability of Bcl-2 to inhibit programmed cell
XX death or apoptosis. The present sequence represents a human Bcl2
XX peptide of the invention.
XX
XX Query Match 100.0%; Score 83; DB 23; Length 25;
XX Best Local Similarity 100.0%; Pred. No. 2.1e-07;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 QRYGRELRMSDEFPD 16
Db |||||
6 QRYGRELRMSDEFPD 21

```

Best Local Similarity 100.0%; Pred. No. 2.1e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRYGRELRMSDEFVD 16  
    |||||  
Db 6 QRYGRELRMSDEFVD 21

Search completed: September 15, 2003, 17:22:14  
Job time : 23.6286 secs

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OM protein - protein search, using sw model 1

Run on: September 15, 2003, 17:22:21 ; Search time 8.34286 Seconds  
(without alignments)  
81.144 Million cell updates/sec

Title: US-09-544-664-29

Perfect score: 83

Sequence: 1 QRYGRELRRMSDEFVD 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*

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- 5: /cgn2.6/ptodata/1/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2.6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	166	1	US-08-665-617-2
2	83	100.0	168	2	US-08-717-123-2
3	83	100.0	168	3	US-08-985-335-1
4	83	100.0	168	3	US-08-985-335-7
5	83	100.0	168	3	US-09-410-372-1
6	83	100.0	168	3	US-09-410-372-7
7	83	100.0	168	4	US-09-375-257-2
8	73	88.0	23	1	US-08-333-565-10
9	73	88.0	23	2	US-08-661-479-10
10	73	88.0	59	2	US-08-733-505A-55
11	73	88.0	59	2	US-08-733-505A-56
12	73	88.0	59	2	US-08-733-505A-57
13	73	88.0	59	2	US-08-733-505A-58
14	73	88.0	204	1	US-08-333-565-2
15	73	88.0	204	2	US-08-661-479-2
16	73	88.0	204	2	US-08-733-505A-1
17	73	88.0	204	2	US-08-733-505A-12
18	73	88.0	204	2	US-08-733-505A-13
19	73	88.0	204	2	US-08-733-505A-14
20	70	84.3	204	2	US-08-717-123-3
21	70	84.3	204	4	US-09-375-257-3
22	67	80.7	16	1	US-08-333-565-26
23	67	80.7	16	2	US-08-661-479-26
24	44	53.0	1125	4	US-09-252-991A-18729
25	42	50.6	11	2	US-08-733-505A-34
26	42	50.6	11	2	US-08-706-741B-69
27	42	50.6	11	2	US-08-924-695A-69

28 42 50.6 876 1 US-08-785-429-2 Sequence 2, Appli  
29 42 50.6 876 3 US-08-996-621-2 Sequence 2, Appli  
30 42 50.6 888 4 US-09-134-001C-3032 Sequence 3032, Ap  
31 41 49.4 284 4 US-09-328-352-6559 Sequence 6559, Ap  
32 40 48.2 394 4 US-09-252-991A-31592 Sequence 31592, A  
33 40 48.2 724 4 US-09-328-352-7710 Sequence 7710, Ap  
34 39 47.0 333 4 US-09-252-991A-28443 Sequence 28443, A  
35 38.5 46.4 1112 4 US-09-252-991A-27256 Sequence 27256, A  
36 38 45.8 376 4 US-09-252-991A-26270 Sequence 26270, A  
37 38 45.8 432 3 US-09-075-087-2 Sequence 2, Appli  
38 38 45.8 432 3 US-09-472-971-1 Sequence 1, Appli  
39 38 45.8 575 3 US-08-913-805A-2 Sequence 2, Appli  
40 38 45.8 575 3 US-08-913-805A-10 Sequence 10, Appli  
41 38 45.8 575 3 US-09-442-629-2 Sequence 2, Appli  
42 38 45.8 575 3 US-09-442-629-10 Sequence 10, Appli  
43 37 44.6 338 4 US-09-252-991A-30165 Sequence 30165, A  
44 37 44.6 520 4 US-09-391-104-10 Sequence 10, Appli  
45 36 43.4 80 4 US-09-328-352-8004 Sequence 8004, Ap

#### ALIGNMENTS

RESULT 1  
US-08-665-617-2  
; Sequence 2, Application US/08665617  
; Patent No. 5663316  
; GENERAL INFORMATION:  
; APPLICANT: Xudong, Yin  
; TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/665,617  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: CL-8  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (352) 375-8100  
; TELEFAX: (352) 372-5800  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 166 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-665-617-2

Query Match 100.0%; Score 83; DB 1; Length 166;  
Best Local Similarity 100.0%; Pred. No. 2.2e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEFVD 16

Db 106 QRYGRELRRMSDEFVD 121

RESULT 2

US-08-717-123-2  
; Sequence 2, Application US/08717123  
; Patent No. 5965703  
; GENERAL INFORMATION:  
; APPLICANT: Horne, William A.  
; APPLICANT: Oltersdorf, Tilman  
; TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic  
; TITLE OF INVENTION: Acids and Methods of Use  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/717.123  
; FILING DATE: 20-SEP-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-ID 1929  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 168 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-717-123-2

Query Match 100.0%; Score 83; DB 2; Length 168;  
Best Local Similarity 100.0%; Pred. No. 2.2e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEFVD 16  
|||||

Db 108 QRYGRELRRMSDEFVD 123

RESULT 3  
US-08-985-335-1  
; Sequence 1, Application US/08985335  
; Patent No. 6080847  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Yue, Henry  
; APPLICANT: Lal, Preeti  
; APPLICANT: Shah, Purvi  
; APPLICANT: Corley, Neil C.  
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL  
; TITLE OF INVENTION: PROLIFERATION  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Dr.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
US-08-985-335-1

SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/985,335  
; FILING DATE: Filed Herewith  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0421 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 168 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: SYNORAB01  
; CLONE: 358673  
US-08-985-335-1

Query Match 100.0%; Score 83; DB 3; Length 168;  
Best Local Similarity 100.0%; Pred. No. 2.2e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEFVD 16  
|||||

Db 108 QRYGRELRRMSDEFVD 123

RESULT 4  
US-08-985-335-7  
; Sequence 7, Application US/08985335  
; Patent No. 6080847  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Yue, Henry  
; APPLICANT: Lal, Preeti  
; APPLICANT: Shah, Purvi  
; APPLICANT: Corley, Neil C.  
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL  
; TITLE OF INVENTION: PROLIFERATION  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Dr.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/985,335  
; FILING DATE: Filed Herewith  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0421 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:  
LENGTH: 168 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 1683637  
US-08-985-335-7

Query Match 100.0%; Score 83; DB 3; Length 168;  
Best Local Similarity 100.0%; Pred. No. 2.2e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEFVD 16  
|||||  
Db 108 QRYGRELRRMSDEFVD 123

## RESULT 5

US-09-410-372-1  
Sequence 1, Application US/09410372  
Patent No. 6281334

## GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.  
APPLICANT: Yue, Henry  
APPLICANT: Lal, Preeti  
APPLICANT: Shah, Purvi  
APPLICANT: Corley, Neil C.  
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/410,372

FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/985,335  
FILING DATE:

## ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0421 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 168 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: SYNORAB01  
CLONE: 358673  
US-09-410-372-1

Query Match 100.0%; Score 83; DB 3; Length 168;  
Best Local Similarity 100.0%; Pred. No. 2.2e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEFVD 16

Db 108 QRYGRELRRMSDEFVD 123  
|||||

## RESULT 6

US-09-410-372-7  
Sequence 7, Application US/09410372  
Patent No. 6281334

## GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.  
APPLICANT: Yue, Henry  
APPLICANT: Lal, Preeti  
APPLICANT: Shah, Purvi  
APPLICANT: Corley, Neil C.  
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/410,372

## FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/985,335

## FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0421 US  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 168 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GenBank

CLONE: 1683637

US-09-410-372-7

Query Match 100.0%; Score 83; DB 3; Length 168;  
Best Local Similarity 100.0%; Pred. No. 2.2e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEFVD 16  
|||||

Db 108 QRYGRELRRMSDEFVD 123

## RESULT 7

US-09-375-257-2  
Sequence 2, Application US/09375257  
Patent No. 6504022

## GENERAL INFORMATION:

APPLICANT: Horne, William A.  
APPLICANT: Oltersdorf, Tilman  
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC  
TITLE OF INVENTION: ACIDS AND METHODS OF USE  
FILE REFERENCE: 480140.428D1  
CURRENT APPLICATION NUMBER: US/09/375,257

```

; CURRENT FILING DATE: 1999-08-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-375-257-2

```

```

Query Match      100.0%; Score 83; DB 4; Length 168;
Best Local Similarity 100.0%; Pred. No. 12.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 QRYGRELRMSDEFVD 16
        |||||
Db      108 QRYGRELRMSDEFVD 123

```

```

RESULT 8
US-08-333-565-10
; Sequence 10, Application US/083333565
; Patent No. 5622852
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/333,565
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000700
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-333-565-10

```

```

Query Match      88.0%; Score 73; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 QRYGRELRMSDEF 14
        |||||
Db      8 QRYGRELRMSDEF 21

RESULT 9
US-08-661-479-10
; Sequence 10, Application US/08661479
; Patent No. 5834209
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,505A
; FILING DATE: 11-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/333,565
; FILING DATE: 31-OCT-1994
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000700
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-333-565-10

```

```

Query Match      88.0%; Score 73; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 QRYGRELRMSDEF 14
        |||||
Db      8 QRYGRELRMSDEF 21

```

```

RESULT 9
US-08-661-479-10
; Sequence 10, Application US/08661479
; Patent No. 5834209
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/661,479
; FILING DATE: 11-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/333,565
; FILING DATE: 31-OCT-1994
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000700
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-661-479-10

```

```

; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/661,479
; FILING DATE: 11-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/333,565
; FILING DATE: 31-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000700
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-661-479-10

Query Match      88.0%; Score 73; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QRYGRELRMSDEF 14
        |||||
Db      8 QRYGRELRMSDEF 21

RESULT 10
US-08-733-505A-55
; Sequence 55, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,505A
; FILING DATE: 11-JUN-1995
; CLASSIFICATION: 530

```

ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 965458  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 59 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-733-505A-55

Query Match 88.0%; Score 73; DB 2; Length 59;  
Best Local Similarity 100.0%; Pred. No. 4.2e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEF 14  
|||||  
Db 46 QRYGRELRRMSDEF 59

RESULT 11  
US-08-733-505A-56  
Sequence 56, Application US/08733505A  
Patent No. 5856445  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, STANLEY J.  
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF  
CELL DEATH REGULATORS  
REFERENCE/DOCKET NUMBER: 965458  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 59 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-733-505A-56

Query Match 88.0%; Score 73; DB 2; Length 59;  
Best Local Similarity 100.0%; Pred. No. 4.2e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEF 14  
|||||  
Db 46 QRYGRELRRMSDEF 59

ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 965458  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 59 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-733-505A-56

Query Match 88.0%; Score 73; DB 2; Length 59;  
Best Local Similarity 100.0%; Pred. No. 4.2e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEF 14  
|||||  
Db 46 QRYGRELRRMSDEF 59

RESULT 12  
US-08-733-505A-57  
Sequence 57, Application US/08733505A  
Patent No. 5856445  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, STANLEY J.  
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF  
CELL DEATH REGULATORS  
REFERENCE/DOCKET NUMBER: 965458  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 59 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-733-505A-57

Query Match 88.0%; Score 73; DB 2; Length 59;  
Best Local Similarity 100.0%; Pred. No. 4.2e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEF 14  
|||||  
Db 46 QRYGRELRRMSDEF 59

RESULT 13  
US-08-733-505A-58  
Sequence 58, Application US/08733505A  
Patent No. 5856445  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, STANLEY J.  
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF  
CELL DEATH REGULATORS  
REFERENCE/DOCKET NUMBER: 965458  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 59 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-733-505A-58

Query Match 88.0%; Score 73; DB 2; Length 59;  
Best Local Similarity 100.0%; Pred. No. 4.2e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEF 14  
|||||  
Db 46 QRYGRELRRMSDEF 59

;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/733,505A  
;/ FILING DATE:  
;/ CLASSIFICATION: 530  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: HOLLAND, DONALD R.  
;/ REGISTRATION NUMBER: 35,197  
;/ REFERENCE/DOCKET NUMBER: 965458  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (314) 727-5188  
;/ TELEFAX: (314) 727-6092  
;/ INFORMATION FOR SEQ ID NO: 58:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 59 amino acids  
;/ TYPE: amino acid  
;/ STRANDEDNESS:  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: peptide  
;/ US-08-733-505A-58

Query Match 88.0%; Score 73; DB 2; Length 59;  
Best Local Similarity 100.0%; Pred. No. 4.2e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRYGRELRRMSDEF 14  
Db 46 QRYGRELRRMSDEF 59

RESULT 14  
US-08-333-565-2  
; Sequence 2, Application US/08333565  
; Patent No. 5622852  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, Stanley J.  
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH  
; TITLE OF INVENTION: REGULATOR  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/333,565  
; FILING DATE: 31-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 15726A-000700  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 204 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..204  
; OTHER INFORMATION: /note= "Deduced amino acid sequence  
; OF mouse BAD."

US-08-333-565-2

Query Match 88.0%; Score 73; DB 1; Length 204;  
Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRYGRELRRMSDEF 14  
Db 145 QRYGRELRRMSDEF 158

RESULT 15  
US-08-661-479-2  
; Sequence 2, Application US/08661479  
; Patent No. 5834209  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, Stanley J.  
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH  
; TITLE OF INVENTION: REGULATOR  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/661,479  
; FILING DATE: 11-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/333,565  
; FILING DATE: 31-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 15726A-000700  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 204 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..204  
; OTHER INFORMATION: /note= "Deduced amino acid sequence  
; OF mouse BAD."

US-08-661-479-2  
Query Match 88.0%; Score 73; DB 2; Length 204;  
Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRYGRELRRMSDEF 14  
Db 145 QRYGRELRRMSDEF 158

Search completed: September 15, 2003, 17:45:06  
Job time : 8.34286 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 15, 2003, 17:25:56 ; Search time 12.6857 Seconds  
(without alignments)  
184.034 Million cell updates/sec

Title: US-09-544-664-29

Perfect score: 83

Sequence: 1 QRYGRLRMSDFVD 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 541936 seqs, 145912426 residues

Total number of hits satisfying chosen parameters: 541936

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*

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- 2: /cgn2\_5/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_5/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_5/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_5/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_5/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_5/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_5/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_5/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_5/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_5/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_5/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_5/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_5/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_5/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_5/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_5/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_5/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	100.0	25	15	US-10-059-261-258
2	83	100.0	168	9	US-09-922-378-2
3	83	100.0	168	9	US-09-894-657-1
4	83	100.0	168	9	US-09-894-657-7
5	83	100.0	168	14	US-10-066-179-2
6	70	84.3	204	9	US-09-922-378-3
7	70	84.3	204	14	US-10-066-179-3
8	56	67.5	15	15	US-10-174-105A-147
9	44	53.0	215	15	US-10-156-761-9145
10	42	50.6	647	15	US-10-156-761-9735
11	42	50.6	810	9	US-09-815-242-12636
12	42	50.6	875	9	US-09-815-242-13003
13	42	50.6	879	9	US-09-815-242-5312
14	41	49.4	312	15	US-10-156-761-7630
15	41	49.4	312	15	US-10-156-761-7867

16	40.5	48.8	1265	15	US-10-198-070-69	Sequence 69, Appl
17	40	48.2	113	9	US-09-815-242-13424	Sequence 13424, A
18	40	48.2	380	15	US-10-156-761-13594	Sequence 13594, A
19	39	47.0	454	15	US-10-166-087-46	Sequence 46, Appl
20	39	47.0	959	12	US-10-342-224-40	Sequence 40, Appl
21	38.5	46.4	588	15	US-10-156-761-10330	Sequence 10330, A
22	38	45.8	35	15	US-10-092-750-1	Sequence 1, Appl
23	38	45.8	50	10	US-09-971-980-64	Sequence 64, Appl
24	38	45.8	64	10	US-09-971-980-62	Sequence 62, Appl
25	38	45.8	138	15	US-10-092-750-241	Sequence 241, App
26	38	45.8	313	10	US-09-738-626-3724	Sequence 3724, Ap
27	38	45.8	320	10	US-09-738-626-4522	Sequence 4522, Ap
28	38	45.8	515	15	US-10-106-698-4658	Sequence 4658, Ap
29	38	45.8	575	9	US-09-839-136-2	Sequence 2, Appli
30	38	45.8	575	9	US-09-839-136-10	Sequence 10, Appl
31	37	44.6	391	15	US-10-163-198-19	Sequence 19, Appl
32	37	44.6	543	15	US-10-156-761-9820	Sequence 9820, Ap
33	37	44.6	556	12	US-09-949-029-36	Sequence 36, Appl
34	37	44.6	1270	15	US-10-223-070-8	Sequence 8, Appli
35	36	43.4	78	15	US-10-083-357-1237	Sequence 1237, Ap
36	36	43.4	80	15	US-10-106-698-5539	Sequence 5539, Ap
37	36	43.4	103	10	US-09-738-626-4453	Sequence 4453, Ap
38	36	43.4	270	11	US-09-934-455-162	Sequence 162, App
39	36	43.4	284	15	US-10-156-761-10335	Sequence 10335, A
40	36	43.4	292	10	US-09-738-626-4426	Sequence 4426, Ap
41	36	43.4	350	11	US-09-940-244-394	Sequence 394, App
42	36	43.4	393	10	US-09-950-510-22	Sequence 22, Appl
43	36	43.4	394	10	US-09-712-363-205	Sequence 205, App
44	36	43.4	404	15	US-10-156-761-14659	Sequence 14659, A
45	36	43.4	445	10	US-09-950-510-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1  
US-10-059-261-258  
; Sequence 258, Application US/10059261  
; Publication No. US20030077826A1  
; GENERAL INFORMATION:  
; APPLICANT: EDELMAN, LENA  
; APPLICANT: JACOTOT, ETIENNE DANIEL FRANCOIS  
; APPLICANT: BRAND, JEAN-PAUL  
; TITLE OF INVENTION: CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET  
; TITLE OF INVENTION: SPECIFIC CELLS AND A MODULE REGULATING THE APTOTOGENIC  
; TITLE OF INVENTION: FUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX  
; TITLE OF INVENTION: (PTPC)  
; FILE REFERENCE: 03495.0216  
; CURRENT APPLICATION NUMBER: US/10/059,261  
; CURRENT FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: 60/265,594  
; PRIOR FILING DATE: 2001-02-02  
; NUMBER OF SEQ ID NOS: 325  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 258  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: TOX peptide  
US-10-059-261-258  
  
Query Match 100.0%; Score 83; DB 15; Length 25;  
Best Local Similarity 100.0%; Pred. No. 5.3e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRLRMSDFVD 16

Db 6 QRYGRLRMSDFVD 21

RESULT 2

US-09-922-378-2

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; Sequence 2, Application US/09922378
; Patent No. US20020037869A1
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
; TITLE OF INVENTION: ACIDS AND METHODS OF USE
; FILE REFERENCE: 480140.428D3
; CURRENT APPLICATION NUMBER: US/09/922,378
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-922-378-2

Query Match      100.0%; Score 83; DB 9; Length 168;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QRYGRELRRMSDEFVD 16
Db      108 QRYGRELRRMSDEFVD 123

RESULT 3
US-09-894-657-1
; Sequence 1, Application US/09894657
; Patent No. US20020098569A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; PROLIFERATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/894,657
; FILING DATE: 28-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/410,372
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0421 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1683637
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-894-657-1

Query Match      100.0%; Score 83; DB 9; Length 168;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QRYGRELRRMSDEFVD 16
Db      108 QRYGRELRRMSDEFVD 123

RESULT 4
US-09-894-657-7
; Sequence 7, Application US/09894657
; Patent No. US20020098569A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; PROLIFERATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/894,657
; FILING DATE: 28-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/410,372
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0421 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1683637
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-894-657-7

Query Match      100.0%; Score 83; DB 9; Length 168;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QRYGRELRRMSDEFVD 16
Db      108 QRYGRELRRMSDEFVD 123

RESULT 5
```

Cell Signaling Technology, Inc.  
 APPLICANT: ZHANG, Hui  
 APPLICANT: COMB, Michael J.  
 APPLICANT: TAN, Yi  
 APPLICANT:

; TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PROSPERO PROTEIN  
 ; NAME OF INVENTOR: CONTEXT-INDEPENDENT ANTIBODIES COUPLED WITH  
 ; FILE REFERENCE: CST-138 CIP3  
 ; CURRENT APPLICATION NUMBER: US/10/174.105A

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; PRIOR APPLICATION NUMBER: US 05/110,712
; PRIOR FILING DATE: 1998-03-04
; PRIOR APPLICATION NUMBER: US 09/535,364
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 147
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (8)..(8)
; OTHER INFORMATION: PHOSPHORYLATION; serine at position 8 is phosphorylated
US-10-174-105A-147

Query Match          67.5%; Score 56; DB 15; Length 15;
Best Local Similarity 100.0%; Pred No. 0.0084;

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QY	LI, CONSERVATIVE	MISMATCHES	INDEXES	GAPS
4 GRELRMSDEF 14				

DO I GETLANSDEF 11

RESULT 9

/ Publication No. US20030119018A1  
 / GENERAL INFORMATION:  
 / APPLICANT: OMURA, SATOSHI  
 / APPLICANT: IKEDA, HARUO  
 / APPLICANT: ISHIKAWA, JUN  
 / APPLICANT: HORIKAWA, HIROSHI  
 / APPLICANT: SHIBA, TADAYOSHI  
 / APPLICANT: SAKAKI, YOSHIYUKI  
 / APPLICANT: HATTORI, MASAHIRA  
 / TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
 / FILE REFERENCE: 249-262  
 / CURRENT APPLICATION NUMBER: US/10156,761  
 / CURRENT FILING DATE: 2002-05-29  
 / PRIOR APPLICATION NUMBER: JP 2001-204089  
 / PRIOR FILING DATE: 2001-05-30  
 / PRIOR APPLICATION NUMBER: JP 2001-272697

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; PRIOR FILING DATE: 2001-09-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9145
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9145
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Query Match          53.0%; Score 44; DB 15; Length 215;
Best Local Similarity 61.5%; Pred. NO. 12;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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QY 1 QYGRELRMSDE 13
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Db 108 ERWGGDLRMRDE 120
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## RESULT 10

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US-10-156-761-9735
; Sequence 9735, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9735
; LENGTH: 647
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9735
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Query Match          50.6%; Score 42; DB 15; Length 647;
Best Local Similarity 57.1%; Pred. NO. 83;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
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QY 3 YGRELRMSDEFVD 16
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Db 565 YARGLRHGHDELID 578
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## RESULT 11

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US-09-815-242-12636
; Sequence 12636, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
```

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; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
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; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12636
; LENGTH: 810
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12636
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Query Match          50.6%; Score 42; DB 9; Length 810;
Best Local Similarity 61.5%; Pred. NO. 1.1e+02;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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Db 185 GRELPILADEYVD 197
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## RESULT 12

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US-09-815-242-13003
; Sequence 13003, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13003
; LENGTH: 876
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-13003
```

```
Query Match          50.6%; Score 42; DB 9; Length 876;
Best Local Similarity 61.5%; Pred. NO. 1.1e+02;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```

QY      4 GRELRMSDFVD 16
      IIII :III:II
Db      251 GRELFIADEYVD 263

RESULT 13
US-09-815-242-5312
; Sequence 5312, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, John J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version
; SEQ ID NO 5312
; LENGTH: 879
; TYPE: PR1
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(879)
; - OTHER INFORMATION: Xaa = Any Amino A
US-09-815-242-5312

```

```

Query Match          50.6%;   Score 42;   DB 9;   Length 879;
Best Local Similarity 61.5%;   Pred. No. 1.1e+02;
Matches 8; Conservative 3; Mismatches 2; Indels

QY      4 GRELRMSDEFVD 16
      |||| :||:|
Db      255 GRELPILADEYVD 267

```

RESULT 14  
US-10-156-761-7630  
; Sequence 7630, Application US/10156761  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI  
; APPLICANT: HATORI, MASAHIRO  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156-761

```

; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 7630
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-7630

Query Match 49.4%; Score 41; DB 15; Length 312;
Best Local Similarity 50.0%; Pred. No. 57;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 QRYGRELRMSDEFVD 16
      | | | | | | | | | |
Db 125 QLSGEERRRLDDFMD 140

RESULT 15
US-10-156-761-7867
; Sequence 7867, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 7867
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-7867

```

Query Match	49.4%;	Score 41;	DB 15;	Length 312;
Best Local Similarity	50.0%;	Pred. No. 57;		
Matches	8;	Conservative 3;	Mismatches 5;	Indels 0;
Gaps	0;			
QY	1	QRYGRELRRMSDEEVD	16	
Db	125	OLSGERRRLIDDFMD	140	

Search completed: September 15, 2003, 17:47:53  
Job time : 13.6857 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 15, 2003, 17:16:55 ; Search time 3.77143 Seconds  
(without alignments)  
199.507 Million cell updates/sec

Title: US-09-544-664-29

Perfect score: 83

Sequence: 1 QRYGRELRRMSDEFVD 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	168	1 BAD_HUMAN	Q92934 homo sapien
2	73	88.0	204	1 BAD_MOUSE	Q61337 mus musculu
3	73	88.0	205	1 BAD_RAT	Q35147 rattus norv
4	42	50.6	196	1 BIM_MOUSE	Q54918 mus musculu
5	42	50.6	196	1 BIM_RAT	Q88498 rattus norv
6	42	50.6	457	1 HGD_RHILO	Q983j4 rhizobium l
7	42	50.6	653	1 HT2A_HUMAN	Q13049 homo sapien
8	41	49.4	370	1 AROG_CANAL	P79023 candida alb
9	41	49.4	861	1 GCR3_YEAST	P34160 saccharomyc
10	40	48.2	261	1 YGFG_ECICHA	P52045 escherichia
11	40	48.2	380	1 PHLC_TRYCR	O15886 trypanosoma
12	40	48.2	429	1 MTAL_ACEPA	O52702 acetobacter
13	40	48.2	631	1 RPSD_BORBU	P52323 borrelia bu
14	39	47.0	220	1 6PGL_THEMEA	Q9x0n8 thermotoga
15	39	47.0	365	1 RA51_SCHPO	P36601 schizosacch
16	39	47.0	418	1 VSI2_REOVD	P03525 reovirus (t
17	39	47.0	418	1 VSI2_REOVL	P11314 reovirus (t
18	39	47.0	432	1 TIG_SALTY	Q8xf04 salmonella
19	39	47.0	503	1 MTBR_BPRH1	P09915 bacterioph
20	39	47.0	545	1 SYFB_METAC	O8tpf7 methanosarc
21	39	47.0	545	1 SYFB_METWA	Q8pta5 methanosarc
22	39	47.0	880	1 SYV_BACST	P11931 bacillus st
23	39	47.0	1967	1 YG5O_YEAST	P53327 saccharomyc
24	39.5	46.4	172	1 DEFL_RHIME	Q92qd0 rhizobium m
25	39.5	46.4	468	1 SELA_PSEAE	Q9hv01 pseudomonas
26	38	45.8	87	1 Y152_UREPA	Q9pgz2 ureaplasma
27	38	45.8	185	1 RRF_THEMEA	Q9xlb9 thermotoga
28	38	45.8	198	1 BIM_HUMAN	O43521 homo sapien
29	38	45.8	251	1 KDKA_VIBCH	Q9xvb9 vibrio chol
30	38	45.8	384	1 ODP2_MYCGE	P47514 mycoplasma
31	38	45.8	402	1 ODP2_MYCPN	P75392 mycoplasma
32	38	45.8	432	1 TIG_ECOL6	O8fka7 escherichia
33	38	45.8	432	1 TIG_ECOLI	P22257 escherichia

## RESULT 1

ID	BAD_HUMAN	STANDARD;	PRT;	168 AA.
AC	Q92934; O14803;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component 6) (Bcl-XL/Bcl-2 associated death promoter) (BCL2-like 8 protein).			
DE	GN BAD OR BBC6 OR BCL2L8.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Yin D.X., Li Z., Huang B., Chen S., Zhou H.;			
RT	"A human protein that interacts with Bcl-2 and have homology to mouse BAD.";			
RT	BAD.";			
RL	Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A., AND PHOSPHORYLATION BY RAF-1.			
RX	MEDLINE=97083574; PubMed=8929532;			
RA	Wang H.-G., Rapp U.R., Reed J.C.;			
RT	"Bcl-2 targets the protein kinase Raf-1 to mitochondria.";			
RL	Cell 87:629-638(1996).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Takayama S., Reed J.C.;			
RL	Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A., AND DIMERIZATION.			
RC	TISSUE=Bone marrow;			
RX	MEDLINE=98049554; PubMed=9388232;			
RA	Ottlie S., Diaz J.L., Horne W., Chang J., Wang Y., Wilson G.,			
RA	Chang S., Weeks S., Fritz L.C., Oltersdorf T.;			
RT	"Dimerization properties of human BAD.";			
RL	J. Biol. Chem. 272:30866-30872(1997).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lung;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			

## ALIGNMENTS

34	38	45.8	575	1 FUT8_BOVIN	Q9n0w2 b alpha-(1,
35	38	45.8	575	1 FUT8_HUMAN	Q9byc5 h alpha-(1,
36	38	45.8	575	1 FUT8_PIG	P79282 s alpha-(1,
37	38	45.8	631	1 EMP2_ARATH	O816y4 arabidopsis
38	38	45.8	1521	1 EMB5_CAEEL	P34703 caenorhabdi
39	38	45.8	1535	1 LML1_CAEEL	Q18823 caenorhabdi
40	37	44.6	375	1 DP3B_MYCCA	P24117 mycoplasma
41	37	44.6	391	1 UBIF_ECOLI	P75728 escherichia
42	37	44.6	398	1 PSMP_ARCFU	O28303 archaeoglob
43	37	44.6	481	1 Y335_SYNY3	Q55587 synechocyst
44	37	44.6	777	1 BARL_HUMAN	Q99728 homo sapien
45	37	44.6	787	1 RELA_MYCLE	Q49640 mycobacteri



```

CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL; L37296; AAB64465.1; -
CC PIR; A55671; A55671.
CC HSP; Q92934; IG5J.
CC MGI; 1096330; Bad.
CC InterPro; IPR000712; Bcl2_BH.
CC PROSITE; PS01259; BH3; FALSE_NEG.
CC Apoptosis; Phosphorylation.
CC FT DOMAIN 147 161 BH3.
CC FT MOD_RES 112 112 PHOSPHORYLATION (BY PKA AND PKB).
CC FT MOD_RES 136 136 PHOSPHORYLATION (BY PKA AND PKB).
CC FT MOD_RES 155 155 PHOSPHORYLATION (BY PKA AND PKB).
CC FT MUTAGEN 112 112 S->A: NO PHOSPHORYLATION.
CC FT MUTAGEN 136 136 S->A: NO PHOSPHORYLATION.
CC FT MUTAGEN 155 155 S->A: NO PHOSPHORYLATION; INTERACTS WITH
CC FT BCL-X(L).
CC SQ SEQUENCE 204 AA; 22080 MW; 6C2BA910205053F7 CRC64;

Query Match 88.0%; Score 73; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 9e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRELRLMSDEF 14
| | | | | | | | | | | | | | | |
Db 145 QRYGRELRLMSDEF 158

RESULT 3
BAD_RAT
ID BAD_RAT STANDARD; PRT; 205 AA.
AC O35147; O70256; Q9JHX1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component
DE 6) (Bcl-xL/Bcl-2 associated death promoter).
GN BAD.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF SER-113 AND SER-137.
RC TISSUE=Ovary;
RX MEDLINE=98034386; PubMed=9369453;
RA Hsu S.Y., Kaipia A., Zhu L., Hsueh A.J.W.;
RT "Interference of BAD (Bcl-xL/Bcl-2-associated death promoter)-induced
RT apoptosis in mammalian cells by 14-3-3 isoforms and P11.";
RL Mol. Endocrinol. 11:1858-1867(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98194755; PubMed=9535132;
RA D'Agata V., Magro G., Travali S., Musco S., Cavallaro S.;
RT "Cloning and expression of the programmed cell death regulator BAD in
RT the rat brain.";
RL Neurosci. Lett. 243:137-140(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC TISSUE=Brain;
RX MEDLINE=21109372; PubMed=11161472;
RA Hanner S., Arumae U., Yu L.-Y., Sun Y.-F., Saarma M., Lindholm D.;
RT "Functional characterization of two splice variants of rat BAD and

```

```

RT their interaction with Bcl-w in sympathetic neurons.";
RL Mol. Cell. Neurosci. 17:97-106(2001).
CC -!- FUNCTION: Promotes cell death. Successfully competes for the
CC binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level
CC of heterodimerization of these proteins with BAX. Can reverse the
CC death repressor activity of Bcl-x(L), but not that of Bcl-2 (By
CC similarity). Appears to act as a link between growth factor
CC receptor signaling and the apoptotic pathways.
CC -!- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-
CC x(L), Bcl-2 and Bcl-w. Also binds protein S100A10. The Ser-
CC 113/Ser-137 phosphorylated form binds 14-3-3 proteins.
CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon
CC phosphorylation, locates to the cytoplasm (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Alpha;
CC IsoId=O35147-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=O35147-2; Sequence=VSP_000534;
CC -!- TISSUE SPECIFICITY: Expressed in all tissues tested, including
CC brain, liver, spleen and heart. In the brain, restricted to
CC epithelial cells of the choroid plexus. Isoform alpha is the more
CC abundant form.
CC -!- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND
CC BAX for their pro-apoptotic activity and for their interaction
CC with anti-apoptotic members of the Bcl-2 family.
CC -!- PTM: Phosphorylated on Ser-113 in response to survival stimuli.
CC Subsequent phosphorylation on Ser-137 promotes heterodimerization
CC with 14-3-3 proteins. This interaction then facilitates the
CC phosphorylation at Ser-156, a site within the BH3 domain, leading
CC to the release of Bcl-x(L) and the promotion of cell survival.
CC Ser-137 is the major site of AKT/PKB phosphorylation, Ser-156 the
CC major site of protein kinase A (CAPK) phosphorylation (By
CC similarity).
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC -----
CC EMBL; AF003523; AAC53374.1; -
CC EMBL; AF031227; AAC15100.1; -
CC EMBL; AF279910; AAF91427.1; -
CC EMBL; AF279911; AAF91428.1; -
CC HSP; Q92934; IG5J.
CC InterPro; IPR000712; Bcl2_BH.
CC PROSITE; PS01259; BH3; FALSE_NEG.
CC Apoptosis; Phosphorylation; Alternative splicing.
CC FT DOMAIN 148 162 BH3.
CC FT MOD_RES 113 113 PHOSPHORYLATION (BY PKA AND PKB)
CC (BY SIMILARITY).
CC FT MOD_RES 137 137 PHOSPHORYLATION (BY PKA AND PKB)
CC (BY SIMILARITY).
CC FT MOD_RES 156 156 PHOSPHORYLATION (BY PKA AND PKB)
CC (BY SIMILARITY).
CC FT VARSPLIC 166 205 LPRPKSAGTATQMSASWTRIIQSWDRNLGKGSPTSQ
CC -> EELTVSEVFLPYRAIMEGWLPLWSFQSFHTLPPTPP
CC EVAMFLRYWTALRLIC (in isoform Beta).
CC /FTId=VSP_000534.
CC S->A: NO EFFECT ON HETERODIMERIZATION
CC WITH 14-3-3 PROTEINS.
CC S->A: NO HETERODIMERIZATION WITH 14-3-3
CC PROTEINS. NO EFFECT ON HETERODIMERIZATION
CC WITH BCL2 NOR WITH PROTEIN P11.
CC FT MUTAGEN 113 113 SDAGGR -> ERRGRK (IN REF. 1).
CC FT MUTAGEN 137 137
CC FT CONFLICT 29 34
CC FT SEQUENCE 205 AA; 22228 MW; 7AFA71DAE9CF4A81 CRC64;

Query Match 88.0%; Score 73; DB 1; Length 205;

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Best Local Similarity 100.0%; Pred. NO. 9e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRLRRMSDEF 14  
| | | | | | | | | |  
Db 146 QRYGRLRRMSDEF 159

```

RESULT 4
BIM_MOUSE
ID BIM_MOUSE STANDARD; PRT; 196 AA.
AC OS4918; OS4919; OS4920;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE BCL2-like protein 11 (BCL2 interacting mediator of cell death).
GN BCL2L11 OR BIM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, TISSUE
RP SPECIFICITY, AND ALTERNATIVE SPLICING.
RX MEDLINE=98094360; PubMed=9430630;
RA O'Connor L., Strasser A., O'Reilly L.A., Hausmann G., Adams J.M.,
RA Cory S., Huang D.C.S.;
RT "Bim: a novel member of the Bcl-2 family that promotes apoptosis.";
RL EMBO J. 17:384-395(1998).
CC -!- FUNCTION: INDUCES APOPTOSIS. THE ISOFORMS VARY IN CYTOTOXICITY
CC WITH ISOFORM BIMs BEING THE MOST POTENT AND ISOFORM BIMEL BEING
CC THE LEAST POTENT.
CC -!- SUBUNIT: FORMS HETERODIMERS WITH A NUMBER OF ANTIAPOPTOTIC BCL-2
CC PROTEINS INCLUDING MCL-1, BCL-2, BCL-XL, BFL-1, AND BHRF-1. DOES
CC NOT HETERODIMERIZE WITH PROAPOPTOTIC PROTEINS SUCH AS BAD, BOK,
CC BAX OR BAK (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: ASSOCIATED WITH INTRACYTOSOLIC MEMBRANES.
CC Event=Alternative splicing; Named isoforms=3;
CC Name=BimL;
CC IsoId=OS4918-1; Sequence=VSP_000536;
CC Name=BimS;
CC IsoId=OS4918-2; Sequence=VSP_000536;
CC -!- TISSUE SPECIFICITY: EXPRESSED IN A NUMBER OF B-AND T-LYMPHOID CELL
CC LINES.
CC -!- DOMAIN: THE BH3 DOMAIN IS REQUIRED FOR BCL-2 BINDING AND
CC CYTOTOXICITY.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
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CC -----
DR EMBL; AF032459; AAC40029.1; -
DR EMBL; AF032460; AAC40030.1; -
DR EMBL; AF032461; AAC40031.1; -
DR MGD; MGI:1197519; Bcl2l11.
DR InterPro; IPR000712; Bcl2_BH.
DR PROSITE; PS01259; BH3; FALSE_NEG.
KW Apoptosis; Alternative splicing; Membrane.
FT DOMAIN 146 160 BH3.
FT VARSPPLIC 42 97 Missing (in isoform BimL).
FT VARSPPLIC 42 127 /FTId=VSP_000536.
FT VARSPPLIC 42 127 Missing (in isoform Bims).
FT VARSPPLIC 42 127 /FTId=VSP_000537.
SQ SEQUENCE 196 AA; 22066 MW; 531C1765FAC9AA CRC64;

```

Query Match 50.6%; Score 42; DB 1; Length 196;  
Best Local Similarity 61.5%; Pred. NO. 8.7;  
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 RYGRRLRRMSDEF 14  
| : | | | | | | |  
Db 145 RYGRRLRRMSDEF 157

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RESULT 5
BIM_RAT
ID BIM_RAT STANDARD; PRT; 196 AA.
AC OS8498; OS8497; Q9WUI8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE BCL2-like protein 11 (BCL2 interacting mediator of cell death)
DE (Bcl-2 related ovarian death protein).
GN BCL2L11 OR BIM OR BOD.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, SUBUNIT, AND TISSUE SPECIFICITY
RP (ISOFORMS BOD-L; BOD-M AND BOD-S).
RC TISSUE=Ovary;
RX MEDLINE=98400436; PubMed=9731710;
RA Hsu S.Y., Lin P., Hsueh A.J.W.;
RT "BOD (Bcl-2-related ovarian death gene) is an ovarian BH3 domain-
RT containing proapoptotic Bcl-2 protein capable of dimerization with
RT diverse antiapoptotic Bcl-2 members.";
RL Mol. Endocrinol. 12:1432-1440(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM BIML).
RA Chen D., Simon R.P., Chen J.;
RT "Cloning of rat bimL and bimL, and their differential expression in
RT ischemia and normal rat brain.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INDUCES APOPTOSIS.
CC -!- SUBUNIT: FORMS HETERODIMERS WITH A NUMBER OF ANTIAPOPTOTIC BCL-2
CC PROTEINS INCLUDING MCL-1, BCL-2, BCL-XL, BFL-1, AND BHRF-1. DOES
CC NOT HETERODIMERIZE WITH PROAPOPTOTIC PROTEINS SUCH AS BAD, BOK,
CC BAX OR BAK.
CC -!- SUBCELLULAR LOCATION: ASSOCIATED WITH INTRACYTOSOLIC MEMBRANES
CC (BY SIMILARITY).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=BOD-L;
CC IsoId=OS8498-1; Sequence=Displayed;
CC Note=Isoform BOD-S is produced by alternative initiation at
CC Met-104 of isoform BOD-L;
CC Name=BimL;
CC IsoId=OS8498-2; Sequence=VSP_000538;
CC Name=BOD-M;
CC IsoId=OS8498-3; Sequence=VSP_000539;
CC Event=Alternative initiation;
CC Comment=2 isoforms, BOD-L (shown here) and BOD-S, are produced
CC by alternative initiation at Met-1 and Met-104;
CC -!- TISSUE SPECIFICITY: Widely expressed.
CC -!- DOMAIN: THE BH3 DOMAIN IS REQUIRED FOR BCL-2 BINDING AND
CC CYTOTOXICITY.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
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CC -----
DR EMBL; AF065433; AAC23595.1; -

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DR EMBL; AF065431; AAC23593.1; -.
DR EMBL; AF065432; AAC23594.1; -.
DR EMBL; AF136927; AAD26594.1; -.
DR InterPro; IPR000712; Bcl2_BH.
DR PROSITE; PS01259; BH3; FALSE_NEG.
KW Apoptosis; Alternative splicing; Membrane; Alternative initiation.
FT CHAIN 1 196 BCL2-LIKE PROTEIN 11, ISOFORM BOD-L.
FT CHAIN 104 196 BCL2-LIKE PROTEIN 11, ISOFORM BOD-S.
FT INIT_MET 104 104 FOR ISOFORM BOD-S.
FT DOMAIN 146 160 BH3.
FT VARSPLIC 42 97 Missing (in isoform BimL).
FT VARSPLIC 42 127 /FTId=VSP_000538.
FT VARSPLIC 42 127 Missing (in isoform BOD-M).
FT CONFLICT 136 136 E -> D (IN REF. 1; AAC23594).
SQ SEQUENCE 196 AA; 22055 MW; B4D2146F9C0B37A0 CRC64;

Query Match 50.6%; Score 42; DB 1; Length 196;
Best Local Similarity 61.5%; Pred. No. 8.7;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 RYGRELRMSDEF 14
| :|||:|
DB 145 RIAQLRRIGDEF 157

RESULT 6
HGD_RHILO
ID HGD_RHILO STANDARD; PRT; 457 AA.
AC Q983J4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Homogentisate 1,2-dioxygenase (EC 1.13.11.5) (Homogentisicase)
DE (Homogentisate oxygenase) (Homogentisic acid oxidase).
GN HMG A OR MUR8303.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asanizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RA "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti."
RL DNA Res. 7:331-338(2000).
CC -!- CATALYTIC ACTIVITY: Homogentisate + O(2) = 4-maleylacetoacetate.
CC -!- COFACTOR: Iron (By similarity).
CC -!- PATHWAY: Catabolism of tyrosine; third step.
CC -!- PATHWAY: Catabolism of phenylalanine; fourth step.
CC -!- SIMILARITY: Belongs to the homogentisate dioxygenase family.
CC -----
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CC -----
DR EMBL; AP003013; BAB53887.1; -.
DR HAMAP; MF_00334; -.
DR InterPro; IPR005708; HmgA.
DR Pfam; PF04209; HmgA; 1.
DR TIGRfam; TIGR01015; hmgA; 1.
KW Oxidoreductase; Dioxygenase; Phenylalanine catabolism;
Tyrosine catabolism; Metal-binding; Iron; Complete proteome.

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FT METAL 351 351 IRON (BY SIMILARITY).
FT METAL 357 357 IRON (BY SIMILARITY).
FT METAL 387 387 IRON (BY SIMILARITY).
SQ SEQUENCE 457 AA; 51046 MW; 6A20B69E9A2B2BD1 CRC64;

Query Match 50.6%; Score 42; DB 1; Length 457;
Best Local Similarity 46.7%; Pred. No. 21;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 RYGRELRMSDEFVD 16
| | | | | | :|
DB 425 RYGALETRQDNYID 439

RESULT 7
HT2A_HUMAN
ID HT2A_HUMAN STANDARD; PRT; 553 AA.
AC Q13049; Q9NQP8;
DT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Zinc-finger protein HT2A (72 kDa Tat-interacting protein) (Tripartite
DE motif-containing protein 32).
GN TRIM32 OR HT2A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95297135; PubMed=7778269;
RA Fridell R.A., Harding L.S., Bogerd H.P., Cullen B.R.;
RT "Identification of a novel human zinc finger protein that
RT specifically interacts with the activation domain of lentiviral Tat
RT proteins."
RL Virology 209:347-357(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Sehra H.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Narusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: MAY PLAY A SIGNIFICANT ROLE IN MEDIATING THE BIOLOGICAL
CC ACTIVITY OF THE HIV-1 TAT PROTEIN IN VIVO. BINDS SPECIFICALLY TO
CC THE ACTIVATION DOMAIN OF HIV-1 TAT AND CAN ALSO INTERACT WITH THE
CC HIV-2 AND EIAY TAT PROTEINS IN VIVO.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: SPLEEN, THYMUS, PROSTRATE, TESTIS, OVARY,
CC INTESTINE AND COLON.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC -!- SIMILARITY: Contains 1 B box-type zinc finger.

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CC -----
CC EMBL; U18543; AAA86474.1; -
CC EMBL; AL133284; CAB92723.1; -
CC EMBL; BC003154; ARA03154.1; -
CC HSP; P29590; LBOR.
CC Genew; HGNC:16380; TRIM32.
CC MIN; 602290; -
CC GO; GO:0005634; C:nucleus; TAS.
CC GO; GO:0003713; F:transcription co-activator activity; TAS.
CC InterPro; IPR001258; NHL.
CC InterPro; IPR001841; Znf_ring.
CC InterPro; IPR000315; Znf_Bbox.
CC Pfam; PF01436; NHL; 5.
CC Pfam; PF00643; zf-B_box; 1.
CC Pfam; PF00097; zf-C3HC4; 1.
CC SMART; SM00336; BBOX; 1.
CC SMART; SM00184; RING; 1.
CC PROSITE; PS01119; ZF-BBOX; 1.
CC PROSITE; PS00518; ZF_RING_1; 1.
CC PROSITE; PS00089; ZF_RING_2; 1.
KW Zinc-finger; Nuclear protein.
FT DOMAIN 2 6 POLY-ALA.
FT ZN_FING 20 65 RING-TYPE.
FT ZN_FING 103 133 B_BOX-TYPE.
FT CONFLICT 27 27 F -> I (IN REF. 1).
SQ SEQUENCE 653 AA; 71988 MW; D83B1595CA8378FD CRC64;

Query Match 50.6%; Score 42; DB 1; Length 653;
Best Local Similarity 61.5%; Pred.No. 30;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QYGRRLRRMSDE 13
Db 186 QYGHERRVQDE 198

RESULT 8
AROG_CANAL STANDARD; PRT; 370 AA.
ID AROG_CANAL STANDARD; PRT; 370 AA.
AC P79023;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited
DE (EC 4.1.2.15) (Phospho-2-keto-3-deoxyheptonate aldolase) (DAHP
DE synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase).
GN ARO4.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 11651 / B792;
RA Sousa S., Pereira S.A., Livi G.P.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP PARTIAL SEQUENCE FROM N.A.
RC MEDLINE=96207468; PubMed=8625423;
RA Pereira S.A., Livi G.P.;
RT "Aromatic amino-acid biosynthesis in Candida albicans: identification
RT of the ARO4 gene encoding a second DAHP synthase.";
RL Curr. Genet. 29, 441-445 (1996).
CC -!- FUNCTION: STEROSPECIFIC CONDENSATION OF PHOSPHONOLPYRUVATE (PPV)
CC AND D-ERYTHROSE-4-PHOSPHATE (E4P) GIVING RISE TO 3-DEOXY-D-

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CC ARABINO-HEPTULOSONATE-7-PHOSPHATE (DAHP).
CC -!- CATALYTIC ACTIVITY: 2-dehydro-3-deoxy-D-arabino-heptonate 7-
CC phosphate + phosphate = phosphoenolpyruvate + D-erythrose 4-
CC phosphate + H(2)O.
CC -!- ENZYME REGULATION: INHIBITED BY TYROSINE (BY SIMILARITY).
CC -!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC first step.
CC -!- SIMILARITY: BELONGS TO CLASS-I DAHP SYNTHETASE FAMILY.
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CC -----
CC EMBL; U53216; ABA48240.1; -
CC HSP; P00886; IQR7.
CC InterPro; IPR006219; AroFGH.
CC InterPro; IPR006218; DAHP1/KDSA.
CC Pfam; PF00793; DAHP_synth_1; 1.
CC ProDom; PD005060; AroFGH; 1.
CC TIGRfams; TIGR00034; aroFGH; 1.
KW Aromatic amino acid biosynthesis; Lyase; Multigene family.
SQ SEQUENCE 370 AA; 40291 MW; 11E5E324C8D7B6DB CRC64;

Query Match 49.4%; Score 41; DB 1; Length 370;
Best Local Similarity 42.9%; Pred.No. 24;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 3 YGRRLRRMSDEFVD 16
Db 77 YGRRLKLADELKD 90

RESULT 9
GCR3_YEAST STANDARD; PRT; 861 AA.
ID GCR3_YEAST STANDARD; PRT; 861 AA.
AC P34160;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE GCR3 protein (STO1 protein) (SUT1 protein).
GN GCR3 OR STO1 OR SUT1 OR YMR125W OR YMR564.07 OR YMR553.01.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92380925; PubMed=1512188;
RA Demura H., Jigami Y.;
RT "GCR3 encodes an acidic protein that is required for expression of
RT glycolytic genes in Saccharomyces cerevisiae.";
RL J. Bacteriol. 174:5526-5532 (1992).
RN [2]
RP SEQUENCE FROM N.A.
RA Pandit S., Sternglanz R.;
RL Submitted (DEC-1992) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Guo Z., Russo P., Sherman F.;
RL Submitted (XXX-1994) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RX PubMed=9169872;
RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
RA Jagers K., Iyer G., Moule S., Odell C., Pearson D., Rajandream M.A.,
RA Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome

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RT XIII. ";
RL Nature 387:90-93(1997).
CC -!- FUNCTION: REQUIRED FOR EXPRESSION OF GLYCOLYTIC GENES. HAS
CC CERTAIN CHARACTERISTICS OF A TRANSCRIPTIONAL ACTIVATOR.
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- SIMILARITY: SOME, TO HUMAN CBP80.
CC -!- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 708
CC ONWARD AND IS SHORTER (725 AA) DUE TO A FRAMESHIFT.
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CC -----
CC EMBL; D10224; BAA01076.1; ALT_SEQ.
DR EMBL; L07650; -; NOT_ANNOTATED_CDS.
DR EMBL; L27744; -; NOT_ANNOTATED_CDS.
DR EMBL; Z49273; CAA89274.1; -.
DR EMBL; Z48622; CAA88950.1; -.
DR F1R; A44919; A44919.
DR SGD; S0004732; ST01.
DR GO; GO:0000243; C:commitment complex; IPI.
DR GO; GO:0005846; C:snRNA cap binding complex; IDA.
DR GO; GO:0003729; F:snRNA binding activity; IPI.
DR GO; GO:0006371; P:snRNA splicing; IPI.
DR InterPro; IPR003890; IF_EIF4G.
DR Pfam; PF02854; MIF4G; 1.
DR SMART; SMC0543; MIF4G; 1.
KW DNA-binding; Nuclear protein.
FT DOMAIN 22 30 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 774 801 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 802 825 ARG/LYS-RICH (BASIC).
FT CONFLICT 164 164 D -> V (IN REF. 3).
FT CONFLICT 633 633 R -> I (IN REF. 3).
FT CONFLICT 704 704 A -> R (IN REF. 3).
SQ SEQUENCE 861 AA; 100017 MW; EDD04907BDC9207D CRC64;

Query Match 49.4%; Score 41; DB 1; Length 861;
Best Local Similarity 40.0%; Pred. No. 58;
Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 QRYGRELFRMSDEFV 15
Db 821 RYSHEVRELADKFI 835

RESULT 10
YGFGL_ECOLI STANDARD; PRT; 261 AA.
AC P52045; P76643;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein ygfg.
GN YGFGL OR B2919.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
CC -!- SIMILARITY: BELONGS TO THE ENOYL-COA HYDRATASE/ISOMERASE FAMILY.

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CC -----
CC EMBL; U28377; AAA69086.1; ALT_INIT.
DR EMBL; AE000375; AAC75956.1; ALT_INIT.
DR PDB; 1EF8; 24-MAY-00.
DR PDB; 1EF9; 24-MAY-00.
DR EcoGene; Egl2972; ygfg.
DR InterPro; IPR001753; EnCoA_hydratase.
DR Pfam; PF00378; ECH; 1.
DR PROSITE; PS00166; ENOYL_COA_HYDRATASE; 1.
KW Hypothetical protein; Lyase; Complete proteome; 3D-structure.
SQ SEQUENCE 261 AA; 29172 MW; B6A8A13EC2C2EBE0 CRC64;

Query Match 48.2%; Score 40; DB 1; Length 261;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 YGRELFRMSDEFVD 16
Db 21 YGRKLNALSKVFID 34

RESULT 11
PHLC_TRYCR STANDARD; PRT; 380 AA.
AC O13886;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Variant-surface-glycoprotein phospholipase C (EC 3.1.4.47) (VSG
DE lipase) (Glycosylphosphatidylinositol-specific phospholipase C)
DE (GPI-PLC).
OS Trypanosoma cruzi.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5693;
RN [1]
RP SEQUENCE FROM N.A.
RA Redpath M., Carnall N., Webb H., Couriel M., Amorim A.,
RA Cardoso de Almeida M.L., Carrington M.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: BY HYDROLYSIS OF THE ATTACHED GLYCOLIPID, RELEASES
CC SOLUBLE VARIANT SURFACE GLYCOPROTEIN CONTAINING PHOSPHOINOSITOL
CC FROM THE CELL WALL OF T.BRUCI AFTER CELL LYSIS. IT ALSO CLEAVES
CC SIMILAR MEMBRANE ANCHORS ON SOME MAMMALIAN PROTEINS. VSG LIPASE
CC MAY PLAY A ROLE IN PROCESSES SUCH AS PARASITE DIFFERENTIATION OR
CC ANTIGENIC VARIATION (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: Variant-surface-glycoprotein 1,2-didecanoyl-
CC sn-phosphatidylinositol + H(2)O = 1,2-didecanoylglycerol + soluble
CC variant-surface-glycoprotein.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Membrane-associated.
CC -!- SIMILARITY: DOMAIN X IS CONSERVED IN DIFFERENT FORMS OF PLC AND IS
CC ESSENTIAL FOR CATALYTIC ACTIVITY.
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CC -----
CC EMBL; AJ000079; CAA03904.1; -.
DR InterPro; IPR000909; PI_PLC_Xdom.
DR InterPro; IPR003633; Varsurfglyc_PLIC.
DR Pfam; PF00388; PI-PLC-X; 1.

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DR Pfam; PF03490; Varsurf_PPLC; 1.
DR ProDom; PD041675; Varsurfglyc_PPLC; 1.
DR SMART; SM00148; PLCXC; 1.
DR PROSITE; PS50007; PPLC_X_DOMAIN; 1.
KW Hydrolase; Membrane.
FT DOMAIN 31 205 DOMAIN X.
SQ SEQUENCE 380 AA; 42736 MW; 273CD402B52068C5 CRC64;

Query Match 48.2%; Score 40; DB 1; Length 380;
Best Local Similarity 50.0%; Pred. No. 36;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 RYGRLELRMSDEFV 15
::|||:|:|:|
Db 165 KFFRELDRLSDRFI 178

RESULT 12
MTAL_ACEPA STANDARD; PRT; 429 AA.
AC Q52702;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Modification methylase ApaLI (EC 2.1.1.73) (Cytosine-specific
DE methyltransferase ApaLI) (M.ApaLI).
GN APALIM.
OS Acetobacter pasteurianus (Acetobacter turbidans).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Acetobacteraceae; Acetobacter.
OX NCBI_TaxID=438;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12875;
RX MEDLINE=99077292; PubMed=9862476;
RA Xu S.-Y., Xiao J.-P., Ettwiller L., Holden M., Aliotta J., Poh C.L.,
RA Dalton M., Robinson D.P., Petronzio T.R., Moran L., Ganatra M.,
RA Ware J., Slatko B., Benner J. II;
RT "Cloning and expression of the ApaLI, NspI, NspHI, SacI, ScaI, and
RT SapI restriction-modification systems in Escherichia coli.";
RL Mol. Gen. Genet. 260:226-231(1998).
CC -!- FUNCTION: THIS METHYLASE RECOGNIZES THE DOUBLE-STRANDED SEQUENCE
CC GTGCAC, CAUSES SPECIFIC METHYLATION ON C-? ON BOTH STRANDS, AND
CC PROTECTS THE DNA FROM CLEAVAGE BY THE APALI ENDONUCLEASE.
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + DNA cytosine = S-
CC adenosyl-L-homocysteine + DNA 5-methylcytosine.
CC -!- SIMILARITY: BELONGS TO THE C5-METHYLTRANSFERASE FAMILY.
CC -----
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CC -----
CC EMBL; AF044847; AAC97180.1; -.
CC REBASE; 3281; M.ApaLI.
CC InterPro; IPR001525; C5_DNA_meth.
CC Pfam; PF00145; DNA_methylase; 1.
CC PRINTS; PR00105; C5METRFRASE.
CC TIGRfams; TIGR00675; dcm; 1.
CC PROSITE; PS00094; C5_MYASE_1; FALSE_NEG.
KW Transferase; Methyltransferase; Restriction system.
FT ACT_SITE 81 81 BY SIMILARITY.
SQ SEQUENCE 429 AA; 46547 MW; E011C7D15B33F3 CRC64;

Query Match 48.2%; Score 40; DB 1; Length 429;
Best Local Similarity 61.5%; Pred. No. 41;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 GREELRRMSDEFV 16
||:|:|:|:|

Db 129 GRDLARLYREFVD 141

RESULT 13
RPSD_BORBU STANDARD; PRT; 631 AA.
AC P52323;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE RNA polymerase sigma factor rpoD (Sigma-70).
GN RPOD OR BB0712.
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE OF 89-631 FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RA Pan M.;
RL Thesis (1994), National Taiwan University, Taiwan.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RX MEDLINE=98065943; PubMed=9403685;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White C., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
RA Utterback T., Wattley L., McDonald L., Artiach P., Bowman C.,
RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochaete, Borrelia
RT burgdorferi.";
RL Nature 390:580-586(1997).
RN [3]
RP SEQUENCE OF 165-614 FROM N.A.
RC STRAIN=297;
RA Pan M., Yeh J., Tsai C.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES
CC ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND
CC THEN IS RELEASED. THIS IS THE PRIMARY SIGMA-FACTOR OF THIS
CC BACTERIA.
CC -!- SIMILARITY: Belongs to the sigma-70 factor family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U17591; AAC44104.1; -.
CC EMBL; AE001171; AAC67061.1; -.
CC EMBL; U68006; AAC45100.1; -.
CC PIR; G70188; G70188.
CC HSSP; P00579; 1SIG.
CC TIGR; BB0712; -.
CC InterPro; IPR000943; Sigma_70.
CC Pfam; PF03979; sigma70_r1_1; 1.
CC Pfam; PF00140; sigma70_r1_2; 1.
CC Pfam; PF04542; sigma70_r2; 1.
CC Pfam; PF04539; sigma70_r3; 1.
CC Pfam; PF04545; sigma70_r4; 1.
CC PROSITE; PS00715; SIGMA70_1; 1.
CC PROSITE; PS00716; SIGMA70_2; 1.
KW Transcription regulation; Sigma factor; DNA-directed RNA polymerase;
KW DNA-binding; Complete proteome.
FT DOMAIN 419 432 POLYMERASE CORE BINDING (POTENTIAL).
FT DNA_BIND 589 608 H-T-H MOTIF (BY SIMILARITY).
SQ SEQUENCE 631 AA; 73642 MW; BD565AB7D8F4796 CRC64;
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Query Match          48.2%; Score 40; DB 1; Length 631;
Best Local Similarity 50.0%; Pred. No. 61;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 YGRELRMSDEFVD 16
DQ 279 YQELRIFSDYID 292
I ||| ||::|

RESULT 14
6PGL_THEME
ID 6PGL_THEME STANDARD; PRT; 220 AA.
AC QXON8;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 6-phosphogluconolactonase (EC 3.1.1.31) (6PGL).
GN PGL OR DEVB OR TM1154.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RX MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Otterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima.";
RL Nature 399:323-329(1999).
CC -!- FUNCTION: HYDROLYSIS OF 6-PHOSPHOGLUCONOLACTONE TO 6-
CC PHOSPHOGLUCONATE.
CC -!- CATALYTIC ACTIVITY: 6-phospho-D-glucono-1,5-lactone + H(2)O = 6-
CC phospho-D-gluconate.
CC -!- PATHWAY: Pentose phosphate pathway; second step.
CC -!- SIMILARITY: BELONGS TO THE GLUCOSAMINE/GALACTOSAMINE-6-PHOSPHATE
CC ISOMERASE FAMILY. 6-PHOSPHOGLUCONOLACTONASE SUBFAMILY.
CC -----
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CC -----
DR EMBL; AE001772; AAD36230.1; -
DR PIR; F72289; F72289.
DR TIGR; TM1154; -.
DR InterPro; IPR006148; Gluc_gal_isom.
DR InterPro; IPR005900; Phosphogluconlac.
DR Pfam; PF01182; Glucosamine_iso; 1.
DR TIGRFAMs; TIGR01198; pgl; 1.
KW Hydrolase; Complete proteome.
SQ SEQUENCE 220 AA; 25325 MW; 9B0FD07EE01E60C3 CRC64;

Query Match          47.0%; Score 39; DB 1; Length 220;
Best Local Similarity 42.9%; Pred. No. 30;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 QRYGRLRMSDEF 14
DQ 113 EKYERLRSATDQF 126
::| ||:| :|:|

RESULT 15
RA51_SCHPO
ID RA51_SCHPO STANDARD; PRT; 365 AA.

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AC P36601;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA repair protein rhp51 (RAD51 homolog).
GN RHP51 OR RAD51 OR SPAC644.14C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94051565; PubMed=8233794;
RA Muris D.F.R., Vreeken K., Carr A.M., Broughton B.C., Lehmann A.R.,
RA Lohman P.H.M., Pastink A.;
RT "Cloning the RAD51 homologue of Schizosaccharomyces pombe.";
RL Nucleic Acids Res. 21:4586-4591(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93364417; PubMed=8358431;
RA Shinohara A., Ogawa H., Matsuda Y., Ushio N., Ikeo K., Ogawa T.;
RT "Cloning of human, mouse and fission yeast recombination genes
RT homologous to RAD51 and recA.";
RL Nat. Genet. 4:239-243(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=94252568; PubMed=8194753;
RA Jang Y.K., Jin Y.H., Kim E.M., Hong S.H., Fabre F., Park S.D.;
RT "Cloning and sequence analysis of rhp51+, a Schizosaccharomyces pombe
RT homologue of the Saccharomyces cerevisiae RAD51 gene.";
RL Gene 142:207-211(1994).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Scours J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grynoprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Sipakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -!- FUNCTION: REQUIRED BOTH FOR RECOMBINATION AND FOR THE REPAIR OF
CC DNA DAMAGE CAUSED BY X-RAYS.
CC -!- SIMILARITY: BELONGS TO THE RECA FAMILY. RAD51 SUBFAMILY.
CC -----
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CC  EMBL; Z22691; CAA80399.1; -.
DR  EMBL; D13805; BAA02963.1; -.
DR  EMBL; Z24756; CAA80879.1; -.
DR  EMBL; Z24756; CAA80878.1; ALT_INIT.
DR  EMBL; AL355012; CAB90141.1; -.
DR  PIR; S42107; S42107.
DR  HSSP; Q06609; 1B22.
DR  GeneDB_SPombe; SPAC64.14c; -.
DR  InterPro; IPR003593; AAA_ATPase.
DR  InterPro; IPR000445; HhH.
DR  InterPro; IPR003583; HhH_1.
DR  InterPro; IPR001553; RecA.
DR  Pfam; PF00633; HhH; 1.
DR  ProDom; PD000229; RecA; 1.
DR  SMART; SM00382; AAA; 1.
DR  SMART; SM00278; HhH1; 1.
DR  PROSITE; PS50162; RECA_2; 1.
DR  PROSITE; PS50163; RECA_3; 1.
KW  DNA damage; DNA repair; ATP-binding; DNA recombination.
FT  NP_BIND 149 156 ATP (POTENTIAL).
FT  CONFLICT 15 15 T -> M (IN REF. 2 AND 4).
SQ  SEQUENCE 365 AA; 39823 MW; 9F26EB9FA4F3C2BA CRC64;

Query Match      47.0%; Score 39; DB 1; Length 365;
Best Local Similarity 53.8%; Pred. No. 50;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      2 RYGRRLRMSDEF 14
Db      269 RFWRLQLADEF 281
```

Search completed: September 15, 2003, 17:23:01  
Job time : 4.77143 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 15, 2003, 17:17:31 ; Search time 17.3714 Seconds  
(without alignments)  
237.680 Million cell updates/sec

Title: US-09-544-664-29

Perfect score: 83

Sequence: 1 QRYGRELRRMSDEFVD 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL\_23.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	71.1	146	13 Q9I9N2	Q9I9n2 brachydanio
2	46	55.4	458	5 Q8SV57	Q8sv57 encephalito
3	46	53.4	477	5 Q8SVF8	Q8svf8 encephalito
4	46	55.4	641	5 Q8SU90	Q8su90 encephalito
5	45	54.2	230	16 Q8XXS6	Q8xxs6 ralstonia s
6	45	54.2	564	16 Q9RUK9	Q9ruk9 deinococcus
7	44	53.0	247	2 Q9AJL5	Q9ajl5 streptomyce
8	44	53.0	726	16 Q8G3Z1	Q8g3z1 bifidobacte
9	44	53.0	1248	16 Q9HZQ3	Q9hzzq3 pseudomonas
10	43	51.8	205	10 Q8L757	Q8l757 arabidopsis
11	43	51.8	804	16 Q8EW78	Q8ew78 mycoplasma
12	43	51.8	5635	5 Q9N9N1	Q9n9n1 leishmania
13	42	50.6	213	17 Q8TJ31	Q8tj31 methanosarc
14	42	50.6	260	16 Q8RCC4	Q8rcc4 thermoanaer
15	42	50.6	297	5 Q8MZ90	Q8mz90 drosophila
16	42	50.6	339	10 Q9FQ05	Q9fq05 atrichum an

17	42	50.6	548	2 P71029	P71029 burkholderi
18	42	50.6	592	5 Q9V7Y6	Q9v7y6 drosophila
19	42	50.6	592	5 Q960B3	Q960b3 drosophila
20	42	50.6	876	16 Q931Q1	Q931q1 staphylococ
21	42	50.6	876	16 Q99TJ8	Q99tj8 staphylococ
22	42	50.6	876	16 Q8CS83	Q8cs83 staphylococ
23	42	50.6	990	17 Q8TUT0	Q8tut0 methanopyru
24	41.5	50.0	191	16 Q8YG63	Q8yg63 brucella me
25	41.5	50.0	191	16 Q8GIQ8	Q8giq8 brucella su
26	41	49.4	216	16 Q9KZC5	Q9kzc5 streptomyce
27	41	49.4	447	10 Q9M0B1	Q9m0b1 arabidopsis
28	41	49.4	497	10 Q8L517	Q8l517 arabidopsis
29	41	49.4	577	3 Q59699	Q59699 schizosacch
30	41	49.4	1303	12 Q9QBU0	Q9qbu0 potato mop-
31	41	49.4	2381	5 Q8IKD7	Q8ikd7 plasmodium
32	40.5	48.8	792	4 P78313	P78313 homo sapien
33	40.5	48.8	1224	4 P78311	P78311 homo sapien
34	40.5	48.8	1265	4 P78312	P78312 homo sapien
35	40	48.2	84	17 Q9HNU7	Q9hnu7 halobacteri
36	40	48.2	109	16 Q97SI9	Q97si9 streptococc
37	40	48.2	113	16 Q8DR57	Q8dr57 streptococc
38	40	48.2	164	17 Q8ZTI1	Q8zti1 pyrobaculum
39	40	48.2	219	17 Q9UZ00	Q9uzq0 pyrococcus
40	40	48.2	259	17 Q8PUZ1	Q8puzi methanosarc
41	40	48.2	275	16 Q8XD14	Q8xd14 escherichia
42	40	48.2	335	10 Q64692	Q64692 arabidopsis
43	40	48.2	360	16 Q9IOH8	Q9ioh8 pseudomonas
44	40	48.2	361	10 Q9FIC1	Q9fic1 arabidopsis
45	40	48.2	411	16 Q9A3L1	Q9a3l1 caulobacter

ALIGNMENTS

RESULT 1

Q9I9N2	PRELIMINARY;	PRT;	146 AA.
ID Q9I9N2	AC Q9I9N2;		
DT 01-OCT-2000	(TREMBLrel. 15, Created)		
DT 01-DEC-2001	(TREMBLrel. 19, Last sequence update)		
DT 01-OCT-2002	(TREMBLrel. 22, Last annotation update)		
DE Bad.			
GN BAD.			
OS Brachydanio rerio (zebrafish) (Danio rerio).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;			
OC Cyprinidae; Danio.			
OX NCBI_TaxID=7955;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=20373792; PubMed=10917738;			
RA Inohara N.; Nunez G.;			
RT "Genes with homology to mammalian apoptosis regulators identified in zebrafish."			
RL Cell Death Differ. 7:509-510(2000).			
DR EMBL; AF231017; AAF66962.2; -.			
DR HSSP; Q92934; 1G5J.			
DR ZFIN; ZDB-GENE-000616-1; bad.			
SQ SEQUENCE 146 AA; 16546 MW; 28A5650BB5107ECB CRC64;			

Query Match 71.1%; Score 59; DB 13; Length 146;  
Best Local Similarity 71.4%; Pred. No. 0.047;  
Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEF 14

Db 93 KKYGOQLRRMSDEF 106

RESULT 2

Q8SV57	PRELIMINARY;	PRT;	458 AA.
ID Q8SV57			
AC Q8SV57;			

DT 01-JUN-2002 (TReMBLrel. 21, Created)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)  
 DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
 DE Hypothetical protein ECU06\_1680.  
 GN ECU06\_1680.  
 OS Encephalitozoon cuniculi.  
 OC Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.  
 OX NCBI\_TaxID=6035;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=GB-M1;  
 RA Genoscope;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=GB-M1;  
 RX MEDLINE=21576510; PubMed=11719806;  
 RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarar F.,  
 RA Prensier G., Barbe V., Peyretailade E., Brottier P., Wincker P.,  
 RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,  
 RA Weissenbach J., Vivares C.P.;  
 RT "Genome sequence and gene compaction of the eukaryote parasite  
 RT Encephalitozoon cuniculi.";  
 RL Nature 414:450-453(2001).  
 DR EMBL; AL590446; CAD25329.1; -.  
 KW Hypothetical protein.  
 SQ SEQUENCE 458 AA; 51914 MW; 24111BF78D4A534D CRC64;

Query Match 55.4%; Score 46; DB 5; Length 458;  
 Best Local Similarity 46.7%; Pred. No. 24;  
 Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 RYGRRLRMSDEFVD 16  
 Db 13 RYGRVWRMLDDMIE 27

RESULT 3  
 Q8SVF8 PRELIMINARY; PRT; 477 AA.  
 ID Q8SVF8  
 AC Q8SVF8;  
 DT 01-JUN-2002 (TReMBLrel. 21, Created)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)  
 DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
 DE Hypothetical protein ECU06\_0040.  
 GN ECU06\_0040.  
 OS Encephalitozoon cuniculi.  
 OC Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.  
 OX NCBI\_TaxID=6035;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=GB-M1;  
 RA Genoscope;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=GB-M1;  
 RX MEDLINE=21576510; PubMed=11719806;  
 RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarar F.,  
 RA Prensier G., Barbe V., Peyretailade E., Brottier P., Wincker P.,  
 RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,  
 RA Weissenbach J., Vivares C.P.;  
 RT "Genome sequence and gene compaction of the eukaryote parasite  
 RT Encephalitozoon cuniculi.";  
 RL Nature 414:450-453(2001).  
 DR EMBL; AL590446; CAD25364.1; -.  
 KW Hypothetical protein.  
 SQ SEQUENCE 477 AA; 54039 MW; B5DC96299724CC96 CRC64;

Query Match 55.4%; Score 46; DB 5; Length 477;  
 Best Local Similarity 46.7%; Pred. No. 25;  
 Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 RYGRRLRMSDEFVD 16  
 Db 32 RYGRVWRMLDDMIE 46

RESULT 4  
 Q8SU90 PRELIMINARY; PRT; 641 AA.  
 ID Q8SU90  
 AC Q8SU90;  
 DT 01-JUN-2002 (TReMBLrel. 21, Created)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
 DE Hypothetical protein ECU11\_0030.  
 GN ECU11\_0030.  
 OS Encephalitozoon cuniculi.  
 OC Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.  
 OX NCBI\_TaxID=6035;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=GB-M1;  
 RA Genoscope;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=GB-M1;  
 RX MEDLINE=21576510; PubMed=11719806;  
 RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarar F.,  
 RA Prensier G., Barbe V., Peyretailade E., Brottier P., Wincker P.,  
 RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,  
 RA Weissenbach J., Vivares C.P.;  
 RT "Genome sequence and gene compaction of the eukaryote parasite  
 RT Encephalitozoon cuniculi.";  
 RL Nature 414:450-453(2001).  
 DR EMBL; AL590450; CAD25913.1; -.  
 KW Hypothetical protein.  
 SQ SEQUENCE 641 AA; 72408 MW; A87E6EBE49732FC2 CRC64;

Query Match 55.4%; Score 46; DB 5; Length 641;  
 Best Local Similarity 46.7%; Pred. No. 34;  
 Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 RYGRRLRMSDEFVD 16  
 Db 203 RYGRVWRMLDDMIE 217

RESULT 5  
 Q8XXS6 PRELIMINARY; PRT; 230 AA.  
 ID Q8XXS6  
 AC Q8XXS6;  
 DT 01-MAR-2002 (TReMBLrel. 20, Created)  
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)  
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
 DE Probable ATP-binding ABC transporter protein.  
 GN RSC2037 OR RS03602  
 OS Ralstonia solanacearum (Pseudomonas solanacearum).  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Ralstoniaceae; Ralstonia.  
 OX NCBI\_TaxID=305;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=GM11000;  
 RX MEDLINE=21681879; PubMed=11823852;  
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,  
 RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,  
 RA Chandler M., Choise N., Claudel-Renard C., Gunnac S., Demange N.,  
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,  
 RA Sigulier P., Thebault P., Whalen M., Wincker P., Levy M.,  
 RA Weissenbach J., Boucher C.A.;  
 RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";  
 RL Nature 415:497-502(2002).  
 DR EMBL; AL646067; CAD15739.1; -.  
 InterPro; IPR003593; AAA\_ATPase.

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DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
KW Complete proteome.
SQ SEQUENCE 230 AA; 25231 MW; 7C3FDA1E7A19A2A4 CRC64;

Query Match 54.2%; Score 45; DB 16; Length 230;
Best Local Similarity 64.3%; Pred. No. 17;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QYGRELRMSDEF 14
DB 168 QEIGRTLRRLVDEF 181

RESULT 6
Q9RUK9
ID Q9RUK9 PRELIMINARY; PRT; 564 AA.
AC Q9RUK9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Glycosyl hydrolase, family 13.
GN DR1375.
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RI;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Hart D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans RI.";
RL Science 286:1571-1577(1999).
DR EMBL; AE001983; AAF10944.1; -.
DR HSP; P21332; IUOK.
DR TIGR; DR1375; -.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
KW Hydrolase; Complete proteome.
SQ SEQUENCE 564 AA; 63667 MW; B8F50B9B0DFC8D51 CRC64;

Query Match 54.2%; Score 45; DB 16; Length 564;
Best Local Similarity 64.3%; Pred. No. 44;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 YGRELRMSDEFVD 16
DB 283 YVEMRRVDEFD 296

RESULT 7
Q9AJL5
ID Q9AJL5 PRELIMINARY; PRT; 247 AA.
AC Q9AJL5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Varr.
GN VARR.
OS Streptomyces virginiae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1961;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21125565; PubMed=11222601;
RA Nawat W., Lee C.K., Kinoshita H., Yamada Y., Nihira T.;
RT "Identification of the varr gene as a transcriptional regulator of
RT virginiamycin S resistance in Streptomyces virginiae.";
RL J. Bacteriol. 183:2025-2031(2001).
CC -!- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
DR EMBL; AB046994; BAB32408.1; -.
DR HSP; P09164; 2TCT.
DR InterPro; IPR001647; HTH_Tetr.
DR InterPro; IPR004111; Tetr_C.
DR Pfam; PF00440; tetr; 1.
DR Pfam; PF02909; tetr_C; 1.
DR PRINTS; PR00455; HTHTETR.
KW DNA-binding; Transcription; Transcription regulation.
SQ SEQUENCE 247 AA; 27328 MW; B6326F4374598A8 CRC64;

Query Match 53.0%; Score 44; DB 2; Length 247;
Best Local Similarity 50.0%; Pred. No. 27;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 3 YGRELRMSDEFVD 16
DB 186 YGKVGRTADEFLE 199

RESULT 8
Q8G3Z1
ID Q8G3Z1 PRELIMINARY; PRT; 726 AA.
AC Q8G3Z1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Narrowly conserved hypothetical protein.
GN BL1609.
OS Bifidobacterium longum.
OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
OC Bifidobacteriaceae; Bifidobacterium.
OX NCBI_TaxID=216816;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCC 2705;
RX MEDLINE=22294977; PubMed=12381787;
RA Schell M.A., Karmirantzou M., Snel B., Villanova D., Berger B.,
RA Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,
RA Pridmore R.D., Arigoni F.;
RT "The genome sequence of Bifidobacterium longum reflects its adaptation
RT to the human gastrointestinal tract.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
DR EMBL; AE014794; AAN25398.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 726 AA; 81866 MW; 6BEB86B61FCBC586 CRC64;

Query Match 53.0%; Score 44; DB 16; Length 726;
Best Local Similarity 60.0%; Pred. No. 85;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 YGRELRMSDEFVD 16
DB 241 RVGVVRRLSDEFID 255

RESULT 9
Q9HZQ3
ID Q9HZQ3 PRELIMINARY; PRT; 1248 AA.
AC Q9HZQ3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

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DE Cobalam biosynthetic protein CobN.  
 GN COBN OR PA2944.  
 OS Pseudomonas aeruginosa.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 CC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=287;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 15692 / PA01;  
 RX MEDLINE=20437337; PubMed=10984043;  
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,  
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,  
 RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,  
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,  
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;  
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an  
 RT opportunistic pathogen.";  
 RL Nature 406:959-964(2000).  
 DR EMBL: AE004720; AAG06332.1; -;  
 DR InterPro: IPR003672; COBN/Mg\_chltase.  
 DR InterPro: IPR000408; Reg\_chrt\_condens.  
 DR Pfam: PF02514; COBN-Mg\_chel; 1.  
 DR PROSITE: PS00626; RCCL\_2; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 1248 AA; 138499 MW; C3D3DBFEE6736C7A CRC64;

Query Match 53.0%; Score 44; DB 16; Length 1248;  
 Best Local Similarity 50.0%; Pred. No. 1.5e+02;  
 Matches 9; Conservative 4; Mismatches 3; Indels 2; Gaps 1;

QY 1 QRYG--RELRRMSDEFVD 16  
 :|||:|:|:|:|:|  
 Db 615 ESYGPLERLERLAEFYD 632

RESULT 10  
 Q8L757  
 ID Q8L757 PRELIMINARY; PRT; 205 AA.  
 AC Q8L757;  
 DT 01-OCT-2002 (TremBLrel. 22, Created)  
 DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 GN AT4G02715.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,  
 RA Carninci P., Chen H., Cheuk K., Chan M.M., Chang C.H., Dale J.M.,  
 RA Deng J.M., Hayashizaki Y., Hsuan V.W., Lee J.M., Ishida J., Kamiya A.,  
 RA Kawai J., Kim C.J., Narusaka M., Quach H.L., Sakurai T., Satou M.,  
 RA Seki M., Shinn P., Tang C.C., Toroumi M., Wallender E.K., Wong C.,  
 RA Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Becker J.,  
 RA Theologis A., Davis R.W.;  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RA Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,  
 RA Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,  
 RA Hayashizaki Y., Shinozaki K.;  
 RT "Arabidopsis thaliana full-length cDNA.";  
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY136474; AAM97139.1; -;  
 DR EMBL: AK118269; BAC42887.1; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 205 AA; 22583 MW; 1BD8D1358ECFF81 CRC64;

Query Match 51.8%; Score 43; DB 10; Length 205;  
 Best Local Similarity 61.5%; Pred. No. 32;  
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 4 GRELRMSDEFVD 16  
 |::||| |  
 Db 100 GSQIRRCSSSEFYD 112  
 RESULT 11  
 Q8EW78  
 ID Q8EW78 PRELIMINARY; PRT; 804 AA.  
 AC Q8EW78;  
 DT 01-MAR-2003 (TremBLrel. 23, Created)  
 DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)  
 DE Cation-transporting p-type ATPase.  
 GN MYPE3250.  
 OS Mycoplasma penetrans.  
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
 OX NCBI\_TaxID=28227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HF-2;  
 RX MEDLINE=22354719; PubMed=12466555;  
 RA Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K.,  
 RA Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;  
 RT "The complete genomic sequence of Mycoplasma penetrans, an  
 RT intracellular bacterial pathogen in humans.";  
 RL Nucleic Acids Res. 30:5293-5300(2002).  
 DR EMBL: AP004171; BAC44118.1; -;  
 KW Complete proteome.  
 SQ SEQUENCE 804 AA; 88008 MW; 69C71AA628FEF7A3 CRC64;

Query Match 51.8%; Score 43; DB 16; Length 804;  
 Best Local Similarity 66.7%; Pred. No. 1.4e+02;  
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 GRELRMSDEFV 15  
 | | | | | | | | | |  
 Db 428 GSELRRMSDEYL 439  
 RESULT 12  
 Q9N9N1  
 ID Q9N9N1 PRELIMINARY; PRT; 5635 AA.  
 AC Q9N9N1;  
 DT 01-OCT-2000 (TremBLrel. 15, Created)  
 DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)  
 DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)  
 DE Dynein heavy chain, cytosolic.  
 GN L3302.02.  
 OS Leishmania major.  
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.  
 OX NCBI\_TaxID=5664;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Friedlin;  
 RA Hilbert H., Wedler H., Wedler E., Dueterhoeft A., Ivens A.C.,  
 RA Quail M., Rajandream M.A., Barrell B.G.;  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Friedlin;  
 RX MEDLINE=96146435; PubMed=9477341;  
 RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,  
 RA Smith D.F.;  
 RT "A physical map of the Leishmania major Friedlin genome.";  
 RL Genome Res. 8:135-145(1998).  
 DR EMBL: AL359781; CAB95305.1; -;  
 DR InterPro: IPR003593; AAA\_ATPase.  
 DR InterPro: IPR004273; Dynein\_heavy.  
 DR InterPro: IPR000169; SHprot\_acsite.

DR Pfam; PF03028; Dynein\_heavy; 1.  
 DR SMART; SM00382; AAA; 4.  
 DR PROSITE; PS00639; THIOL\_PROTEASE\_HIS; 1.  
 KW ATP-binding.  
 SQ SEQUENCE 5635 AA; 620050 MW; 64A9E81A9B14641 CRC64;

Query Match 51.8%; Score 43; DB 5; Length 5635;  
 Best Local Similarity 72.7%; Pred. No. 1.1e+03;  
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QRYGRLRRMS 11  
 ||:|||||  
 Db 1535 QRFGRDLRRMS 1545

## RESULT 13

Q8TUJ31 PRELIMINARY; PRT; 213 AA.  
 AC Q8TUJ31;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE ABC transporter, ATP-binding protein.  
 GN MA3957.  
 OS Methanosarcina acetivorans.  
 OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;  
 OC Methanosarcinaceae; Methanosarcina.  
 OX NCBI\_TaxID=2214;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=C2A / ATCC 35395 / DSM 2834;  
 RX MEDLINE=21929760; PubMed=11932238;  
 RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., MacDonald P.,  
 RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,  
 RA Allen N., Naylor J., Stange-Thomann N., Dearellano K., Johnson R.,  
 RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,  
 RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,  
 RA Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,  
 RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,  
 RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,  
 RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,  
 RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,  
 RA Metcalf W.W., Birren B.;  
 RT "The genome of Methanosarcina acetivorans reveals extensive metabolic  
 RT and physiological diversity."  
 RL Genome Res. 12:532-542(2002).  
 DR EMBL; AE011107; AAM07308.1; -.  
 DR InterPro; IPR003593; AAA\_AIPase.  
 DR InterPro; IPR003439; ABC\_transporter.  
 DR Pfam; PF00005; ABC\_tran; 1.  
 DR ProDom; PD000006; ABC\_transporter; 1.  
 DR SMART; SM00382; AAA; 1.  
 DR PROSITE; PS00211; ABC\_TRANSPORTER; 1.  
 KW ATP-binding; Complete proteome.  
 SQ SEQUENCE 213 AA; 23676 MW; B548F93D94D109C9 CRC64;

Query Match 50.6%; Score 42; DB 17; Length 213;  
 Best Local Similarity 80.0%; Pred. No. 49;  
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 GRELRRMSDE 13  
 ||:|||||  
 Db 59 GRDLRRMSDE 68

## RESULT 14

Q8RCC4 PRELIMINARY; PRT; 260 AA.  
 AC Q8RCC4;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE ABC-type amino acid transport system, periplasmic component.

GN ARTI OR TTE0512.  
 OS Thermoanaerobacter tengcongensis.  
 OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;  
 OC Thermoanaerobacteriaceae; Thermoanaerobacter.  
 OX NCBI\_TaxID=119072;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MB4 / JCM 11007;  
 RX MEDLINE=21992816; PubMed=11997336;  
 RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,  
 RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,  
 RA Tan H., Chen R., Wang J., Yu J., Yang H.;  
 RT "A complete sequence of T. tengcongensis genome."  
 RL Genome Res. 12:689-700(2002).  
 DR EMBL; AE013022; AAM23788.1; -.  
 DR InterPro; IPR003439; ABC\_transporter.  
 DR InterPro; IPR001311; SBP\_glu\_receptor.  
 DR InterPro; IPR001638; SBP\_bac\_3.  
 DR Pfam; PF00497; SBP\_bac\_3; 1.  
 DR SMART; SM00062; PBPb; 1.  
 DR PROSITE; PS00211; ABC\_TRANSPORTER; 1.  
 DR PROSITE; PS01039; SBP\_BACTERIAL\_3; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 260 AA; 28849 MW; F3D87ED16B18DCBC CRC64;

Query Match 50.6%; Score 42; DB 16; Length 260;  
 Best Local Similarity 58.3%; Pred. No. 61;  
 Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 RELRRMSDEFVD 15  
 :||:|||||  
 Db 170 QQLNRVSDEFMD 181

## RESULT 15

Q8MZ90 PRELIMINARY; PRT; 297 AA.  
 AC Q8MZ90;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE AT26020P.  
 GN CG30456 OR CG15612 OR CG15613.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Dresnak D., Farfan D., Erise B.,  
 RA George K., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,  
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,  
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
 RA Celniker S.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY113300; AAM29305.1; -.  
 DR FlyBase; FBgn0050456; CG30456.  
 DR InterPro; IPR000219; RhogEF.  
 DR Pfam; PF00621; RhogEF; 1.  
 DR PROSITE; PS50010; DH\_2; 1.  
 SQ SEQUENCE 297 AA; 35804 MW; 58FDBF3DF68D99A CRC64;

Query Match 50.6%; Score 42; DB 5; Length 297;  
 Best Local Similarity 53.3%; Pred. No. 70;  
 Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 QRYGRLRRMSDEFV 15  
 ||:|||||  
 Db 3 QQRNRLKRLDFEFL 17

Search completed: September 15, 2003, 17:25:49  
Job time : 18.3714 secs

1

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run On: September 15, 2003, 17:18:16 ; Search time 7.2 Seconds  
(without alignments)  
213.708 Million cell updates/sec

Title: US-09-544-664-29

Perfect score: 83

Sequence: 1 QRYGRLRRMSDEFVD 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_76.\*

1: Piri:\*

2: Piri2:\*

3: Piri3:\*

4: Piri4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	73	88.0	204	2 A55671	bad protein - mous
2	45	54.2	564	2 H75403	glycosyl hydrolase
3	44	53.0	1248	2 G83278	cobalamin biosynth
4	42	50.6	876	2 E89949	valine-tRNA ligase
5	41.5	50.0	191	2 AD3414	hypothetical cytos
6	41	49.4	447	2 F85356	hypothetical prote
7	41	49.4	577	2 T40297	membrane transport
8	41	49.4	858	2 A44919	GCR3 protein - yea
9	40	48.2	84	2 F84388	hypothetical prote
10	40	48.2	109	2 B95043	conserved hypothet
11	40	48.2	113	2 D97913	conserved hypothet
12	40	48.2	219	2 A75088	hypothetical prote
13	40	48.2	275	2 E91102	probable enzyme [i
14	40	48.2	275	2 A85948	probable enzyme yg
15	40	48.2	275	2 F85076	hypothetical prote
16	40	48.2	335	2 T52577	gibberellin 2beta-
17	40	48.2	360	2 F83311	hypothetical prote
18	40	48.2	411	2 F87644	transcription regu
19	40	48.2	429	2 JC4986	site-specific DNA-
20	40	48.2	445	2 G97123	probable Fe-S oxid
21	40	48.2	631	2 G70188	transcription init
22	40	48.2	5138	2 B96695	hypothetical prote
23	39.5	47.6	198	2 E87441	conserved hypothet
24	39.5	47.6	414	2 B84275	hypothetical prote
25	39	47.0	73	2 AC3365	hypothetical prote
26	39	47.0	172	2 B71339	probable cationic
27	39	47.0	207	2 B95348	hypothetical prote
28	39	47.0	220	2 F72289	oxidoreductase, so
29	39	47.0	275	2 C69808	transporter homolo

#### ALIGNMENTS

##### RESULT 1

A55671

bad protein - mouse

C:Species: Mus musculus (house mouse)

C>Date: 03-Mar-1995 #sequence\_revision 03-Mar-1995 #text\_change 05-Nov-1999

C:Accession: A55671

R:Yang, E.; Zha, J.; Jockel, J.; Boise, L.H.; Thompson, C.B.; Korsmeyer, S.J.

Cell 80, 285-291, 1995

A>Title: Bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promot

A:Reference number: A55671; MUID:95136361; PMID:7834748

A:Accession: A55671

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-204 <YAN>

A:Cross-references: GB:L37296; NID:g639778; PIDN:AAA64465.1; PID:g639779

C:Keywords: heterodimer

Query Match

Best Local Similarity 88.0%; Score 73; DB 2; Length 204;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRLRRMSDEF 14

|||||

Db 145 QRYGRLRRMSDEF 158

##### RESULT 2

H75403

glycosyl hydrolase, family 13 - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans

C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 17-Mar-2000

C:Accession: H75403

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.C.

, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A>Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: H75403

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-564 <WHI>

A:Cross-references: GB:AE001983; GB:AE000513; NID:g6459123; PIDN:AAF10944.1; PID:g645

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR1375

A:Map position: 1

C:Superfamily: alpha-glucosidase; alpha-amylase core homology

Query Match

Best Local Similarity 54.2%; Score 45; DB 2; Length 564;

Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 YGRLRRMSDEFVD 16  
 |||:|: |||  
 Db 283 YVEMRRVDFDD 296

RESULT 3  
 G83278  
 cobalamin biosynthetic protein CobN PA2944 [imported] - Pseudomonas aeruginosa (strain H  
 C:Species: Pseudomonas aeruginosa  
 C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 02-Mar-2001  
 C:Accession: G83278  
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B  
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
 ; Lory, S.; Olson, M.V.  
 Nature 406, 959-964, 2000  
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
 A:Reference number: A82950; MUID:20437337; PMID:10984043  
 A:Accession: G83278  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1248 <STO>  
 A:Cross-references: GB:AE004720; GB:AE004091; NID:g9949032; PIDN:AG06332.1; GSPDB:GN001  
 A:Experimental source: strain PA01  
 C:Genetics:  
 A:Gene: cobN; PA2944  
 C:Superfamily: Rhodobacter capsulatus magnesium-protoporphyrin O-methyltransferase

Query Match 53.0%; Score 44; DB 2; Length 1248;  
 Best Local Similarity 50.0%; Pred. No. 47;  
 Matches 9; Conservative 4; Mismatches 3; Indels 2; Gaps 1;

Qy 1 QRYG--RELRRMSDEFVD 16  
 : || | : | : | : | : |  
 Db 615 ESYGPLRLDLRLADEYD 632

RESULT 4  
 E89949  
 valine-tRNA ligase [imported] - Staphylococcus aureus (strain N315)  
 C:Species: Staphylococcus aureus  
 C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 22-Oct-2001  
 C:Accession: E89949  
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu  
 ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;  
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.  
 Lancet 357, 1225-1240, 2001  
 A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.  
 A:Reference number: A89758; MUID:21311952; PMID:11418146  
 A:Accession: E89949  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-876 <KUR>  
 A:Cross-references: GB:BA000018; PID:g13701460; PIDN:BA842754.1; GSPDB:GN00149  
 A:Experimental source: strain N315  
 C:Genetics:  
 A:Gene: valS  
 C:Superfamily: valine-tRNA ligase

Query Match 50.6%; Score 42; DB 2; Length 876;  
 Best Local Similarity 61.5%; Pred. No. 70;  
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GRELRMSDEFVD 16  
 |||| :||:|  
 Db 251 GRELPILADEYD 263

RESULT 5  
 AD3414  
 hypothetical cytosolic protein BME11298 [imported] - Brucella melitensis (strain 16M)  
 C:Species: Brucella melitensis  
 C:Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 01-Feb-2002

C:Accession: AD3414  
 R:DelVecchio, V.G.; Kapural, V.; Redkar, R.J.; Patra, G.; Mujeer, C.; Los, T.; Ivanov  
 ; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let  
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
 A:Title: The genome sequence of the facultative intracellular pathogen Brucella melit  
 A:Reference number: AD3252; PMID:11756688  
 A:Accession: AD3414  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-191 <KUR>  
 A:Cross-references: GB:AE008917; PIDN:AA152479.1; PID:g17983287; GSPDB:GN00190  
 A:Experimental source: strain 16M  
 C:Genetics:  
 A:Gene: BME11298  
 A:Map position: 1

Query Match 50.0%; Score 41.5; DB 2; Length 191;  
 Best Local Similarity 33.3%; Pred. No. 18;  
 Matches 11; Conservative 2; Mismatches 3; Indels 17; Gaps 1;

Qy 1 QRYGR-----ELRRMSDEFVD 16  
 || ||  
 |||| :||:|  
 Db 131 QRGRKYSVVSTLTTPAMISDELRRQADHFID 163

RESULT 6  
 F85356  
 hypothetical protein AT4g30490 [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cross)  
 C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 16-Feb-2001  
 C:Accession: F85356  
 R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sp  
 Nature 402, 769-777, 1999  
 A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
 A:Reference number: A85001; MUID:20083488; PMID:10617198  
 A:Accession: F85356  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-447 <STO>  
 A:Cross-references: GB:NC\_001268; NID:g7269950; PIDN:CA879767.1; GSPDB:GN00140  
 C:Genetics:  
 A:Gene: AT4g30490  
 A:Map position: 4

Query Match 49.4%; Score 41; DB 2; Length 447;  
 Best Local Similarity 66.7%; Pred. No. 52;  
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 5 RELRRMSDEFVD 16  
 ||||:|: ||  
 Db 84 RELRLYDELVD 95

RESULT 7  
 T40297  
 membrane transporter - fission yeast (Schizosaccharomyces pombe)  
 C:Species: Schizosaccharomyces pombe  
 C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 18-Feb-2000  
 C:Accession: T40297  
 R:Lyne, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Moestl, D.; Duest  
 submitted to the EMBL Data Library, May 1998  
 A:Reference number: Z21919  
 A:Accession: T40297  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-577 <LYN>  
 A:Cross-references: EMBL:AL023589; PIDN:CAA19050.1; GSPDB:GN00067; SPDB:SPBC36.02c  
 A:Experimental source: strain 972h-; cosmid c36  
 C:Genetics:  
 A:Gene: SPDB:SPBC36.02c  
 A:Map position: 2  
 C:Superfamily: benomyl/methotrexate resistance protein

Query Match 49.4%; Score 41; DB 2; Length 577;  
 Best Local Similarity 57.1%; Pred. No. 67;  
 Matches 8; Conservative 3; Mismatches 0; Indels 3; Gaps 0;

QY 3 YGRELRRMSDEFVD 16  
 :||:|||||  
 Db 563 FGKIRRMKMAVD 576

RESULT 8  
 A44919  
 GCR3 protein - yeast (Saccharomyces cerevisiae)  
 N;Alternate names: protein YM8564.07; protein YM9553.01; protein YMR125W  
 C;Species: Saccharomyces cerevisiae  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 29-Oct-1999  
 C;Accession: A44919; S53055; S54494  
 R;Uemura, H.; Jigami, Y.  
 J. Bacteriol. 174, 5526-5532, 1992  
 A;Title: GCR3 encodes an acidic protein that is required for expression of glycolytic ge  
 A;Reference number: A44919; MUID:92380925; PMID:1512188  
 A;Accession: A44919  
 A;Molecule type: DNA  
 A;Residues: 1-958 <DEM>  
 A;Cross-references: GB:D10224; NID:g464221; PIDN:BAA01076.1; PID:d1001545; PID:g464222  
 A;Note: sequence extracted from NCBI backbone (NCBIN:112104, NCBI:P:112106)  
 R;Badcock, K.; Churcher, C.  
 submitted to the EMBL Data Library, March 1995  
 A;Reference number: S53055  
 A;Accession: S53055  
 A;Molecule type: DNA  
 A;Residues: 339-858 <BAD>  
 A;Cross-references: EMBL:Z48622; NID:g728663; PIDN:CAA88550.1; PID:g728664; MIPS:YMR125W  
 R;Lye, G.; Churcher, C.M.  
 submitted to the EMBL Data Library, May 1995  
 A;Reference number: S54014  
 A;Accession: S54494  
 A;Molecule type: DNA  
 A;Residues: 'MFNRKRRG', 6-489 <LYE>  
 A;Cross-references: EMBL:Z49273; NID:g809577; PIDN:CAA89274.1; PID:g809584; MIPS:YMR125W  
 C;Genetics:  
 A;Gene: SGD:STO1; GCR3  
 A;Cross-references: MIPS:YMR125W; SGD:S0004732  
 A;Map position: 13R  
 C;Keywords: DNA binding; nucleus

Query Match 49.4%; Score 41; DB 2; Length 858;  
 Best Local Similarity 40.0%; Pred. No. 1e+02;  
 Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDEFV 15  
 :|| | | :||:  
 Db 818 RRYSHVEYRELADKFI 832

RESULT 9  
 F84388  
 hypothetical protein Vng2379h [imported] - Halobacterium sp. NRC-1  
 C;Species: Halobacterium sp. NRC-1  
 C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
 C;Accession: F84388  
 R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S  
 ; Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl  
 Jung, K.H.; Alam, M.; Freitas, T.  
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
 A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li  
 A;Title: Genome sequence of Halobacterium species NRC-1.  
 A;Reference number: A84160; MUID:20504483; PMID:11016950  
 A;Accession: F84388  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-84 <STO>  
 A;Cross-references: GB:AE004437; NID:g10581786; PIDN:AG20474.1; GSPDB:GN00138  
 C;Genetics:

A;Gene: VNG2379H

Query Match 48.2%; Score 40; DB 2; Length 84;  
 Best Local Similarity 66.7%; Pred. No. 14;  
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 RYGRELRRMSDE 13  
 ||| | |||  
 Db 66 RYGTASRRMDE 77

RESULT 10

B95043  
 conserved hypothetical protein SP0372 [imported] - Streptococcus pneumoniae (strain :  
 C;Species: Streptococcus pneumoniae  
 C;Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 03-Aug-2001  
 C;Accession: B95043  
 R;Fetzelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; I  
 on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapp  
 nson, T.; Hickey, E.K.; Holt, I.E.  
 Science 293, 498-506, 2001  
 A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris  
 A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
 A;Reference number: A95000; MUID:21357209; PMID:11463916  
 A;Accession: B95043  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-109 <KUR>  
 A;Cross-references: GB:AE005672; PIDN:AAK74539.1; PID:g14971841; GSPDB:GN00164; TIGR  
 A;Experimental source: strain TIGR4  
 C;Genetics:  
 A;Gene: SP0372

Query Match 48.2%; Score 40; DB 2; Length 109;  
 Best Local Similarity 45.0%; Pred. No. 18;  
 Matches 9; Conservative 4; Mismatches 3; Indels 4; Gaps 1;

QY 1 QRYGRELRRMS----DEFVD 16  
 | :|||:| : |||:  
 Db 14 QEFGREVGYNKVEVDFLD 33

RESULT 11

D97913  
 conserved hypothetical protein spr0332 [imported] - Streptococcus pneumoniae (strain  
 C;Species: Streptococcus pneumoniae  
 C;Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 22-Oct-2001  
 C;Accession: D97913  
 R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Bargett, S.; DeHoff, B.S  
 e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S  
 y, P.; Sun, P.M.; Winkler, M.E.  
 J. Bacteriol. 193, 5709-5717, 2001  
 A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S  
 A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
 A;Reference number: A97872; MUID:21429245; PMID:11544234  
 A;Accession: D97913  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-113 <KUR>  
 A;Cross-references: GB:AE007317; PIDN:AAK99136.1; PID:g15457889; GSPDB:GN00174  
 C;Genetics:  
 A;Gene: spr0332

Query Match 48.2%; Score 40; DB 2; Length 113;  
 Best Local Similarity 45.0%; Pred. No. 19;  
 Matches 9; Conservative 4; Mismatches 3; Indels 4; Gaps 1;

QY 1 QRYGRELRRMS----DEFVD 16  
 | :|||:| : |||:  
 Db 18 QEFGREVGYNKVEVDFLD 37

RESULT 12

A75088

hypothetical protein PAB1640 - Pyrococcus abyssi (strain Orsay)  
 C:Species: Pyrococcus abyssi  
 C:Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Aug-1999  
 C:Accession: A75088  
 R:anonymous, Genoscope  
 submitted to the EMBL Data Library, July 1999  
 A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure  
 A:Reference number: A75001  
 A:Accession: A75088  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-219 <RAW>  
 A:Cross-references: GB:AJ248286; GB:AL096836; NID:95458366; PIDN:CAB50006.1; PID:el51590  
 A:Experimental source: strain Orsay  
 C:Genetics:  
 A:Gene: PAB1640

Query Match 48.2%; Score 40; DB 2; Length 219;  
 Best Local Similarity 47.1%; Pred. No. 37;  
 Matches 8; Conservative 4; Mismatches 3; Indels 2; Gaps 1;

QY 2 YGRELRRMS--DEVD 16  
 ||| | :| :| :| :|  
 Db 104 YGNEFORVSPQENFID 120

RESULT 13

E91102  
 probable enzyme [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)  
 C:Species: Escherichia coli  
 C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 03-Aug-2001  
 C:Accession: E91102  
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;  
 gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
 DNA Res. 8, 11-22, 2001  
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic  
 A:Reference number: A99629; MUID:21156231; PMID:11258796  
 A:Accession: E91102  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-275 <HAY>  
 A:Cross-references: PIDN:BA000007; PIDN:BA037212.1; PID:gl3363261; GSPDB:GN00154  
 A:Experimental source: strain O157:H7, substrain RIMD 0509952  
 C:Genetics:  
 A:Gene: ECs3789  
 C:Superfamily: naphthoate synthase; enoyl-CoA hydratase homology

Query Match 48.2%; Score 40; DB 2; Length 275;  
 Best Local Similarity 50.0%; Pred. No. 46;  
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 YGRELRRMSDEVD 16  
 ||| | :| :| :| :|  
 Db 35 YGRKLNALSKVFID 48

RESULT 14

A85948  
 probable enzyme ygfG [imported] - Escherichia coli (strain O157:H7, substrain EDL933)  
 C:Species: Escherichia coli  
 C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
 C:Accession: A85948  
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
 Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dinalanta, E.; Potamoudis, K.; Apodaca,  
 Nature 409, 529-533, 2001  
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
 A:Reference number: A85480; MUID:21074935; PMID:11206551  
 A:Accession: A85948  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-275 <STO>  
 A:Cross-references: GB:AE005174; NID:gl2517451; PIDN:AAG58045.1; GSPDB:GN00145; UWGP:242

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: ygfG

C:Superfamily: naphthoate synthase; enoyl-CoA hydratase homology

Query Match 48.2%; Score 40; DB 2; Length 275;  
 Best Local Similarity 50.0%; Pred. No. 46;  
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 YGRELRRMSDEVD 16  
 ||| | :| :| :| :|  
 Db 35 YGRKLNALSKVFID 48

RESULT 15

F65076  
 hypothetical protein b2919 - Escherichia coli (strain K-12)  
 C:Species: Escherichia coli  
 C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 01-Mar-2002  
 C:Accession: F65076  
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;  
 A.; Rose, D.J.; Mau, B.; Shao, Y.  
 Science 277, 1453-1462, 1997  
 A:Title: The complete genome sequence of Escherichia coli K-12.  
 A:Reference number: A64720; MUID:97426617; PMID:9278503  
 A:Accession: F65076  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-275 <BLAT>  
 A:Cross-references: GB:AE000375; GB:U00096; NID:gl789282; PIDN:AAC75956.1; PID:gl789;  
 A:Experimental source: strain K-12, substrain MG1655  
 C:Superfamily: naphthoate synthase; enoyl-CoA hydratase homology  
 F:40-192/Domain: enoyl-CoA hydratase homology <ECH>

Query Match 48.2%; Score 40; DB 2; Length 275;  
 Best Local Similarity 50.0%; Pred. No. 46;  
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 YGRELRRMSDEVD 16  
 ||| | :| :| :| :|  
 Db 35 YGRKLNALSKVFID 48

Search completed: September 15, 2003, 17:27:03

Job time : 9.2 secs